Article

Distinct in vivo roles of secreted APP ectodomain variants APPs α and APPs β in regulation of spine density, synaptic plasticity, and cognition

Max C Richter^{1,†}, Susann Ludewig^{2,†}, Alex Winschel³, Tobias Abel⁴, Charlotte Bold¹ , Leonie R Salzburger², Susanne Klein¹, Kang Han¹, Sascha W Weyer¹, Ann-Kristina Fritz^{5,6}, Bodo Laube³ .
, David P Wolfer^{5,6}, Christian J Buchholz⁴^D, Martin Korte^{2,[7](http://orcid.org/0000-0001-6956-5913)}D & Ulrike C Müller^{1,[*](http://orcid.org/0000-0002-0587-2575)}

Abstract

Increasing evidence suggests that synaptic functions of the amyloid precursor protein (APP), which is key to Alzheimer pathogenesis, may be carried out by its secreted ectodomain (APPs). The specific roles of APPsa and APPsß fragments, generated by nonamyloidogenic or amyloidogenic APP processing, respectively, remain however unclear. Here, we expressed APPs α or APPs β in the adult brain of conditional double knockout mice (cDKO) lacking APP and the related APLP2. APPsa efficiently rescued deficits in spine density, synaptic plasticity (LTP and PPF), and spatial reference memory of cDKO mice. In contrast, APPsß failed to show any detectable effects on synaptic plasticity and spine density. The Cterminal 16 amino acids of APPsa (lacking in APPsß) proved sufficient to facilitate LTP in a mechanism that depends on functional nicotinic a7-nAChRs. Further, APPsa showed high-affinity, allosteric potentiation of heterologously expressed a7-nAChRs in oocytes. Collectively, we identified a7-nAChRs as a crucial physiological receptor specific for APPsa and show distinct in vivo roles for APPsa versus APPsb. This implies that reduced levels of APPsa that might occur during Alzheimer pathogenesis cannot be compensated by APPs β .

Keywords Alzheimer; amyloid precursor protein; nicotinic acetylcholine receptor; soluble APPsa; synaptic plasticity

Subject Categories Neuroscience

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Introduction

Alzheimer's disease (AD) is characterized by the accumulation of β -amyloid peptides $(A\beta)$ that are derived from the amyloid precursor protein (APP) by proteolytic cleavage (Selkoe & Hardy, 2016). Two principal physiological pathways either prevent or promote $A\beta$ generation. Within the amyloidogenic pathway, APP processing is shifted towards the production of $\text{A}\beta$ and secreted APPs β , by consecutive β -secretase (BACE1) and γ -secretase cleavage (Vassar et al, 2014). In AD, BACE1 is upregulated, favoring amyloidogenic APP processing (Holsinger et al, 2002; Ahmed et al, 2010). In the alternative, non-amyloidogenic pathway cleavage of APP within the Ab region by the major a-secretase ADAM10 (a disintegrin and metalloprotease) prevents $\mathbf{A}\beta$ generation and liberates \mathbf{APP} s α that is secreted into the extracellular space (Saftig & Lichtenthaler, 2015). Shifting APP processing towards non-amyloidogenic processing has therefore been suggested as a therapeutic strategy for AD (Mockett et al, 2017). An important and still unresolved question is whether in addition to neurotoxic $A\beta$ accumulation a concomitant reduction in APPs α level, or an altered APPs α /APPs β ratio may contribute to AD symptoms and pathogenesis (reviewed by Mockett et al, 2017). In this regard, it will be crucial to know whether $APPs\alpha$ and $APPs\beta$, that is only 16 amino acids shorter than APPsa, serve largely similar or distinct, possibly even opposite physiological functions. While our previous studies and work from others indicated that APPsa has neurotrophic and neuroprotective effects, including synaptogenic, LTP facilitating and memory enhancing properties (Meziane et al, 1998; Ring et al, 2007; Taylor et al, 2008; Milosch et al, 2014; Weyer et al, 2014; Hick et al, 2015; Hefter et al, 2016; Plummer et al, 2016), only few and mostly conflicting studies have as yet addressed the functions of APPs β (Nikolaev et al, 2009; Li et al, 2010; Weyer et al, 2011; Chasseigneaux & Allinquant, 2012). So far,

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1 Institute of Pharmacy and Molecular Biotechnology (IPMB), Ruprecht-Karls University Heidelberg, Heidelberg, Germany

5 Institute of Anatomy, University of Zurich, Zurich, Switzerland

² Zoological Institute, Division of Cellular Neurobiology, TU Braunschweig, Braunschweig, Germany

³ Department of Biology, Neurophysiology und Neurosensory Systems, TU Darmstadt, Darmstadt, Germany

⁴ Paul-Ehrlich-Institut (PEI), Langen, Germany

⁶ Institute of Human Movements Sciences and Sport, ETH Zurich, Zurich, Switzerland

Helmholtz Centre for Infection Research, AG NIND, Braunschweig, Germany *Corresponding author. Tel: +49 6221 546717; E-mail: u.mueller@urz.uni-heidelberg.de † [†]These authors contributed equally to this work

the molecular basis of any difference compared to $APPs\alpha$ remained unclear. Thus, a more detailed knowledge about the specific functions of the secreted APP ectodomains is essential to understand AD pathogenesis and evaluate risks of ongoing pharmacotherapy, as well as to elucidate APP physiology.

There is a large body of evidence indicating that APP family proteins are multimodal proteins that can function as ligands via their secreted fragments or as cell surface proteins important for synaptic adhesion and signal transduction (Müller et al, 2017). Major insights into the physiological functions of APP and the related APLPs (APP like proteins) were obtained from knockout models (Müller et al, 2017). While most impairments of APP-KO mice emerged only in aged mice (Dawson et al, 1999; Seabrook et al, 1999; Ring et al, 2007; Lee et al, 2010; Tyan et al, 2012), combined APP/APLP2 double knockout mice die shortly after birth, likely due to severe deficits at the neuromuscular junction (von Koch et al, 1997; Heber et al, 2000; Wang et al, 2005; Klevanski et al, 2014). Recently generated forebrain-specific double knockout mice (termed NexCre cDKO), that lack APP from embryonic day 11.5 onwards in excitatory forebrain neurons on a global constitutive APLP2-KO background, showed a severe synaptic phenotype already at young age, including reduced spine density and impaired LTP in the hippocampus, as well as deficits in learning and memory (Hick et al, 2015). Interestingly, the LTP impairment of NexCre cDKO mice could be ameliorated by acute APPsa application onto brain slices in vitro, while the molecular mechanism and receptor(s) mediating its function remained unknown (Hick et al, 2015).

More recently, we showed that AAV-mediated intracranial expression of APPsα can mitigate the Aβ-related synaptic deficits of APP/PS1 mice in vivo (Fol et al, 2016). Intracranial AAV-APPsa injections enhanced spine density, improved LTP deficits and memory, but at the same time also reduced soluble \overrightarrow{AB} levels and plaque load, likely due to enhanced \overrightarrow{AB} clearance (Fol et al, 2016). In addition, APPs α had been reported to lower A β by directly binding to and inhibiting BACE (Obregon et al, 2012). These results raised the question of whether the beneficial in vivo effects of APPsa are mainly due to its $A\beta$ lowering properties.

Here, we asked whether APPs α may also have synaptotrophic effects in an Aß-independent pathology with synaptic impairments and used viral vectors to express APPsa intracranially in NexCre cDKO mice. Moreover, we set out to compare side by side the properties of APPs α and APPs β in vivo. We demonstrate that APPsa is sufficient to fully rescue hippocampal spine density, to restore LTP and partially rescue spatial memory in adult NexCre cDKO mice. In sharp contrast, despite similar expression level, APPs β failed to show any detectable effects on synaptic plasticity and spine density. Finally, we show that the $CT\alpha16$ domain of APPs α (that is lacking in APPs β) is able to facilitate LTP to the same extent as APPsa, in a mechanism that involves functional nicotinic a7 acetylcholine receptors (a7-nAChRs). Moreover, we show that nanomolar concentrations of APPs α (but not APPs β) can directly potentiate a7-nAChRs-mediated currents upon heterologous expression in Xenopus oocytes and increases the apparent agonist affinity as a positive allosteric modulator. Collectively, our analysis identifies the α 7-nAChR as a crucial physiological receptor for APPsa and reveals distinct in vivo roles of APPsa vs. $APPs\beta$.

Results

AAV-APPsa injection mediates efficient and neuron-specific expression of APPs α in the hippocampus of cDKO mice

To investigate whether $APPs\alpha$ is able to rescue the synaptic deficits of NexCre cDKO (further referred to as cDKO) animals in vivo, APPsa was expressed in the adult brain using stereotactic injection. We employed an AAV9-based bicistronic vector (AAV-APPsa; Fig 1A) coding for Venus and codon-optimized HA-tagged murine HA -APPs α that was inserted behind the APP signal peptide (SP). The HA-APPsa reading frame was fused to Venus by a T2A site to enable tracking of transduced cells. Expression was driven by the neuronal synapsin promoter. Monocistronic AAV-Venus vector served as a control (AAV-Venus; Fig 1A). Adult cDKO animals (aged 4–5 months) were either injected with AAV-APPsa or AAV-Venus control vector, whereas littermate control mice (LM control) received only AAV-Venus. Thus, comparison of AAV-Venus-injected cDKO mice with AAV-Venus-injected LM controls was expected to yield similar synaptic impairments as previously observed for uninjected cDKO mice (Hick et al, 2015). Vectors were bilaterally injected (dose: 1.0×10^9 gc/ μ l per injection spot) into the stratum lacunosum-moleculare region of the dorsal hippocampus and into the dentate gyrus (Fig 1B). To evaluate Venus and APPsa expression, animals were sacrificed 6 weeks post-injection and brain samples were analyzed by Western blot and immunohistochemistry using an HA-tag-specific antibody. Analysis of serial anteroposterior coronal brain sections (Bregma -1.10 to Bregma -2.70 ; see Fig EV1C) revealed widespread expression of APPsa in the hippocampus and, to a considerably lower extent, also in adjacent cortical areas (Figs 1C and EV1C). Along the longitudinal (dorsalventral) axis of the hippocampus, APPsa expression was much more pronounced in the dorsal region, whereas expression was not detectable in the ventral hippocampus (Fig EV1C).

As Venus contained a membrane anchor, we observed prominent accumulation in dendritic regions, whereas HA-APPsa staining was intense in intracellular membrane compartments consistent with the transport of APPsa within the secretory pathway to the cell surface for secretion (see also Fig EV2D and E for co-localization with ER and Golgi markers). In the CA3 region, APPsa expression appeared slightly lower compared to the expression obtained in pyramidal cells of the subiculum, the CA1 (Fig 1C) and the CA2 regions. Consistent with previous studies (Jackson et al, 2016), we noted that APPsa was detectable in HEK cells transfected with synapsin promoter driven AAV constructs (see Fig EV2A), likely due to AAV plasmid overload. In vivo, however, AAV-APPsa expression was restricted to neurons, as shown by double immunofluorescence staining against the HA-tag and the neuronal marker NeuN (Fig 1D and E). Consistently, no overlapping expression pattern was detectable in astrocytes (GFAP; Fig 1F) and microglia (Iba1; Fig 1G). The AAV-Venus expression pattern obtained from injections of control vector was largely similar to that of AAV-APPsa (Fig EV1C). Western blot analysis of hippocampal homogenates, using the M3.2 antibody, confirmed efficient AAV-mediated APPsa expression in injected animals (Fig 1H). Note that antibody M3.2 is directed against an epitope located between the α - and β -secretase site and recognizes endogenous APP species (APP full length and APPsa) that are still expressed by interneurons and glia in cDKO mice (see

H

Figure 1. Expression of APPsx in the hippocampus of AAV-APPsx-injected cDKO animals.

