

Functional connectivity favors hyperactivity leading to synapse loss in amyloidosis

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Running title: Functional and synaptic connectivity in amyloidosis

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ABSTRACT

Hyperactivity is observed in early Alzheimer's disease (AD) in multiple brain regions, including the visual cortex. We recently found that the postsynaptic structures favor visual cortex hyperactivity, which disrupts functional connectivity and leads to visual recognition memory deficits in a mouse AD model. It is unclear whether presynaptic structures also favor hyperactivity and whether hyperactivity depends on the target or source of presynaptic terminals. In addition, it is not well understood whether the functional connectivity of brain regions under nonpathological conditions predicts their hyperactivity in amyloid pathology. We used c-Fos immunolabeling under resting state conditions to map brain-wide neural activity and performed network analysis. We also quantified excitatory and inhibitory presynaptic terminals in hyperactive and non-hyperactive brain regions. We found that hyperactivity in the visual network originates in the cortex, and brain regions highly connected to the primary visual cortex in nonpathological conditions tend to be hyperactive in amyloid pathology. Immunolabeling presynaptic terminals from subcortical and cortical neurons show that the source rather than the target brain regions determine the vulnerability of synapses. Furthermore, we observed a reduction in presynaptic structures selectively in the hyperactive region, indicating presynaptic changes are unfavorable to hyperactivity. Brain regions with higher functional connectivity under nonpathological conditions are vulnerable to hyperactivity in amyloid pathology. Furthermore, presynapse loss may serve as an adaptation to maintain neuronal activity homeostasis.

INTRODUCTION

Neuronal hyperactivity occurs early in some Alzheimer's disease (AD) patients and mouse models of amyloidosis[1-21]. Multiple cellular and synaptic mechanisms, including structural synaptic changes, increased excitation, reduced inhibition, altered intracellular calcium levels or extracellular glutamate levels are associated with hyperactivity[1, 2, 6-8, 10, 11, 13-16, 22-44]. Hyperactivity elicited by disruption of any of these factors may occur independently in different brain regions. Alternatively, hyperactivity originating in a brain region may spread globally due to properties of network connectivity. Consistently, the highly connected default mode network has been found to be hyperactive in AD patients[4, 45-50]. Hyperconnectivity and hyperactivity may influence each other under pathological states, but the extent to which functional connectedness under nonpathological conditions predispose circuits to hyperactivity in amyloidosis is unclear.

Neuronal hyperactivity is observed in circuits beyond the default mode network and the hippocampus[1, 21, 23, 51-55]. The visual cortex is one of the understudied brain regions in the context of AD due to the absence of gross structural deficits in this brain region until very late stages[56-59]. However, in some patients the visual cortex is affected early in the disease progression, and these patients exhibit profound visuospatial defects[60-72]. Neuronal hyperactivity and is also observed in the visual cortex of AD patients[52, 54, 60, 73]. Likewise, many mouse models of AD exhibit structural and functional deficits in the visual cortex[1, 2, 23, 51, 53, 74-81]. We recently found that visual cortex hyperactivity disrupts local functional connectivity and impairs visual recognition memory in a mouse model of amyloidosis[1]. Interestingly, the changes to excitatory and inhibitory postsynaptic densities favored hyperactivity[1]. However, it is unclear whether presynaptic structures are differentially

influenced by hyperactivity. Since hyperactive regions progress to a hypoactive state in AD[22, 46, 82-87], increased hyperactivity favored by postsynaptic structures could be compensated by loss of presynaptic structures, leading to eventual hypoactivity.

Using visual network as a model, we test whether functional connectedness under nonpathological conditions favors hyperactivity, which in turn lead to the loss of presynaptic terminals in a mouse model of amyloidosis (J20 line) at a pre-plaque stage. Using immediate early gene expression-based network mapping, we found that functional connectedness under nonpathological conditions is a significant predictor of network hyperactivity. We additionally found that hyperactivity is associated with localized loss of specific excitatory presynaptic markers, indicating that presynaptic changes oppose hyperactivity. Interestingly, the loss of presynaptic terminals is not dependent on hyperactivity in their target brain region, indicating that cell-intrinsic properties may influence synapse loss.

MATERIALS AND METHODS

ANIMALS

All animal procedures are approved by the University of Kansas Institute of Animal Use and Care Committee and meet the NIH guidelines for the use and care of vertebrate animals. PDGF-hAPP transgenic mice (J20 line; Gladstone) were maintained as heterozygotes for the hAPP transgene by breeding heterozygous J20 male mice with WT female mice. A maximum of five mice were housed in a standard cage. Mice were housed on a 12h-light/12h-dark cycle.