- A Schematic representation of monocistronic and bicistronic AAV constructs enabling neuron-specific expression of (i) Venus and (ii) HA-tagged APPsa (+Venus). ITR: inverted terminal repeat, Synapsin: neuron-specific promotor, T2A: Thoseaasigna virus 2A site, SP: signal peptide, HA: influenza hemagglutinin tag.
- B Scheme of the hippocampus with coordinates of the two injection sites (black stars).
- C Overview of the hippocampus of an AAV-APPsa-injected cDKO mouse. HA-tag staining (red) reveals APPsa expression within the CA1, CA3, and DG of the hippocampus. Magnification shows the boxed CA1 region. Scale bars: 500 µm (left), 100 µm (right). DG: Dentate Gyrus, CA: Cornu Ammonis.
- D-G Double immunostaining in CA1 region. APPsa (HA-tag, red) is exclusively expressed in neurons (NeuN, blue, D, E), but not in astrocytes (GFAP, blue, F) or microglia (Iba1, blue, G). Scale bars: 10 μm (D, F, G), 5 μm (E).
- H Western blot analysis of APP expression in hippocampus of LM control (N = 5) and cDKO mice (N = 4) injected with AAV-Venus or AAV-APPs α (N = 5). Age of mice: 5–6 months.

Source data are available online for this figure.

Hick et al, 2015) and vector-derived AAV-APPsa. Collectively, our data demonstrate that AAV-APPsa injection results in efficient and neuron-specific expression of APPsa throughout the dorsal hippocampus.

Impaired synaptic plasticity and reduced spine density of APP/APLP2 cDKO mice are rescued by APPsa expression in the adult brain

Having demonstrated that HA-APPs α is efficiently expressed in the hippocampus of injected animals, we evaluated whether APPsa is sufficient to rescue impairments in functional network activity that were previously reported for cDKO mice (Hick et al, 2015). After 20 min of baseline recording, we induced long-term potentiation (LTP) at the Schaffer collateral to CA1 pathway by application of theta burst stimulation (TBS) in acute hippocampal slices of mice that had been injected with viral vectors 6 weeks earlier (at 4–5 months of age). Consistent with our previous results (Hick et al, 2015), AAV-Venus-injected cDKO mice exhibited significantly lower induction and maintenance of LTP $(n = 25$ slices), as compared to AAV-Venus-injected LM controls $(n = 23;$ Fig 2A). AAV-Venus-injected LM control mice

Figure 2. AAV-APPsa rescues LTP, impaired short-term synaptic plasticity, and spine density of cDKO mice.

- A, B LTP was induced at hippocampal CA3-CA1 synapses after 20 min baseline recordings (arrowhead, TBS). cDKO mice expressing Venus (red) exhibited significant lower induction and maintenance of LTP (128.12 \pm 3.41%) compared to Venus-injected LM controls (white, 156.69 \pm 4.75%, $^{#HH}P$ < 0.001). AAV-mediated expression of APPsa (green) restored potentiation after start of baseline recording and resulted in a LTP curve comparable to that of LM controls. The LTP induction rate is shown as percentage % of mean baseline slope. Data points were averaged over six time points. $n =$ number of slices. N = number of animals.
- C The deficit of PPF in Venus-injected cDKO mice at the 10 ms ($^{\#}P$ < 0.05) and 20 ms ($^{\#}P$ < 0.05) ISI was restored by expression of APPs α . $n =$ number of slices. $N =$ number of animals.
- D Representative images of basal and midapical dendritic segments of CA1 neurons. Scale bar: 5 μ m.
- The spine density deficit of Venus-injected cDKOs mice (11% in basal and 18% in midapical dendrites) is rescued by APPsa to LM control levels. Images are maximum projections of deconvolved z-stacks. Spine density was normalized to LM control levels. $n =$ number of neurons (from five animals per condition).

Data information: Age of mice at analysis: 5–6 months. Data represent mean \pm SEM. Data were analyzed by one-way ANOVA followed by Bonferroni's post hoc test. # indicates significant differences between LM control and cDKO injected with AAV-Venus, * between cDKO injected with AAV-Venus or APPsa. nsp > 0.05, */#P < 0.05, ** $P < 0.01$, *** $^{#H#H}P < 0.001$.

showed a potentiation of $156.69 \pm 4.75\%$ (t75–t80 after start of baseline recording) that was significantly reduced to only $128.12 \pm 3.41\%$ in AAV-Venus-injected cDKO mice (one-way ANOVA followed by Bonferroni's post hoc test, $^{***}P < 0.001$; Fig 2B). In contrast, the LTP curve recorded from acute slices of AAV-APPs α -injected cDKO mice ($n = 24$) closely overlapped with that of AAV-Venus-injected LM controls (Fig 2A). Quantification of the last 5 min of recording revealed that APPsa rescued LTP deficits of cDKO mice to a level statistically indistinguishable from that of Venus-injected LM controls (t75–80: 150.34 \pm 3.55%, ^{ns}P > 0.05; Fig 2B). While basal synaptic transmission was comparable in all groups (see Fig EV3A and B), presynaptic function evaluated by paired pulse facilitation (PPF; Fig 2C) was significantly impaired in AAV-Venus-injected cDKO mice at the 10 ms ($^{#}P < 0.05$) and 20 ms ($^{#}P < 0.05$) interstimulus intervals (ISI) in comparison with AAV-Venus-injected LM controls. Strikingly, AAV-APPs α treatment leads to a highly significant rescue of short-term synaptic plasticity in cDKO mice as evidenced by PPF values statistically indistinguishable from LM controls (Fig 2C).

Next, we evaluated spine density as a correlate of excitatory synapses. To visualize neuronal morphology and spine density, we performed iontophoretic postfixation filling with a fluorescent dye of hippocampal CA1 pyramidal cells in brain slices from injected adult mice (aged 5–6 months). Consistent with our previous study (Hick et al, 2015), we confirmed a prominent reduction in spine density both in basal $(100.00 \pm 3.41 \text{ vs. } 88.77 \pm 3.10 \text{ s})$ spines/ μ m, $^{*}P < 0.05$) and in midapical dendrites (100.00 \pm 3.57 vs. 82.08 \pm 4.73 spines/ μ m, $^{#}P$ < 0.05) of AAV-Venus-injected cDKO CA1 neurons as compared to AAV-Venus-injected LM controls (Fig 2D–F). In contrast, spine density of AAV-APPsainjected cDKO mice did not significantly differ from that of AAV-Venus-injected LM control neurons, indicating that APPsa expression fully restored spine density in CA1 neurons. Collectively, these data demonstrate that acute expression of APPsa in adult mice is sufficient to rescue morphological and functional synaptic deficits in cDKO animals.

APPsa ameliorates dendritic branching abnormalities of cDKO animals

Prompted by the effect of APPs α on spine density, we further evaluated its influence on the overall morphology and complexity of hippocampal CA1 neurons (Fig 3). In view of their different morphology and connectivity, basal and apical dendrites of CA1 neurons were studied separately. Neurons of AAV-Venus-injected cDKO mice showed a significantly reduced total dendritic length and branching (as assessed by the number of nodes) in both basal and apical dendrites compared to AAV-Venus-injected LM controls (Fig 3A–F). Impairments were readily apparent when visually inspecting reconstructed images of individual neurons (Fig 3A).

Although total dendritic length was not significantly increased by APPsa expression in cDKO animals, the total number of nodes was significantly increased in basal dendrites of neurons from AAV-APPsa-injected cDKO mice (Fig 3D) compared to Venus-injected cDKO animals (one-way ANOVA followed by Bonferroni's post hoc test, $*P < 0.05$). To investigate whether changes in dendritic complexity may be more pronounced in distinct dendritic subregions, we performed morphometric Sholl analysis. We plotted the dendritic length measured within circles centered on the soma against the distance from the cell body (see scheme in Fig 3B). In this analysis, an increase in dendritic length per sphere corresponds to an increased dendritic complexity. Comparison of dendritic complexity between pyramidal neurons from AAV-Venus-injected cDKO and LM control mice revealed an overall reduced dendritic complexity in cDKO neurons, both in basal (Fig 3G) and apical dendrites (Fig 3H). Branching deficits of basal dendrites from Venus-injected cDKO neurons were most pronounced in proximal dendritic segments (30–90 µm from the soma). In apical dendrites, both proximal regions (60–180 μ m) and midapical regions (300 μ m, 330 µm) were less complex. Interestingly, neurons of AAV-APPsainjected cDKO mice exhibited an intermediate curve with partially restored dendritic complexity. Sholl analysis revealed significantly increased dendritic complexity in proximal regions $(60 \mu m)$ of basal

- Figure 3. APPsα ameliorates dendritic branching abnormalities of cDKO animals.
A Representative 3D-reconstructions of CA1 pyramidal neurons from AAV-Venus-injected LM controls (left), AAV-Venus-injected cDKOs (middle, red injected cDKOs (right, green).
- B Schematic representation of parameters assessed.
- C–F Compared to LM controls, AAV-Venus-injected cDKO mice show a significantly reduced basal $(^{#H}P < 0.01$, C) and apical $(^{#H}P < 0.01$, E) dendritic length and reduced branching in basal ($^{tt\#P}$ < 0.01, D) and apical ($^{tt\#P}$ < 0.01, F) dendrites. AAV-APPs α injection did neither affect basal (^{ns}P > 0.05, C) nor apical (n° P > 0.05, E) total dendritic length. However, the total number of basal nodes differed significantly compared to AAV-Venus-injected cDKO mice (*P < 0.05, D).
- G Sholl analysis of basal dendritic length reveals a significant group effect (repeated measures ANOVA: genotype $F(2, 29) = 5.038$, $P < 0.05$) and a significant distance effect (repeated measures ANOVA: genotype F(5, 145) = 250.2, P < 0.0001). Due to a significant interaction effect (repeated measures ANOVA: genotype $F(10, 145) = 4.466$, $P < 0.0001$), a post hoc Sidak's multiple comparison test was performed to further evaluate effects between groups at distinct distances from soma. Compared to Venus-injected, AAV-APPs α injection of cDKO significantly increased basal dendritic length at 60 μ m (*P < 0.05).
- H Sholl analysis of apical dendritic length reveals an overall significant group effect (repeated measures ANOVA: genotype F(2, 37) = 4.776, P < 0.05) and a significant distance effect (repeated measures ANOVA: genotype F(18, 666) = 47.54, P < 0.0001). Due to a significant interaction effect (repeated measures ANOVA: genotype F(36, 666) = 1.640, P < 0.05), a post hoc Sidak's multiple comparison test was performed to further evaluate effects between groups at distinct distances from soma. AAV-APPsa expression increased midapical dendritic length at 300 μ m (**P < 0.01) and 330 μ m (**P < 0.01) distance from soma compared to AAV-Venus-injected cDKO mice.

Data information: Age of mice: 5–6 months. $n =$ number of neurons (from 4 to 5 animals per condition). Data represent mean \pm SEM. Data were analyzed by one-way ANOVA followed by Bonferroni's post hoc test (C–F) or repeated measures ANOVA followed by Bonferroni's or Sidak's post hoc test (G–H). # indicates significant differences between LM control and cDKO injected with AVV-Venus, * between cDKO injected with AAV-Venus or APPsa, ● between LM control injected with Venus and cDKO injected with AAV-APPsa. nsp > 0.05, $\frac{1}{2}$ + $\frac{1}{2}$ = 0.05, ** $\frac{1}{2}$ + $\frac{1}{2}$ = 0.001, $\frac{1}{2}$ = 0.0001, $\frac{1}{2}$ = 0.0001.

dendrites of AAV-APPsa-injected cDKO neurons (repeated measures ANOVA followed by Sidak's *post hoc* test, $*P < 0.05$; Fig 3G). Likewise, in apical dendrites of cDKO mice injected with AAV-APPsa, dendritic length was significantly increased at a distance of 300 µm (** $P < 0.01$) and 330 µm (** $P < 0.01$) as compared to neurons of AAV-Venus-injected cDKO neurons. Together, these data indicate that APPsa ameliorates branching deficits of cDKO mice at distinct dendritic regions.

APPsa improves spatial learning and spatial memory in cDKO mice

To evaluate whether improved synaptic density and plasticity is also reflected at the behavioral level, we assessed spatial learning and memory in the Morris water maze (MWM) place navigation task (Fig 4). To this end, cDKO mice were either injected with AAV-Venus ($n = 18$, red circles) or with AAV-APPs α ($n = 18$, green circles) at 4–5 months of age and tested 2 months later at 6– 7 months of age. For comparison, LM controls were injected with AAV-Venus ($n = 22$, white circles). While swim speed was comparable in all groups (Fig 4A), we observed an overall impaired performance in AAV-Venus-injected cDKO mice both during acquisition and reversal training. Although all three groups of mice did show learning, escape latencies (Fig 4B) and swim path lengths (Fig 4C) were significantly increased in Venus-injected cDKO mice compared to Venus-injected LM controls, especially at days 2 and 3 of acquisition, learning and for the last trials of reversal learning. These data are highly consistent with and confirm the deficit in spatial learning observed previously in uninjected cDKO mice (Hick et al, 2015). Overall, APPsa expression in cDKO mice leads to an intermediate performance with significantly improved learning during the reversal phase. AAV-APPsa expression in cDKO mice significantly decreased escape latency ($*P < 0.01$; Fig 4B) and swim path length $(*P < 0.05;$ Fig 4C) at day 5 of reversal learning, as compared to AAV-Venus-injected cDKO mice. During the probe trial that assesses spatial reference memory, analysis of time [%] spend in the target zone (Fig 4D) reveals a significant overall group \times place effect $(F(2, 46) = 9.095, P = 0.0005)$. AAV-Venus-injected cDKO mice were strongly impaired in comparison with AAV-Venus-injected controls $($ ^{***} P < 0.001) and failed to prefer the trained target zone. Time spend in the target zone was not significantly different from chance level. Strikingly, AAV-APPsa expression substantially improved probe trial performance in cDKO mice compared to Venus-injected cDKO mice (**P < 0.01). Moreover, AAV-APPsa-injected cDKOs showed a highly significant preference for the trained target zone over adjacent quadrants (** $P < 0.01$). Together, these data indicate that expression of $APPs\alpha$ in the adult hippocampus substantially improved spatial reference memory.

APPs β does not rescue LTP or spine density in vivo

During AD, BACE expression is upregulated (Holsinger et al, 2002; Ahmed et al, 2010) leading to increased amyloidogenic APP processing and thus increased APPs β levels. Although APPs β has been reported to be less potent in assays of neuroprotection in vitro (Furukawa et al, 1996; Barger & Harmon, 1997; Copanaki et al, 2010), the molecular basis of this property has remained elusive and its in vivo role is currently unknown. We therefore evaluated in a separate set of experiments whether APPs β , being only 16 amino acids shorter compared to APPsa (see Fig 5B), might also be able to rescue the impairments of cDKO mice. Briefly, we stereotactically injected cDKO mice and LM controls (4–5 months of age) with AAV-Venus or a bicistronic vector coding for Venus and HA-tagged murine APPs β (AAV-APPs β ; Fig 5A). Immunohistochemistry of serial brain sections indicated that injection of AAV-APPs β yielded a comparable expression level and distribution to that obtained for HA-APPsa (Figs 5C and EV1C). Western blot analysis of total hippocampal homogenates (containing cell bound and secreted proteins) using an HA-tag-specific antibody further confirmed similar (and statistically not significantly different) levels of HA-APPsß and HA-APPsa expression upon injection of the respective AAVs (unpaired two-tailed Student's t-test, ${}^{ns}P > 0.05$; Fig 5D and E). Ultracentrifugation (UC) of the same hippocampal homogenates was used to specifically detect soluble HA-APPs α and HA-APPs β (Fig 5D, lower boxed panels) and yielded comparable levels of APPs α and APPs β in UC supernatants (unpaired two-tailed Student's t-test, $nsp > 0.05$; Fig 5D and E). Transfection of HEK cells (Fig EV2A) with the APPsα or APPsβ encoding AAV plasmids or transduction of cultured neurons with either of the AAV vectors (Fig EV2B) further confirmed efficient and comparable secretion of APPsa or $APPs\beta$, as evidenced by Western blot analysis of cell supernatants (Fig EV2A and B).

Strikingly, despite comparable levels of expression and secretion, soluble $APPs\beta$ failed to exert any detectable effects on basal synaptic transmission (Fig EV3C and D) or synaptic plasticity in recordings of cDKO slices at 5–6 months of age (Fig 5F–H). AAV-APPsbinjected cDKO mice showed superimposable LTP curves compared to Venus-injected cDKO mice. Potentiation at t75–80 min after start of baseline recording was not significantly different (cDKO + AAV-Venus: $125.58 \pm 2.69\%$ vs. cDKO + AAV-APPs β : $124.42 \pm 1.96\%$, $nsp > 0.05$, unpaired two-tailed Student's *t*-test). Moreover, also in the PPF paradigm AAV-APPs β expression did not lead to any detectable difference compared to AAV-Venus control injections (Fig 5H). Likewise, and consistent with electrophysiological analysis, $AAV-APPs\beta$ failed to rescue spine density deficits of cDKO mice determined upon Golgi staining. AAV-Venus-injected cDKO mice revealed again a significant reduction in spine density in basal and in apical dendrites as compared to Venus-injected LM controls (Fig 5I–K). However, spine density was comparable and statistically indistinguishable in AAV-Venus and APPs β -injected cDKO mice. Basal dendrites from AAV-Venus and AAV-APPsß-injected cDKO mice showed a similar and statistically not significantly different reduction in spine density of 14% (LM control + Venus: 100 ± 2.84 vs. cDKO + Venus: 85.99 ± 3.51 spines/ μ m, $*P < 0.05$) and 12% (LM control + Venus: 100 ± 2.84 vs. cDKO + APPs β : 88.39 \pm 3.26 spines/ μ m, **** $P < 0.0001$), respectively (Fig 5J). In midapical dendritic segments, spine density was reduced by 24% in AAV-Venus-injected cDKO animals (LM control + Venus: 100 ± 4.01 vs. $cDKO + Venus: 76.05 \pm 2.097$ spines/ μ m) or by 18% (LM control + Venus: 100 ± 4.01 vs. $cDKO + APPs\beta$: 82.40 ± 3.28 spines/µm) in AAV-APPs β -injected animals, respectively (Fig 5K). Together, these data indicate a striking difference in the in vivo properties of secreted APPs, with APPsa ameliorating morphological and functional synaptic deficits of cDKO mice, while $APPs\beta$ had no effect.

Figure 4. APPs α improves place navigation and spatial memory of cDKO mice in the MWM.

- A Swim speed during acquisition and reversal learning is comparable in all groups (each point represents 1 day with six trials).
- B During acquisition learning and after platform reversal to the opposite quadrant, AAV-Venus-injected cDKOs (red circles) show considerably longer escape latency compared to AAV-Venus-injected LM controls (white circles). AAV-APPsa-injected cDKO mice (green circles) show an overall intermediate performance (genotype F(2, 46) = 6.361, P = 0.0036) and that differs significantly at day 5 of reversal learning compared to AAV-Venus-injected cDKO mice (genotype × day F(8, 184) = 5.266, P < 0.0001; ** P < 0.01).
- C Measurements of swim path length confirm the training performance deficit of cDKO mice compared to LM controls. During the reversal phase, the performance of AAV-<code>APPs α -injected cDKOs is</code> significantly improved at day 5 (genotype F(2, 46) = 16.70, $P < 0.0001$, genotype \times day F(8, 184) = 5.788, $P < 0.0001;$ * $P < 0.05,$ $^{\bullet}P < 0.01$).
- D In the probe trial, AAV-Venus-injected cDKOs (red) spend significantly less time in the target zone compared to AAV-Venus- ($^{\text{ttt#} \mu}$ < 0.001) injected LM control animals (white) and failed to prefer it significantly over control zones in adjacent quadrants. Note that expression of APPsa (green) largely rescues the deficits of cDKOs. N = 22 (LM controls: AAV-Venus), N = 18 (cDKOs: AAV-Venus), N = 18 (cDKOs: AAV-APPsa).

Data information: Data represent mean ± SEM. Dashed lines: chance level. Data were analyzed using a mixed ANOVA model with conditions (LM control: AAV-Venus, cDKO: AAV-Venus and cDKO: AAV-APPsa) as between subject factor. Within subject, factors were added to explore the dependence of genotype effects on day and place. Significant interactions and main effects were further explored by pairwise FDR-corrected two-tailed Student's t-tests. # indicates significant differences between LM control and cDKO injected with AVV-Venus, * between cDKO injected with AAV-Venus or APPsa, ● between LM control injected with Venus and cDKO injected with AAV- $\mathsf{APPs}\alpha \stackrel{\mathsf{ns}}{\mathsf{p}}>0.05, \star^{\mathsf{/p}}\mathsf{P}<0.05, \star^{\mathsf{pk}\# \# \mathsf{p}\blacktriangleright\blacktriangleright\mathsf{P}}\mathsf{P}<0.01, \stackrel{\mathsf{H}\# \# \mathsf{p}\blacktriangleright\blacktriangleright\mathsf{P}}\mathsf{P}<0.001.$

APPs α facilitates LTP via its C-terminal CT α 16 domain

Prompted by these results, we now focused on the 16 amino acids domain (CT α 16) that distinguishes APPs α from APPs β (Fig 5B and L–Q). Previously, we had demonstrated that a short incubation of slices with recombinant APPs α (recAPPs α) is sufficient to largely rescue the LTP deficits of cDKO mice (Hick et al, 2015). To determine whether this acute function of APPsa is mediated by the

CTa16 domain, we now pre-incubated cDKO slices for 60 min at room temperature either with a synthetic $CT\alpha$ 16 peptide (10 nM), or with $CT\alpha16_{scr}$ (10 nM), a scrambled peptide of the same amino acid composition. After 20 min of baseline recording, LTP was again induced by TBS. During the whole measurement, the peptides diluted in ACSF were circulating in a closed-loop system. Strikingly, we found that the application of $CT\alpha16$ potently facilitated LTP over the whole recording period (Fig 5L and M) including the early phase of post-tetanic potentiation (t20–25, CT α 16: 191.49 \pm 8.82% vs. CT α 16_{scr}: 165.12 \pm 8.82%, $*P < 0.01$; Fig 5L and M) and led to a highly significant increase in LTP values 60 min after TBS (t75–80, CT α 16: 148.08 \pm 3.65% vs. CT α 16_{scr}: 132.18 \pm 4.26%, $*P < 0.01$; Fig 5L and M). In contrast, LTP values obtained for $CT\alpha16_{\text{scr}}$ were very similar to those after AAV-Venus-injection into cDKO mice (t75–80, 128.12 \pm 3.41%; Fig 2B). CT α 16 peptide application also significantly improved and restored PPF of cDKO slices (Fig 5N) to values comparable to that obtained for AAV-Venusinjected LM control mice (see Fig 2C). Next, we directly compared the activity of $CT\alpha16$ and recAPPs α (Fig 50–Q) that was purified from stably transfected HEK cell supernatants. We found that CT α 16 application (10 nM) was as potent as recAPPs α (10 nM) in rescuing both the LTP (t75–80, APPs α : 146.15 \pm 4.21% vs. CT α 16: 148.08 \pm 3.65%, ^{ns}P > 0.05) and PPF deficit of cDKO slices. Values obtained were statistically indistinguishable (Fig 5O and P). Together, these data identify the $CT\alpha16$ domain of APPs α as

sufficient to mediate the functions of APPsa for enhancing synaptic plasticity in vitro.