TISSUE PREPARATION AND IMMUNOHISTOCHEMISTRY

Mouse cages were brought to the surgical suite at least five hours before brain extractions to avoid capturing c-Fos expression elicited by movement or contextual novelty. 3.5-6-month-old (synapse immunohistochemistry) or 5-6-month-old (c-Fos immunohistochemistry) J20-hAPP

and WT littermate mice were deeply anesthetized by intraperitoneal injection of 2% avertin in phosphate-buffered saline (PBS), pH 7.4 and transcardially perfused with cold PBS followed by 4% paraformaldehyde. The brains were extracted and post-fixed in 4% PFA overnight at 4°C, followed by storage in PBS. For 40µm slicing, the brains were embedded in 4% oxidized agarose as previously described[88] to limit artifacts during sectioning and sliced on a vibratome (Leica VT1000 S). For 20µm slicing, brains were cryoprotected overnight at 4°C in 15% (w/v) and then in 30% (w/v) sucrose in phosphate buffer (PB). The brains were sectioned coronally on a microtome (Leica SM 2010R) and collected in PBS with sodium azide (0.02%).

24 evenly spaced 40µm slices from each brain spanning the posterior midbrain to the anterior olfactory bulb were fluorescently immunolabeled for c-Fos, and 3 evenly spaced 20-40µm slices spanning the VIS, AUD, and LGD (1-2 slices for each region per mouse) were fluorescently immunolabeled for VGAT, VGluT1, and VGluT2. Sections were permeabilized for 2h at room temperature in a 1% TritonX-100 and 10% normal goat serum (NGS) solution in PBS followed by incubation with rabbit anti-c-Fos (1:1000, CST) or rabbit anti-VGAT (1:1000, Synaptic Systems), mouse anti-VGluT1 (1:2000, Sigma), and guinea pig anti-VGluT2 (1:1000, Sigma) in a PBS solution containing 0.1% TritonX-100 and 5% NGS overnight at 4°C. Sections were then washed 3X with PBS and incubated with Alexa 555-conjugated goat anti-rabbit antibody (1:2000; Fisher) for c-Fos immunohistochemistry or Alexa 488 conjugated goat anti-rabbit antibody (1:2000, Fisher), Alexa 555-conjugated goat anti-mouse antibody (1:2000, Fisher), and Alexa 647-conjugated goat anti-guinea pig antibody (1:2000, Fisher) for two hours in a PBS solution containing 0.1% TritonX-100 and 5% NGS at room temperature, followed by three washes with PBS before mounting on glass slides. Slices were imaged using an ImageXpress Pico automated imaging system (Molecular Devices, San Jose, CA) with a 10x

objective for c-Fos acquisition (Leica HC PL FLUOTAR 10x/0.32) and a 63x objective for presynaptic termini acquisition (Leica HC PL FLUOTAR 63x/0.70 CORR).

ANALYSIS

Slice registration, cell/synapse detection, and brain region area measurements were performed using NeuroInfo software (MBF Bioscience, Williston, VT). 12-bit slice images were first mapped in 3D to the Allen CCF v3 to allow automated cell/synapse detection and area measurement by region. A total of 31 regions covering the entire cerebral cortex, cerebral nuclei, interbrain, and midbrain, and 17 subregions of the visual network were mapped for analysis. Bright circular objects against a darker background were automatically detected using a scale-space analysis of the response to Laplacian of Gaussian (LoG) within the expected range of labeled cell body or synaptic puncta diameters as described[89]. Briefly, cells/synapses were filtered out from all identified objects with a user-defined threshold based on the strength of the LoG response within an expected range of cell body diameters. The LOG threshold value was set at LoG threshold = 55 for cell bodies and 101 for all synapses (range 0-255). Only objects above this LoG strength threshold were included in the analysis to minimize false positives. All regions in both hemispheres of the 24 brain-wide slices were analyzed for c-Fos⁺ cell detection. For synapse quantification, 1-2 ~230 x 900 μ m columns per mouse spanning all layers of the VIS or AUD were analyzed, and 1-2 ~230 x 375 μ m columns per mouse spanning the ventral to dorsal LGD were analyzed. Automatically identified cells and synapses were manually proofread, and remaining false positive identifications were removed before analysis. Cell/synapse density for each mouse was calculated by dividing the total number of cells or synapses per region by the area per region across all slices for each brain (24 slices for c-Fos, 2-3 slices for synapses). Localized areas containing artifacts were excluded from analysis. 8 WT (6 males, 2 females) and

9 hAPP mice (4 males, 5 females) were used for c-Fos⁺ cell density analysis, and 14 WT (9 males, 7 females) and 12 hAPP mice (6 males, 6 females) were used for presynaptic density analysis. GePhi (Association GePhi, London, England) was used to produce circular network graphs and network statistics. Representative images were generated in FIJI (NIH, Bethesda, MD), and all other figures and statistical tests were produced in GraphPad Prism (GraphPad Software, San Diego, CA).