Inhibition of a7-nAChR by BTX blocks APPsa-mediated effects on LTP

While elevated (micromolar) $\mathbf{A}\mathbf{\beta}$ concentrations and aggregated $\mathbf{A}\mathbf{\beta}$ species exert an inhibitory effect on synaptic function (Kamenetz et al, 2003; Shankar et al, 2007; Gu & Yakel, 2011), picomolar concentrations of soluble Ab have previously been demonstrated to enhance LTP and PTP in a mechanism dependent on the activity of a7 nicotinic acetylcholine receptors (a7-nAChRs; Puzzo et al, 2011, 2008). As the CT α 16 domain of APPs α overlaps with the N-terminus of \overrightarrow{AB} , we therefore tested whether signaling by α 7-nAChR may mediate the LTP facilitating functions of APPsa. First, we hypothesized that if a7-nAChRs are crucially involved in the LTP facilitating effect of APPsa, pharmacological block of a7-nAChR should impair LTP in LM control mice that still express APP and APPs α . Indeed, treatment of slices with 10 nM α -bungarotoxin (α -BTX), a specific inhibitor of a7-nAChRs, significantly reduced LTP during the induction phase (t20–25, LM control: $184.01 \pm 5.59\%$ vs. LM control + BTX: 158.04 \pm 8.35%, $*P < 0.05$) and the maintenance phase (t75–80, LM control: $147.25 \pm 3.87\%$ vs. LM control + BTX: 131.24 \pm 4.99%, *P < 0.05; Fig 6A and B). Values obtained after BTX treatment were very similar to those of $CT\alpha 16_{\text{scr}}$ -treated cDKO

- Figure 5. AAV-APPsß fails to rescue LTP or spine density in vivo, while CT α 16 facilitates LTP in vitro.
A Schematic representation of AAV9 constructs enabling the neuron-specific expression of (i) Venus and (ii) HA-tag Synapsin: neuron-specific promotor, T2A: Thoseaasigna virus 2A site, SP: signal peptide, HA: influenza hemagglutinin tag.
- B APPs *a* differs from APPsB in the last 16 C-terminal amino acids (CT_a16, green). The epitope recognized by the M3.2 antibody is indicated.
- C Overview of the hippocampus of a AAV-APPsß- (HA-tag, red) injected cDKO mouse. APPsß is expressed in CA1, CA3, and DG. Scale bar: 500 µm. DG: dentate gyrus, CA: Cornu Ammonis.
- D Western blot analysis of HA-APPs α and HA-APPsß in hippocampi of injected mice (boxed upper panel) probed with an HA-tag-specific antibody (lower band, arrowhead; *unspecific signal). Homogenates of AAV-injected hippocampi were subjected to ultracentrifugation to detect soluble APPs α and APPs β (UC supernatant; boxed lower panel). The APP C-terminal antibody Y188 was used to confirm the separation of soluble APPsa from membrane bound full-length APP that is detected in total lysates of AAV-Venus-injected littermate controls. Hippocampi of APP^{-/-} mice served as a negative control for antibody specificity.
- E Quantification of HA-APPs α and HA-APPsß expression in total hippocampal homogenates and of soluble HA-APPs after UC normalized to β -tubulin. Note the comparable expression in AAV-APPsa- and AAV-APPs β -injected mice. Age: 5–6 months. N = Number of animals. Data represent mean \pm SEM. Data were analyzed by unpaired two-tailed Student's t-test. $n s_p > 0.05$.
- F-H Activity-dependent synaptic plasticity was investigated in cDKO after injection of AAV-Venus (red) or APPsß (blue). (F, G) AAV-mediated overexpression of APPsß $(n = 23$ slices, blue symbols) failed to rescue the LTP defect of cDKO mice $(n = 24$ slices, red symbols). (G) TBS-induced strengthening of fEPSPs resulted in similar potentiation levels for the last 5 min of recording (t75–80). The LTP induction rate is shown as percentage % of mean baseline slope. Data points were averaged over six time points. (H) PPF paradigm yielded no significant differences between viral vector-injected cDKO mice. Age: 5–6 months. n = number of recorded slices. $N =$ number of animals. Data represent mean \pm SEM. Data were analyzed by unpaired two-tailed Student's t-test.
- Representative images of Golgi-stained midapical and basal dendritic segments of LM control and cDKO animals injected with AAV-Venus or AAV-APPsß. Images are maximum projections of z-stacks. Scale bar: 5 um.
- J, K The significant spine density deficit of AAV-Venus-injected cDKO mice (red bar) in basal (J) and apical dendrites (K) was comparable and not significantly different $\binom{n}{P}$ > 0.05) from that of AAV-APPs β -injected cDKO mice (blue bar). White bar: AAV-Venus-injected LM controls. Spine density is normalized to LM control levels. Age: 5–6 months; $n =$ number of neurons (from five animals per condition). Data represent mean \pm SEM. Data were analyzed by one-way ANOVA followed by Bonferroni's post hoc test. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.0001$.
- L, M Acute hippocampal slices of cDKO were pre-incubated for 1 h either with 10 nM CTa16 or CTa16_{scr} before inducing LTP by TBS (arrowhead). Averaged potentiation levels at LTP induction (t20-25) revealed a significantly enhancement by CTa16 as compared to CTa16_{scr} present over the whole recording time. Potentiation levels at t75–80 are significantly increased in the presence of CTa16 (**P < 0.01). The LTP induction rate is shown as percentage % of mean baseline slope. Data points were averaged over six time points. *P < 0.05, **P < 0.01. $n =$ number of recorded slices. N = number of animals. Data represent mean \pm SEM. Data were analyzed by unpaired two-tailed Student's t-test.
- N CTa16 significantly enhances short-term synaptic plasticity at inter-stimulus intervals of 40 (**P < 0.01), 80 (*P < 0.05), and 160 (**P < 0.01) ms compared to CTa16_{scr}. n = number of recorded slices. N = number of animals. Data represent mean \pm SEM. Data were analyzed by unpaired two-tailed Student's t-test.
- O-Q Acute application of CTa16 and recAPPsa elevates LTP in cDKO slices to the same extent. (O, P) After 1 h pre-incubation with either 10 nM CTa16 or 10 nM recAPPsa, fEPSPs were recorded. The TBS-induced LTP curve was closely overlapping for both conditions and resulted in similar, statistically not significantly different LTP values. (Q) CT α 16 and recAPPs α modulate presynaptic function of cDKO mice in the same manner. Age: 5–6 months. $n =$ number of recorded slices. $N =$ number of animals. Data represent mean \pm SEM. Data were analyzed by unpaired two-tailed Student's t-test.

Source data are available online for this figure.

slices (compare to Fig 5L and M, $CT\alpha16_{scr}$ -treated cDKO slices: $132.18 \pm 4.26\%$).

Next, we tested how α -BTX affects the induction of LTP by exogenous application of recAPPsa or CTa16 (Figs 6C–G and EV4). When α -BTX was added after the incubation of slices with either recAPPsa or CTa16 30 min before TBS (Fig EV4A, scheme), we observed only a small but not significant reduction in LTP (Fig EV4B–E). In contrast, if α -BTX was co-applied together with recAPPsa for 1 h before TBS (Fig 6C, scheme), this leads to a significant inhibition as compared to recAPPsa treatment alone (Fig 6D and E) both during the LTP induction phase (t20–25, recAPPsa: $168.49 \pm 7.20\%$ vs. recAPPs α + BTX: $142.57 \pm 7.75\%$, $*P < 0.05$; Fig 6D and E) and the LTP maintenance phase (t75–80, recAPPsa: $135.59 \pm 3.81\%$ vs. recAPPs α : +BTX: 118.58 \pm 5.51%, *P < 0.05; Fig 6D and E). Similarly, if α -BTX was co-applied together with the CT α 16 peptide for 1 h before TBS (Fig 6F and G), this lead to a significant inhibition as compared to $CT\alpha16$ treatment alone both during the LTP induction phase (t20–25, CT α 16: 176.23 \pm 4.69%) vs. $CT\alpha16 + BTX: 153.75 \pm 5.05\%$, $*P < 0.05$; Fig 6F and G) and the LTP maintenance phase (t75–80, CT α 16: 144.37 \pm 2.34% vs. $CT\alpha16 + BTX: 129.24 \pm 3.40\%, **P < 0.01;$ Fig 6F and G). Together, these data suggest that APPsa exerts its functions on LTP mainly via the CT α 16 domain in a mechanism depending on α 7nAChR function. Further studies are needed to address whether improvements in spine density and behavior that we observed upon AAV-APPsa re-expression might also depend on a7-nAChR function.

APPsa shows high-affinity allosteric potentiation of a7-nAChR expressed in Xenopus oocytes

To investigate whether $CT\alpha16$ can modulate α 7-nAChRs directly, homomeric a7-nAChRs were expressed in Xenopus laevis oocytes, and nicotine- or acetylcholine-induced currents at submaximal EC_{50} agonist concentration (100 μ M) were measured either alone or after pre-application of CTa16 by two-electrode voltage clamp. Upon application of 100 nM of CTa16 alone, no activation of a7-nAChRs was detectable (data not shown). Remarkably, 100 nM of CTa16 significantly potentiated both nicotine- and acetylcholine-induced currents with a 2.58 ± 0.42 -fold $(n = 8)$ and 3.01 ± 0.96 -fold $(n = 7)$ enhancement of α 7-nAChRs responses, respectively (paired two-tailed Student's t-test, *P < 0.05; Fig 7A and B). In contrast, no

significant effect of 100 nM $CT\alpha16_{scr}$ on nicotine-induced currents could be detected $(1.00 \pm 0.06$ -fold increase, paired two-tailed Student's *t*-test, $n = 5$; $^{ns}P > 0.05$; Fig 7A and B). Dose-response analysis of CTa16 concentrations between 1 and 100 nM yielded an EC_{50} value for CT α 16 of 10.7 \pm 4.6 nM with an hill coefficient of 2.1 \pm 0.3 for α 7-nAChRs (*n* = 4; Fig 7C). To establish whether the physiological APPs α fragment that contains the CT α 16 sequence at the C-terminus can also modulate a7-nAChRs, we tested the effect of 20 nM recAPPsa, a concentration close to the 10 nM that facilitated LTP in slices, on nicotine-gated currents (Fig 7D–F). Indeed, 20 nM recAPPsa significantly potentiated nicotine-induced currents $(3.35 \pm 0.81$ -fold enhancement, paired two-tailed Student's t-test, $n = 4$; *P < 0.05) to a similar extent as seen with 100 nM of CT α 16 (Fig 7D and E, see Fig 7A for comparison). This effect could be specifically blocked by BTX (Fig 7D). Notably, and consistent with experiments in slices, no significant potentiation was seen upon preapplication of 20 nM recAPPs β (1.32 \pm 0.18-fold enhancement, paired two-tailed Student's *t*-test, $n = 5$, ^{ns} $P > 0.05$; Fig 7D and E). As a further control, we investigated whether APPs x may also modulate other pentameric ion channels. However, neither recAPPsa nor CTa16 had any effects on the structurally related homomeric α 1-GlyR (Fig EV5), indicating that APPs α specifically acts on a7-nAChRs. Next, to gain further mechanistic insight, we analyzed nicotine dose-responses of α 7-nAChRs in the presence of a potentiating concentration of recAPPsa to see how APPsa modulates a7-nAChRs (Fig 7F). Strikingly, 20 nM recAPPsa shifted the nicotine dose–response curve to the left and lead to an approximately twofold significant decrease in the EC_{50} of nicotine (40.3 \pm 6.0 µM) as compared to recAPPs α -free conditions (EC₅₀ of 80.5 \pm 12.7 µM, paired two-tailed Student's *t*-test, $n = 5$, $*P < 0.05$) without affecting the hill coefficient $(3.3 \pm 0.5 \text{ vs. } 3.7 \pm 0.9)$, paired two-tailed Student's t-test, ${}^{ns}P > 0.05$) and the maximal inducible nicotine currents (Fig 7F). Together, these data indicate that APPsa acts as a potent (nanomolar range) positive allosteric modulator of a7-nAChRs by increasing the apparent agonist affinity.

Discussion

In this study, we provide compelling evidence for distinct functional roles of the two secreted APP ectodomain fragments APPsa and APPs β in vivo and provide functional insight into the underlying

- Figure 6. LTP facilitation by APPs α or CT α 16 requires functional α 7-nAChRs.
A, B Treatment with 10 nM α -BTX (30 min prior to TBS, black circles) significantly reduces LTP induction (t20–25, phase of post-tetan (t75–80) in LM controls expressing endogenous APP and APPsa. The LTP induction rate is shown as percentage % of mean baseline slope. Data points were averaged over six time points.
- C Experimental setup: co-application of recAPPsa or CTa16 and BTX before LTP induction. Peptides and BTX inhibitor used for pre-incubation circulated throughout the whole LTP recording.
- D, E Co-application of BTX and recAPPsa significantly inhibits synaptic plasticity in cDKO mice. After 1 h pre-incubation of acute slices with 10 nM recAPPsa or 10 nM recAPPsa and 10 nM BTX, fEPSPs were recorded. Hippocampal acute slices treated with 10 nM BTX and recAPPsa revealed significantly impaired induction (t20-25) and maintenance (t75–80) of LTP in comparison with slices of cDKO mice recorded in the presence of recAPPs α alone.
- F, G Co-application of BTX and CTa16, the C-terminal domain of APPsa, significantly inhibits synaptic plasticity in cDKO mice. After 1 h pre-incubation of acute slices with 10 nM CTa16, or 10 nM CTa16 and 10 nM BTX, fEPSPs were recorded. Hippocampal acute slices treated with 10 nM BTX and CTa16 revealed similar to recAPPsa, a significantly impaired induction (t20–25) and maintenance (t75–80) of LTP in comparison with slices of cDKO mice recorded in the presence of CTa16 alone.

Data information: Age: 5–6 months of age. $n =$ number of recorded slices. $N =$ number of animals. Data represent mean \pm SEM. Data were analyzed by unpaired twotailed Student's t-test. $*P < 0.05$, $**P < 0.01$.

Figure 6.

Figure 7. Potentiating effect of CT α 16 and APPs α on recombinant homomeric α 7-nAChRs.

- A Nicotine- and acetylcholine-induced whole-cell current traces of a7-nAChRs expressed in Xenopus oocytes recorded in the absence or presence of CTa16 or CTa16 scr, respectively. Note specific robust potentiation of nicotine- and acetylcholine-induced currents by CTa16, but no direct activation of a7-nAChRs by either peptide in the absence of agonist (not shown). Bars indicate application of EC₅₀ agonist concentrations and of the peptide indicated (green: CTa16: gray: CTa16_{scr}).
- B Quantification of potentiation shows that CTa16 enhances nicotine- and acetylcholine-induced currents to a similar extend, whereas CTa16scr had no effect.
- C CTa16 dose–response curve obtained with submaximal nicotine concentrations (100 µM) with a corresponding EC₅₀ value of 10.7 \pm 4.6 nM and a hill coefficient of 2.1 ± 0.3 (n = 4).
- D Nicotine-induced whole-cell current traces of a7-nAChRs in the presence of 20 nM recAPPsa (green bar) or 20 nM recAPPs β (blue bar). Note that only recAPPsa efficiently potentiates a7-nAChRs, which is blocked by BTX (orange bar).
- E Quantification of potentiation shows that recAPPsa enhances nicotine-induced currents to a similar extend as CTa16 (see for comparison Fig 7B) while recAPPsß had no effect.
- F Nicotine dose–response curve obtained either in the presence of 20 nM recAPPsa (green circles, left) or without treatment (black circles, right). Note that recAPPsa treatment shifts the curve to the left, significantly reducing the apparent agonist affinity by about twofold (EC₅₀ of 40.3 \pm 6.0 µM, green curve vs. EC₅₀ of 80.5 \pm 12.7 µM, black curve; n = 5).

Data information: For statistical evaluation of potentiation, we performed a paired two-tailed Student's t-test of the agonist-induced currents in the absence and presence of the indicated peptide. $n =$ number of oocytes. Data represent mean \pm SEM. ^{ns}P > 0.05, *P < 0.05.

mechanism. Long-term AAV-mediated expression of either APPsa or APPsb in the hippocampus of adult NexCre cDKO (cDKO) mice revealed several important new findings: (i) In vivo expression of APPsa efficiently rescued deficits in spine density, synaptic plasticity (LTP and PPF) and spatial reference memory of cDKO mice. (ii) In contrast to APPs α , APPs β expression had no detectable effects on spine density and synaptic plasticity in cDKO mice indicating distinct functional roles in the adult CNS. (iii) The C-terminal 16 amino acids (CTa16) of APPsa proved sufficient to enhance LTP to the same extent as full-length APPsa. (iv) Nanomolar concentrations of APPsa and CTa16 function as potent positive allosteric modulators of a7-nAChRs in vitro increasing the apparent agonist affinity. (v) Pharmacological blockade of a7-nAChRs impaired the APPsa (or $CT\alpha16$ -induced LTP facilitation, thus identifying α 7-nAChRs as physiological APPsa receptors that are involved to mediate its LTPenhancing effects.

Our previous studies indicated that LTP deficits of cDKO mice can be rescued by acute application of nanomolar amounts of APPsa, but not APPs β , in vitro. Despite this, it remained unclear whether these acute in vitro effects observed for a short time of recording would also be relevant in vivo and whether reduced spine density and behavioral deficits might also be rescued. Lastly, the mechanism by which APPsa regulates LTP including the relevant receptor was unknown. In principle, synaptic deficits of cDKO mice may either arise from developmental deficits such as impaired synaptogenesis that could lead to miswired circuits or may be due to a lack of APP (or APLP2)-mediated functions in the adult brain. To address these questions and to assess the specific role(s) of the secreted ectodomains APPs α and APPs β , we used a reverse genetic approach employing AAV-mediated re-expression of APPsa or $APPs\beta$ in the hippocampus of adult cDKO mice. Expression of the AAV-Venus control vector in cDKO mice or littermate controls fully reproduced and confirmed the phenotype of cDKO mice (Hick et al, 2015) including reduced dendritic complexity (Fig 3) and spine density of CA1 neurons (Fig 2), deficits in synaptic plasticity (Fig 2), and impaired spatial memory (Fig 4). This indicates that the cDKO phenotype is robust and that AAV vectors are suitable to confer neuron-specific, long-lasting and widespread expression throughout the dorsal hippocampus (see Figs 1 and EV1). Using this in vivo reconstitution approach, we show that APPs α is not only able to acutely modulate synaptic strength when applied in vitro (Hick et al, 2015), but has the ability to mediate a long-lasting rescue of synaptic plasticity, with facilitating effects on both the induction and maintenance phase of LTP. Moreover, we show that APPsa re-expression rescued spine density, a correlate of excitatory synapses. These data are perfectly in line with our recent observation that a lack of APP and thus APPsa in APP-KO mice leads to impairments in structural spine plasticity in the cortex (Zou et al, 2016). While synaptic plasticity and spine density were completely restored, APPsa expression led only to a partial rescue of dendritic complexity of CA1 neurons with effects most pronounced close to the soma and in the midapical region of apical dendrites. These more subtle effects might in part be related to a potential nonuniform secretion of APPsa along dendritic regions of individual neurons that may become limiting at more distant regions. Alternatively, it is conceivable that APPsa is not sufficient to fully restore neurite outgrowth and dendritic arbors due to an inability to compensate early developmental defects or an additional

requirement for APLP2 (Weyer et al, 2014; Hick et al, 2015). In this regard, neither deficiency of APP nor APLP2 alone results in reduced dendritic complexity in young adult knockout mice (Lee et al, 2010; Midthune et al, 2012; Tyan et al, 2012), while a combined absence in cDKO mice profoundly impairs neuronal morphology and total neurite length (Hick et al, 2015; Weyer et al, 2014 and this study) indicating a combined role of APP and APLP2 for dendritic complexity. Although the underlying mechanism is still unknown, it appears likely that domains conserved between APP and APLP2 (and not divergent sequences as those close to the secretase sites) are involved.

The ability of synapses to undergo long-term potentiation is considered as a cellular mechanism underlying learning and memory (reviewed by Korte & Schmitz, 2016). Indeed, restoration of LTP by APPsa at the CA3/CA1 pathway was associated with a significantly improved performance in water maze place navigation during reversal learning (Fig 4B and C) and a substantial increase of spatial reference memory, as assessed during the probe trial. In mice, emotional reactions to the swim stress are a limiting factor for performance during task acquisition that becomes less relevant during reversal learning as mice get habituated to the stressful experience (Lipp & Wolfer, 1998; Strange et al, 2014). The dorsal hippocampus that is known to mediate spatial processing (Strange et al, 2014) was efficiently targeted by AAV-APPsa injections, whereas AAV-APPsa was undetectable in ventral portions of the hippocampus (Fig EV1C) that mediate emotional responses. Thus, a failure to compensate emotional problems due to selective targeting may explain why AAV-APPsa treatment effects were only seen during probe trial and reversal learning. Although hippocampal lesions have been demonstrated to impair hippocampus-dependent behavior (Morris et al, 1982), learning and memory also involves other brain regions that were not targeted by the injections including the dorsomedial striatum-prefrontal cortex network which is strongly involved in the initial acquisition of the place navigation task (Woolley et al, 2013). The entorhinal cortex constitutes a crucial interface between the hippocampus and the rest of the cortex and is the source of most spatial information that is processed in the hippocampus (Hales et al, 2014; Vorhees & Williams, 2014). The fact that AAV-APPsa expression was largely restricted to the hippocampus may thus underlie the partial but not complete rescue of performance by APPs α in the MWM. In addition, part of the behavioral deficits may also be due to developmental effects of the mutation.

Consistent with an important function of $APPs\alpha$ in the mature brain, acute depletion of APPs α in wild-type animals by either pharmacological inhibition of α -secretase (Taylor et al, 2008), or infusion of antibodies directed against the C-terminus of APPsa (Taylor et al, 2008; Puzzo et al, 2011) was reported to impair LTP and cognitive behavior. However, these previous approaches lacked specificity, as secretase inhibitors target also other substrates besides APP and antibodies employed bind not only to APPsa, but also full-length APP and A β . Collectively, our findings indicate an important synaptotrophic role of APPsa in the mature CNS for spine density, synaptic plasticity, and behavior. Importantly, this role in cDKO mice (lacking endogenous APP and all its fragments including $\Delta\beta$) is completely independent of any indirect $\Delta\beta$ related effects, in contrast to the previously reported A β lowering properties of APPs α in transgenic APP/PS1 mice (Obregon et al, 2012; Fol et al, 2016).

As APPs α and APPs β are identical in primary sequence except for the last 16 amino acids, one may expect that they should exhibit largely overlapping functions. Accordingly, only few studies have so far directly compared the effects mediated by either APPsa or APPs β . In vitro, recombinant APPs β was shown to more efficiently induce the differentiation of human embryonic stem cells into neuronal precursor cells as compared to APPsa (Freude et al, 2011), whereas a similar increase in axonal outgrowth was observed when cortical neurons were treated with recombinant APPs β or APPs α (Chasseigneaux et al, 2011). With regard to in vitro assays of neuroprotection, however, APPs β was considerably less potent to protect neurons against glucose deprivation, excitotoxicity, Ab peptide (Furukawa et al, 1996; Barger & Harmon, 1997), or epoxomicininduced proteasomal stress (Copanaki et al, 2010).

Here, we compared the in vivo functions of the secreted APP ectodomains in the adult brain. A surprising key finding was that APPs α and APPs β exert strikingly different effects in vivo, despite a similar level and pattern of AAV-mediated expression (Figs 1, 5C–E, EV1, and EV2). Of note, the absence of beneficial effects by AAV- $APPs\beta$ cannot be simply explained by possible adverse effects associated with $AAV-APPs\beta$ expression, as we found no signs of increased cell death, nor any evidence for increased astrogliosis or microgliosis (see Appendix Fig S1) as unspecific signs of neurodegeneration. Although earlier studies had indicated that a fragment (N-APPs1-286) derived for APPsb may induce caspase activation and death of sensory neurons in a mechanism requiring DR6 (Nikolaev et al, 2009), these data have recently been revised to exclude a requirement for β -secretase activity and thus APPs β (Olsen et al, 2014). Our notion that AAV-APPs β does not induce adverse effects is further in agreement with previous data from fully viable and apparently normal APPsß-knockin (KI) mice expressing solely APPs β on an APLP2 wildtype background (Li et al, 2010). However, whether a lack of APPs α in APPs β -KI mice might lead to synaptic deficits had remained unknown.

We demonstrate that APPs α but not APPs β rescues spine density and synaptic plasticity in cDKO mice and identified the $CT\alpha16$ peptide of APPs α as a crucial LTP-enhancing functional domain that stimulated LTP to the same extent as recAPPsa. Mechanistically, facilitation of LTP by APPs α or the CT α 16 peptide required functional a7-nAChRs since BTX, a selective antagonist of a7-nAChRs, blocked its effects. Moreover, when expressed in oocytes a7 nAChRs could be directly potentiated by nanomolar amounts of either recAPPs α (but not recAPPs β) or CT α 16 in the presence of ACh or nicotine. Together with the ability of APPsa to enhance the sensitivity of a7-nAChRs for the agonist nicotine, these data establish APPs α as a potent positive allosteric modulator (PAM). These findings also suggest that APPsa might function as an endogenous PAM of cholinergic signaling in the hippocampus, although further studies are required to confirm its activity in vivo. Several studies have shown that nAChR activation facilitates LTP induction (for review see Yakel, 2014) and a7-nAChRs are abundantly expressed in the hippocampus (Fabian-Fine et al, 2001). Several mechanisms of a7-nAChR signaling are thought to contribute to its role in LTP: (i) Activation of presynaptic a7-nAChR can increase glutamate release and (ii) activation of postsynaptic α 7-nAChRs that have a high $Ca²⁺$ permeability may confer membrane depolarization and induce plasticity evoking Ca^{2+} signaling (reviewed by McKay et al, 2007; Yakel, 2014).

Although more work is needed to understand precisely how APPs α affects α 7-nAChR signaling, we hypothesize that both preand postsynaptic mechanisms are likely to play a role. When applied to slices of cDKO mice, both APPsa and CTa16 enhanced, in a BTX-sensitive manner, the early phase of post-tetanic potentiation (PTP) during the first minutes after start of baseline recording, which is believed to involve Ca^{2+} build up in presynaptic terminals. In line with an important endogenous role of APPsa for LTP, APPsa secretion is activity dependent (Fazeli et al, 1994; Mills & Reiner, 1999; Gakhar-Koppole et al, 2008; Hoey et al, 2009) and can thus be increased through plasticity-inducing protocols. The enhancement of PTP by APPsa, as observed in our study, is consistent with previous studies that reported increased $Ca²⁺$ influx in synaptoneurosomes and a7-nAChRs transfected neuroblastoma cells upon application of low (picomolar) amounts of $A\beta$ or N-terminal $A\beta$ -peptides that are overlapping with the C-terminus of APPs α (Dougherty et al, 2003; Lawrence et al, 2014). Recently, low (picomolar) amounts of $\Lambda\beta$ were shown to increase synaptic vesicle recycling via a7-nAChRs signaling in hippocampal neurons (Lazarevic et al, 2017). Moreover, low amounts of A β had been found to stimulate synaptic plasticity and memory in wild-type mice (Puzzo et al, 2011; Lawrence et al, 2014). In addition to presynaptic effects, it is likely that APPsa will also modulate signaling at the postsynaptic site (for a review, see Ludewig & Korte, 2016). Postsynaptic membrane depolarization due to Ca^{2+} influx through α 7-nAChRs may increase the probability of NMDAR activation that is crucial to induce stable LTP. In this regard, NMDAR inhibition has been shown to prevent the nicotine-induced conversion of short-term plasticity into LTP at CA3/CA1 synapses (Ji et al, 2001). Moreover, also activation of septal cholinergic input to induce a7-nAChRsdependent LTP required the activation of NMDARs (Gu & Yakel, 2011). In addition to signaling via α 7-nAChRs, APPs α may also modulate NMDARs more directly, as APPsa was shown to potentiate tetanically evoked NMDAR currents recorded at granule cells of the dentate gyrus in rat brain slices (Taylor et al, 2008) and fulllength APP can biochemically interact with GluN1/GluN2 receptors (Cousins et al, 2009), although it is not known whether this also holds true for APPsa.

Our findings of distinct in vivo functions of APPs α and APPs β have important implications for AD therapy. Pharmacological BACE1 inhibition has been a major approach to reduce $\mathbf{A}\mathbf{\beta}$ in animals and clinical trials. More recently, however, concerns have been raised that therapeutic BACE1 inhibition may also compromise important physiological functions of BACE (Yan & Vassar, 2014). Indeed, BACE-KO mice display deficits in synaptic morphology and synaptic plasticity in the hippocampus (Dominguez et al, 2005; Laird et al, 2005). Our data indicate that APPs β deficiency that will result from BACE1 inhibition is unlikely to lead to toxic effects. A number of recent studies demonstrated that very low concentrations of $A\beta$ may stimulate transmitter release and modulate synaptic plasticity and memory. Strikingly, we now show that it is the C-terminal domain of APPsa that is required to increase spine density, rescues LTP, and improves memory. As this C-terminal domain is also present in $A\beta$, it is conceivable that signaling of $APPs\alpha$ and soluble, non-aggregated $\mathsf{A}\beta$ species may at least in part converge, for example, regarding the activation of α 7-nAChRs. From this, one may speculate that APPsa may be able to rescue potential unwanted effects due to limited $\mathsf{A}\beta$ levels. It is also clear, however, that

sequence context and structural accessibility of the CTa16 domain is crucial. Indeed, the presence of the $CT\alpha16$ domain appears to alter the conformation of APPsa in a critical way. Analysis by small-angle X-ray diffraction indicated that the 3D structure of APPsa and APPsb is quite different, with APPs α exhibiting an extended conformation with an exposed CTa16 region (Gralle et al, 2006; Peters-Libeu et al, 2015), while in APPs β the E1 domain folds back towards the C-terminal juxtamembrane region (Peters-Libeu et al, 2015). Thus, different 3D structures may enable or prevent binding to receptors, which may contribute to the distinct in vivo functions of APPs α and APPsb.

Regarding AD pathogenesis, our data indicate that a shift towards b-secretase processing that may occur during AD (Holsinger et al, 2002; Ahmed et al, 2010) could result in insufficient amounts of APPsa that cannot be functionally compensated by APPs β . A lack or reduction of APPs α might thus contribute to deficits in synaptic plasticity and cognitive function in AD patients. Consistent with this notion, in AD patients hippocampal levels of synaptically localized ADAM10/SAP97 complexes are reduced (Epis et al, 2010) and an activity attenuating mutation in the human ADAM10 gene leading to reduced APPsa levels has been associated with AD (Kim et al, 2009; Suh et al, 2013). In familial AD cases carrying the Swedish mutation (APP_{SWE}), cerebrospinal fluid (CSF) levels of APPsa were found to be reduced already at early stages of AD (Lannfelt et al, 1995; Almkvist et al, 1997). With regard to sporadic AD cases, however, no consensus has been reached whether reduced APPsa levels are associated with AD (Mockett et al, 2017). Early on, total soluble APPs was reported to be severely reduced in sporadic AD (Van Nostrand et al, 1992). Several more recent studies specifically detecting APPsa reported reduced APPsa levels in mild (Sennvik et al, 2000) to moderate AD (Rosen et al, 2012), or in APOE4 positive AD patients (Olsson et al, 2003), while several other studies found no difference in APPsa at early stages of sporadic AD (Perneczky et al, 2011, 2013; Rosen et al, 2012; Brinkmalm et al, 2013). These mixed results may in part be related to different assays systems used and the recent finding of considerable diurnal variability of APPsa and other APP fragments in the CSF (Dobrowolska et al, 2014). Thus, more detailed studies are needed to resolve these important issues.

In preclinical AD research, numerous studies have been conducted using APP transgenic mouse models ([https://www.alzfo](https://www.alzforum.org/research-models) [rum.org/research-models\)](https://www.alzforum.org/research-models) which (over)express huAPP_{SWE} that undergoes enhanced β -secretase processing. Consequently, reduced levels of neuroprotective and synaptotrophic APPsa relative to increased amounts of A β (that is a reduced APPs α /A β ratio) may fail to adequately balance and antagonize the detrimental effects of $A\beta$ and thus contribute to the phenotypic and synaptic impairments in these transgenic mice.

APPsa also plays an important role in processes of natural aging. Not only is memory performance correlated with APPsa levels in rats (Anderson et al, 1999), but also aging-related deficits in LTP and cognitive behavior can be rescued by exogenous APPsa (Moreno et al, 2015; Xiong et al, 2016). Collectively, our findings indicate distinct functions for APPs α in the adult brain to modulate spine density, synaptic plasticity, and cognition. Our findings lend further support to therapeutic approaches aimed at directly or indirectly increasing APPsa expression in the brain (Mockett et al, 2017; Müller et al, 2017) to ameliorate synaptic deficits in AD or possibly also for other diseases in which neurons are damaged.

Materials and Methods

Mice

Experiments on animals were performed in accordance with the guidelines and regulations set forth by the German Animal Welfare Act, the Regierungspräsidium Karlsruhe (Germany) and the Regierungspräsidium Darmstadt (Germany). Generation and genotyping of NexCre cDKO mice (further referred as cDKO mice) were as described previously (Hick et al, 2015). Genotype of experimental animals: NexCre cDKO $(=APP^{flox/flox} APLP2^{-/-} NextCre⁺)$ and Cre⁻ littermate (LM) controls (= $APP^{flox/flox} APLP2^{-/-}$).

AAV plasmid design and vector production

The mouse APPsa coding sequence (derived from Uniprot: P12023- 2) was codon optimized (Geneart, Germany) and then cloned under control of the synapsin promoter into a single-stranded rAAV2 based shuttle vector, as described previously (Fol et al, 2016). Briefly, the bicistronic DNA constructs harbor a T2A site that connects the cDNA of lckVenus and muAPPsa. Venus contains a lymphocyte-specific protein tyrosine kinase (lck)-derived peptide motif which tethers it to the plasma membrane. For easy detection, an N-terminal double HA-tag was inserted downstream of the APP signal peptide (SP) at the N-terminus of APPsa. The monocistronic control vector, AAV-Venus, encodes only the yellow fluorescent protein Venus. All constructs were packaged into AAV9 capsids. Briefly, viral particles were produced by transient cotransfection of HEK-293 cells with the transfer vector containing the above-mentioned expression cassettes and the helper plasmid pDP9rs. 72 h following transfection, virions were purified and concentrated from cell lysate and supernatant by ultracentrifugation on a iodixanol density gradient followed by buffer exchange to 0.01% pluronic/phosphate-buffered saline (PBS) via a 100 kDa Amicon centrifugal filter unit. Genome copies in the vector stocks were determined by free inverted terminal repeat (ITR)-specific quantitative TaqMan PCR and expressed as genomic copies per ul of concentrated stocks (gc/µl) as described (D'Costa et al, 2016).

Stereotactic injection of AAVs

Mice were anesthetized by intraperitoneal injection of sleep mix (Medetomedin: 500 µg/kg, Midazolam: 5 mg/kg, Fentanyl: 50 µg/ kg in isotonic NaCl solution) and positioned on a stereotactic frame (World Precision Instruments, USA). Vector particles (either AAV-Venus, AAV-APPsα or AAV-APPsβ) were injected into the hippocampus at two injection spots per hemisphere using $1 \mu l$ vector stock (titer: 1×10^9 gc/µl) per spot at a rate of 0.2 µl/min. When injection was completed, the cannula was left to rest for 1 min to prevent efflux of viral vector solution. Stereotactic coordinates of injection sites from bregma were as follows: anteroposterior (A/P): -2 mm, mediolateral (M/L): ± 1 mm, dorsoventral (D/V):

 -2.25 mm and -1.75 mm. Procedures were approved by the local animal care and use committee (35-9185.81/G-304/14, Regierungspräsidium Karlsruhe, Germany).

Brain samples

Mice were sacrificed 6 weeks post-injection at 5–6 months of age. Following anesthesia, mice were transcardially perfused with PBS before dissection. For immunohistochemistry, one cerebral hemisphere was dissected and post-fixed in 4% paraformaldehyde (PFA) for 48 h and afterwards stored in PBS at 4° C. 40-um coronal sections were cut using a vibratome (HM650V Vibratome, Thermo Fisher Scientific, USA) and collected in PBS. The other hemisphere was dissected to segregate hippocampus and cortex for biochemical analysis. Samples were then homogenized using a Polytron homogenizer (Polytron PT-MR 2100, Kinematica AG, Switzerland) in tissue homogenization buffer (THB, 250 mM sucrose, 1 mM EGTA, 20 mM Tris–HCl, pH 7.4) containing $1 \times$ protease inhibitor (Complete[™] #04693124001, Roche, Switzerland). After centrifugation (10 min, 15,700 g, 4 $^{\circ}$ C), the supernatant was collected and the protein concentration was quantified by BCA assay. Lysate aliquots were snap-frozen in liquid N_2 and stored at -80° C. For the detection of the soluble ectodomain fragments APPs, hippocampal lysates were subjected to high-speed centrifugation (60 min at $100,000 \times g$ and membrane-free supernatant was used for further analysis.

Western blot analysis

Total brain homogenate or supernatant from ultracentrifugation (10 lg protein) was used for SDS–PAGE. Proteins were separated using 12% Tris-Glycine gels at 20 mA/gel in Laemmli buffer (0.25 M Tris, 2 M glycine and 1% SDS) and transferred to 0.45 μ m PVDF membranes (GE Healthcare, USA) using a tank blot at 450 mA for 1 h (for samples after ultracentrifugation: 450 mA for 1.5 h). After blocking in PBS-T (2.5% Tween in PBS) containing 5% (w/v) dried milk powder at room temperature for 60 min, membranes were incubated with the primary antibodies at 4°C overnight. The following antibodies were used: a-HA-tag (rabbit, 1:1,000, #3724, Cell Signaling Technology, USA, was used for total hippocampal homogenates or mouse, 1:1,000, #2367, Cell Signaling Technology, USA, used for analysis after ultracentrifugation), a-GFAP (rabbit, 1:3,000, #173002, Synaptic Systems, Germany), a-Iba1 (rabbit, 1:500, #234003, Synaptic Systems, Germany), a-GFP (chicken, 1:1,000, #A10262, Thermo Fisher Scientific, USA), anti-b-Tubulin (mouse, 1:10,000, #MAB3408, Merck Millipore, USA), M3.2 (mouse, 1:1,000, kind gift from Paul Mathews), Y188 (rabbit, 1:1,000, #ab32136, Abcam, UK). Membranes were then washed with PBS-T, incubated with a horseradish peroxidase-coupled secondary antibody (goat-a-mouse HRP, 1:10,000, #115-165-146, Dianova, Germany; donkey-a-rabbit HRP, 1:10,000, #711-035-152, Dianova, Germany; goat-a-chicken HRP, 1:10,000, #103-035-155, Dianova, Germany), and washed again and developed using Signal-Fire ECL Reagent (#6883, Cell Signaling Technology, USA) or Signal-Fire™ Elite ECL Reagent (used for analysis after ultracentrifugation, #12757, Cell Signaling Technology, USA). Signals were detected with the Bio-Rad Chemidoc MP imager (Bio-Rad, Hercules, USA) and analyzed using Bio-Rad Image Lab software.

Immunostaining

Slices were blocked/permeabilized in blocking buffer (5% BSA, 5% NGS, 0.4% Triton X-100 in PBS) overnight at 4°C. To detect AAVencoded HA-tagged HA-APPs α , slices were incubated with α -HA antibody (rabbit-a-HA, 1:1,000, #3724, Cell Signaling Technology, USA or mouse-a-HA, 1:1,000, #H3667, Sigma-Aldrich, USA) overnight at 4°C. After three successive washes with PBS-T (2.5% Tween in PBS), slices were incubated in secondary antibody (goata-rabbit Cy3, 1:1,500, #711-165-152, Jackson ImmunoResearch Laboratories, USA; goat-a-rabbit Cy5, 1:1,500, #111-175-144, Jackson ImmunoResearch Laboratories, USA; donkey-a-mouse Cy3, 1:1,500, #715-165-150, Jackson ImmunoResearch Laboratories, USA; goat-a-mouse Cy5, 1:1,500, #A10524, Thermo Fisher Scientific, USA). For expression analysis, HA-APPsa was coimmunostained overnight with the following primary antibodies: a-NeuN (mouse, 1:1,500, #MAB377, Merck Millipore, USA), a-GFAP (rabbit, 1:3,000, #173002, Synaptic Systems, Germany), and a-Iba1 (rabbit, 1:500, #234003, Synaptic Systems, Germany). Images were taken with a Axio Observer Z1 (Zeiss, Germany) and a Leica TCS SP5II (Leica, Germany).

Electrophysiology

In vitro extracellular recordings were performed on acute hippocampal slices of LM controls stereotactically injected with the AAV-Venus ($N = 5$) and cDKO mice injected either with AAV-Venus $(N = 4)$ or AAV-APPs α ($N = 5$). In a separate set of experiments, cDKO mice were injected either with AAV-Venus ($N = 5$) or AAV-APPs β (N = 5). Investigation of synaptic plasticity was done 7– 8 weeks after AAV injection. In-between animals were housed in a temperature- and humidity-controlled room with a 12 h light–dark cycle and had access to food and water ad libitum.

Slice preparation

Acute hippocampal transversal slices were prepared from isoflurane anesthetized individuals. Following decapitation, the brain was removed and quickly transferred into ice-cold carbogenated (95% O2, 5% CO2) artificial cerebrospinal fluid (ACSF) containing 125.0 mM NaCl, 2.0 mM KCl, 1.25 mM NaH₂PO₄, 2.0 mM MgCl₂, 26.0 mM NaHCO₃, 2.0 mM CaCl₂, and 25.0 mM glucose. The hippocampus was sectioned into 400-µm-thick transversal slices with a vibrating microtome (VT1200S, Leica, Germany) and maintained in carbogenated ACSF at room temperature for at least 1.5 h. Before recording, each slice of the injected animals was inspected for Venus expression in area CA1 and CA3 (Axiovert 35, Zeiss). Slices lacking fluorescence in the recording areas were excluded from further analysis.

Peptides and inhibitor

Acute hippocampal slices of LM controls and cDKO mice were preincubated in 30 ml gently carbogenated ACSF containing synthetic CT α 16 (DAEFGHDSGFEVRHQK) or a scrambled CT α 16_{scr} peptide (RFDQHGVEDHAFGESK) of the same amino acid composition as a control. Recombinant recAPPsa was purified from the supernatant of stably transfected HEK cells as described (Hick et al, 2015) and was used at a concentration of 10 nM, in a custom-made incubation chamber for 1 h at RT. Afterwards slices were transferred into the

recording chamber where again 30 ml of ACSF with the respective peptide was circulating in a closed loop during the entire experiment. In another set of experiments, the α 7-nicotinic acetylcholine receptor antagonist (a7-nAChR) a-Bungarotoxin (BTX, Merck Millipore, Germany) solved in Aqua dest. was used at a final concentration of 10 nM and either co-applied already at the step of pre-incubation (1 h before TBS) together with 10 nM $CT\alpha$ 16 (or 10 nM APPsa) on acute slices or washed in 10 min before baseline recording started.

Extracellular field recordings

Slices were placed in a submerged recording chamber and perfused with carbogenated ACSF (32°C, 125.0 mM NaCl, 2.0 mM KCl, $1.25 \text{ mM } \text{NaH}_2\text{PO}_4$, $2.0 \text{ mM } \text{MgCl}_2$, $26.0 \text{ mM } \text{NaHCO}_3$, 2.0 mM $CaCl₂$, and 25.0 mM glucose) at a rate of 1.2–1.5 ml/min. Field excitatory postsynaptic potentials (fEPSPs) were recorded in stratum radiatum of CA1 region with a borosilicate glass micropipette (resistance 2–4 MΩ) filled with 3 M NaCl at a depth of \sim 150–200 μm. Monopolar tungsten electrodes were used for stimulating the Schaffer collaterals at a frequency of 0.1 Hz. Stimulation intensity was adjusted to \sim 40% of maximum fEPSP slope for 20 min baseline recording. LTP was induced by applying theta burst stimulation (TBS: 10 trains of four pulses at 100 Hz in an 200 ms interval, repeated three times).

Basal synaptic transmission properties were analyzed via input– output (IO) measurements, and short-term plasticity was examined via PPF. The IO measurements were performed either by application of defined current values (25–250 μ A) or by adjusting the stimulus intensity to certain fiber volley (FV) amplitudes (0.1–0.8 mV). Presynaptic function and short-term plasticity were assessed with the PPF paradigm by applying a pair of two closely spaced stimuli in inter-stimulus intervals (ISI) ranging from 10 to 160 ms.

Data analysis and statistics

Data of electrophysiological recordings were collected, stored, and analyzed with LABVIEW software (National Instruments, USA). The initial slope of fEPSPs elicited by stimulation of the Schaffer collaterals was measured over time, normalized to baseline, and plotted as average \pm SEM. Analysis of the PPF data was performed by calculating the ratio of the slope of the second fEPSP divided by the slope of the first one and multiplied by 100. The statistical analysis was performed using Microsoft Excel or GraphPad Prism version 6.0 (GraphPad, USA). Data obtained between two genotypes or two different experimental conditions were compared using an unpaired two-tailed Student's t-test. Data including more than two different groups were analyzed using a one-way ANOVA followed by a post hoc Bonferroni's test. All data are indicated as mean \pm SEM. Values of $P < 0.05$ were considered significant and plotted as follows $*P < 0.05$, $*P < 0.01$, $**P < 0.001$.

Xenopus oocyte expression and electrophysiological recording

The rat α 7-nAChR, kindly provided by A. Nicke (Kendel et al, 2013), and the human α 1-GlyR (Laube et al, 2000) cDNAs were subcloned into the oocyte expression vector pNKS2. The original rat a7-nAChR cDNA had been provided by J. Patrick (Baylor College of Medicine, Houston, USA). The rat a7-nAChR or the human a1-GlyR cDNA was linearized, and cRNA was synthesized with the SP6 or T7 mMessage mMachine kit, respectively (Ambion, USA). For electrophysiological analysis, X. laevis oocytes were injected with 50 ng of the cRNA in a volume of 50 nl. Oocytes were isolated and maintained as described previously (Laube et al, 1997) and approved by the local animal care and use committee (II25.3-19c20/15, RP Darmstadt, Germany). 1–3 days after injection, whole-cell currents were recorded at -70 mV by twoelectrode voltage clamp according to Laube et al (2000). Currents were acquired at 200 Hz with a Geneclamp 500B amplifier, a Digidata 1322A digitizer, and Clampex 9.2 software (Molecular Devices, USA). The agonists nicotine, acetylcholine, or glycine, dissolved in bath solution, was applied either alone for 10 s or after 15 s preapplication of the respective peptides ($CT\alpha 16$, $CT\alpha 16$ _{scr}, recAPPs α , or recAPPs β) also dissolved in bath solution. All experiments were performed at room temperature.

Data analysis and statistics

Currents were measured with Clampfit 9.2 software (Molecular Devices, USA), and results were analyzed using the KaleidaGraph program (Synergy Software, USA) and GraphPad Prism version 6.0 (GraphPad, USA). Peak current responses to nicotine in the absence or presence of APPsa were plotted against agonist concentration and fit with variable slope nonlinear regression to establish agonist EC₅₀ parameter (Laube et al, 2000). For peptide modulation, responses to EC_{50} nicotine (100 μ M), acetylcholine (100 μ M), or glycine $(100 \mu M)$ after application were analyzed. Normalized CTa16-induced fold enhancement of nicotine-induced currents was fit with variable slope nonlinear regression (GraphPad Prism version 6.0, GraphPad, USA), yielding EC_{50} parameters for each individual experiment (Laube et al, 1998). All experiments were from at least two batches of oocytes. Data were compared by paired two-tailed Student's *t*-test. Values of $P < 0.05$ were considered significant and plotted as follows $*P < 0.05$, $**P < 0.01$, $**P < 0.001$. All data are indicated as mean \pm SEM.

Neuronal morphology and spine density

Iontophoretic fillings

In brief, CA1 pyramidal cells were visualized by postfixation filling with Alexa 568 in 200-µm horizontal brain sections of 5- to 6-monthold mice (see Appendix Table S1 for sex of animals). For iontophoretic fillings of CA1 pyramidal neurons, one brain slice at a time was placed in a custom-made chamber filled with cold PBS and visualized on an Olympus BX51WI fixed stage upright microscope (Olympus, Japan). Sharp quartz glass electrodes (Quartz electrodes with filament, O.D: 1.0 mm, I.D.: 0.7 mm, 10 cm length, Sutter instruments, USA) were pulled using the Sutter P-2000 Laser Puller. The tip of the electrode was loaded with 5 mM Alexa 568 dye dissolved in distilled water and backfilled with 0.1 M LiCl dissolved in distilled water. Using a motorized 3D micromanipulator, the electrode was lowered into the hippocampal CA1 region under visual control using a Calcium Crimson filter cube (HQ580/20×, U-Q595LP (339038), HQ630/60 m) while applying a negative voltage pulse (-1 V, 1 Hz) to the electrode via a silver wire in line with a 500 M Ω resistor. When piercing of a cell body was observed, the cell was filled by application of a negative 1 Hz current pulse $({\sim} 5 \text{ nA})$ to the electrode. Filling was for 10 min or until no further filling was observed. Afterwards slices were fixed for 2 days in 4% PFA at 4°C, washed three times in cold PBS, and finally mounted in Mowiol.

Image acquisition

Images of filled neurons were acquired on a Leica TCS SP5II (Leica, Germany) upright confocal microscope. Overview images of complete neurons used for reconstruction were taken with a 20× objective (Apo 20×/0.75). The complete volume of one filled neuron was imaged with a z-step size of 1 μ m and a 2,048 \times 2,048 resolution. Basal and apical segments were imaged individually with two overlapping stacks. Detailed images of dendritic segments and spines were acquired using a $63 \times$ objective (Apo $63 \times /1.4$ oil) and a digital zoom of 5. To fulfill the Nyquist criteria for deconvolution, z-stacks of dendritic segments were captured with a pixel size of 80 nm and a z-step of 130 nm. Laserpower, gain and offset varied from cell to cell as the parameters were always chosen so that the complete range of the grayscale was used. Images for spine counts were deconvoluted with the AutoQuantX3 software (Media Cybernetics, USA).

Neuronal morphology and spine counts

Filled CA1 pyramidal neurons were manually reconstructed using the Neurolucida software (MicroBrightField, USA) by an experimentator blind to genotype and injected viral vector. Neurons were only included into Sholl analysis if they showed a completely filled apical or basal tree and well-defined dendritic endings. The morphometric Sholl analysis was done using the NeuroExplorer software (MicroBrightField, USA). In short, a series of concentric spheres (centered around the soma) was drawn with an intersection interval of 30 µm and the number of dendrites crossing each sphere, as well as the dendritic length in between each sphere was calculated. This analysis was done separately for basal and apical dendrites and was plotted against the distance from the soma. For evaluation of basal dendritic spine density, at least three different randomly chosen dendritic segments of the basal dendritic arbor were imaged. They had to fulfill the following criteria: (i) lie mostly horizontally to the slice surface, (ii) be at least $20 \mu m$ away from the soma, (iii) have a comparable thickness. The minimum basal dendritic length imaged per neuron was 100 µm. For evaluation of midapical dendritic spine density, at least three different dendritic segments of the apical tree were imaged. Midapical was defined as the middle third of the length of the apical dendrite measured from the origin of the apical dendrite from the soma to the endpoint of the tufts. Dendritic segments used for evaluation had to fulfill the following criteria: (i) be of second or third order to assure comparable shaft thickness, (ii) lie in the middle third of the main apical dendrite, (iii) be longer than $10 \mu m$. The minimum midapical dendritic length imaged per neuron was $100 \mu m$. Files in the ND2 format were imported into ImageJ (NIH) using the BioFormats Importer. After adjusting, images were saved in the TIFF format. Dendritic spines were manually counted using the Neurolucida and NeuroExplorer software (MicroBrightField, USA) following the criteria of Holtmaat (Holtmaat et al, 2009) with minor modifications: (i) All spines that protruded laterally from the dendritic shaft and exceeded a length of $0.4 \mu m$ were counted. (ii) Spines that protruded into the z-plane were only counted if they exceeded the dendritic shaft more than $0.4 \mu m$ to the lateral side. (iii) Spines that bisected were counted as two spines. (iv) Spines had to be at least $10 \mu m$ away from branching points and the soma. Spine density was expressed as spines per μ m of dendrite. Prior to statistical analysis and blind to genotype, neurons were excluded if the

image quality (poor signal to noise ratio) was not sufficient for counting of spines or for deconvolution.

Golgi staining

Golgi staining was done using the Rapid Golgi Staining Kit (FD NeuroTechnologies, USA) according to the manufacturer's instructions. All procedures were performed under dark conditions. One hemisphere of each mouse was used for Western blot analysis and the other hemisphere for Golgi staining (see Appendix Table S1 for sex of animals). Hemispheres were immersed in 2.5 ml mixtures of equal parts of kit solutions A and B and incubated at room temperature for 2 weeks. After 24 h solution $(A + B)$ was renewed. Afterwards brain tissues were stored in solution C at 4°C for at least 72 h, once exchanged after 24 h. Brains were snap-frozen on dry ice, and coronal sections of $100 \mu m$ were cut with a cryotome (Hyrax C50, Zeiss). Each section was mounted with Solution C on an adhesive microscope slide pre-coated with 1% gelatin/0.1% chrome alum on both sides and stained according to the manufacturer's protocol with the exception that RotiClear (Roth, Germany) was used instead of xylene. Finally, slices were cover-slipped with Permount (Thermo Fisher Scientific, USA).

Imaging and analysis of spine density after Golgi staining

Imaging of second- or third-order dendritic branches of hippocampal pyramidal neurons of area CA1 was done with an Axio Observer Z1 (Zeiss) for Golgi-stained neurons using a 63× oil objective. Z-stack thickness was held constant at 130 nm. The number of spines was determined per micrometer of dendritic length (in total 100 µm per neuron) at apical and basal compartments using Neurolucida software (MicroBrightField, USA). Spines in the area around branching points and the soma were excluded from analysis. Five animals per genotype and 3–4 neurons per animal were analyzed blind to genotype and injected viral vector.

Behavioral analysis

Animals

Mice (cDKO + AAV-APPsa: 9M + 9F, cDKO + AAV-Venus: 8M + 10F, LM control + AAV-Venus: 12M + 10F) were housed under a 12/12 h light–dark cycle (lights on at 20:00) in groups of 2–5, unless individual housing was required by experimental protocols or to prevent fighting. Testing occurred during the dark phase under dim light (approximately 12 lux). Mice were transferred to the testing room 30 min before testing. Procedures were approved by the Veterinary Office of the Kanton of Zurich (license 44/2015).

Behavioral procedures

Morris water maze place navigation. The round white polypropylene pool had a diameter of 150 cm with 68 cm high walls. It was filled with water (24–26°C, depth 15 cm) and rendered opaque by addition of 1 l of milk (UHT whole milk 3.5% fat, Coop, Switzerland). The white quadratic goal platform $(14 \times 14 \text{ cm})$ was made of metallic wire mesh. It was hidden 0.5 cm below the water surface in the center of one of the four quadrants, 30 cm from the side wall. Salient extra-maze cues were placed on the walls of the testing room. Animals performed 30 training trials (max. duration 120 s), 6 per day with intertrial intervals of 30–60 min and varying starting positions. During the first 18 trials, the hidden platform was held in

the same position (acquisition phase) and then moved to the opposite quadrant for the remaining 12 trials (reversal phase). The first 60 s of the first reversal trial served as probe trial to test for spatial retention. Time spent in a circular target zone comprising 12.5% of the pool surface was compared with corresponding control zones in adjacent quadrants.

Data analysis and statistics

The path of moving mice was tracked using Noldus EthoVision 3.1 (Noldus, Netherlands). For analysis, all data were imported in custom programmed software Wintrack [\(www.wintrack.ch;](http://www.wintrack.ch) Wolfer et al, 2001). Data were evaluated using an ANOVA model with genotype (cDKO + AAV-APPsa, cDKO + AAV-Venus, LM control + AAV-Venus) and sex as between subject factors. Within subject factors were added as needed to explore the dependence of genotype effects on place or time. Significant interactions and where necessary significant main effects were further explored by pairwise t-tests or by splitting the ANOVA model, as appropriate. Variables with strongly skewed distributions or strong correlations between variances and group means were subjected to Box-Cox transformation before statistical analysis. The significance threshold was set at 0.05. The false discovery rate (FDR) control procedure of Hochberg was applied to groups of conceptually related variables within single tests to correct significance thresholds for multiple comparisons. Similarly, FDR correction was applied during post hoc testing. As genotype and treatment effects were independent of sex, the sex factor is not reported in results and figures. Statistical analyses were run using R version 3.2.3 complemented with the packages psych and moments.

For further methods related to EV Figures, see Appendix Supplementary Methods.

Expanded View for this article is available [online.](https://doi.org/10.15252/embj.201798335)

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Author contributions

UCM designed and conceived the study. MCR, SK, and SW performed intracranial AAV injections and analyzed data. CB and KH produced recombinant APPs. MCR performed and analyzed experiments related to APPs expression analysis in vitro and in vivo including Western blots, and performed immunochemistry and Sholl analysis including spine density measurements. SL, LRS, and MK performed extracellular electrophysiological recordings in brain slices, analyzed data, and interpreted results. AW and BL performed electrophysiological recordings in oocytes, analyzed data, and interpreted results. TA and CJB generated AAV vectors and analyzed APPs expression in neurons. A-KF and DPW conducted, analyzed, and interpreted behavioral experiments. UCM wrote the manuscript with help from MCR and input from all authors.

Conflict of interest

The authors declare that they have no conflict of interest.

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