RESULTS

VISUAL NETWORK HYPERACTIVITY IS LOCALIZED TO CORTICAL REGIONS IN HAPP MICE

We recently found increased c-Fos⁺ cell density in the primary visual cortex in ~5-month-old hAPP-overexpressing mice compared to control siblings, indicating hyperactivity in pre-plaque stage amyloidosis[1]. Primary visual cortex hyperactivity may arise due to hyperactivity in subcortical structures that project to the visual cortex. In turn, the primary visual cortex may influence hyperactivity in other brain regions through their functional connections. Therefore, we characterized c-Fos⁺ cell density across 24 evenly spaced slices spanning the brain in hAPP mice and WT littermate controls (Figure 1A-C., see Supplementary Table 1 for region abbreviations). To test whether subcortical brain regions that project to visual cortex are hyperactive, we compared c-Fos⁺ cell density in the lateral geniculate nuclei and superior colliculus and found no significant difference between hAPP and WT mice (Figure 1D, left). However, c-Fos⁺ cell density was significantly increased in the primary visual cortex. Within the primary visual cortex, we compared c-Fos⁺ cell density between hAPP and WT mice in different layers to test whether hyperactivity originates in specific layers. We found that all layers, including layer 4, which receives subcortical inputs, show hyperactivity (Figure 1D, right). We next tested whether

hyperactivity is limited to the primary visual cortex or spread out in the rest of the higher visual cortical areas. We found that c-Fos⁺ cell density was significantly higher in all higher order visual cortical areas in hAPP mice (Figure 1D, right). These results indicate that visual network hyperactivity originates in cortex in early-stage amyloidosis.

HYPERACTIVITY-ASSOCIATED SYNAPSE LOSS DEPENDS ON THE SOURCE OF PRESYNAPTIC INPUTS

Increases and decreases in synaptic density are likely to enhance or lower regional neuronal activity, respectively. We first tested whether synaptic density differs between hAPP and control mice depending on the hyperactivity state of a brain region. We performed immunolabeling for excitatory presynaptic proteins of cortical and thalamic neurons (VGluT1 and VGluT2, respectively) and inhibitory presynaptic proteins (VGAT) in two visual network regions: the primary visual cortex (hyperactive) and the dorsal lateral geniculate nucleus (non-hyperactive) (Figure 2A). We found a significant reduction in VGluT1, but not VGluT2 or VGAT densities in hAPP mice in the primary visual cortex and a similar trend of reduction in the dorsal lateral geniculate nucleus (Figure 2B-D). Excitatory synapse loss from cortical neurons may be a global feature in hAPP mice, or it may preferentially occur within broadly hyperactive visual network. To test this possibility, we compared synapse densities in another primary sensory cortex, the auditory cortex, which is neither hyperactive in hAPP mice nor part of the visual network. Consistent with the idea that excitatory synapse loss is preferentially associated with network hyperactivity, we did not observe synapse loss in the auditory cortex (Figure 2B-D). Interestingly, the primary visual and auditory cortexes exhibit similar hAPP burden at this stage despite differences in activity and synaptic adaptation (Figure 2E). These results suggest that

presynaptic loss is likely to be a network-related adaptation to hyperactivity rather than a causal or brain-wide alteration in amyloidosis.

VGluT2 in the visual cortex represents thalamic presynaptic inputs[90-92]. The lack of reduction in VGluT2 (thalamic synapses) density in the hyperactive primary visual cortex of hAPP mice suggests that the activity levels at the source (lateral geniculate nucleus) of presynaptic terminals rather than their target (visual cortex) may influence synapse loss. If this is the case, we expected that cortical synapses expressing VGluT1 in the non-hyperactive lateral geniculate nucleus in hAPP mice to be more reduced than VGluT2 expressing thalamic synapses. To test this, we normalized the synaptic density in individual hAPP mice to the average WT density for each synapse type. We found that the reduction in VGluT1 is higher than VGluT2 in both the visual cortex and lateral geniculate nucleus, though it did not reach statistical significance in the latter ($p = 0.08$; Figure 2F). These results indicate that presynaptic loss is not due to hyperactivity in their target brain regions.

HYPERCONNECTIVITY WITHIN THE VISUAL NETWORK AND ACROSS THE BRAIN IN AMYLOIDOSIS

Previous studies have shown hyperconnectivity in AD networks is associated with hyperactivity[9, 12, 22, 73]. To confirm if this is the case in hAPP mice, we compared functional connectivity, or correlated c-Fos⁺ cell densities between brain regions, both within the visual network and across the brain. Brain-wide and visual network functional connectivity matrices revealed a general increase in pairwise correlation strength between brain regions with the exception of the dentate gyrus (Figure 3A). Similar results were seen for the visual network, though the cortical correlations were high even in nonpathological condition (Figure 3B). We next filtered out regional pairwise activity correlations with a p-value > 0.05 and quantified the

number of remaining connections for each node (node degree) both across the brain and within the visual network (Fig 3C-D). We observed an average of a 1.9-fold increase in node degree, both across the whole-brain network and within the visual network.

FUNCTIONAL CONNECTIVITY IN NONPATHOLOGICAL CONDITIONS ARE PREDICTIVE OF REGIONAL HYPERACTIVITY IN AMYLOIDOSIS

Multiple brain regions in ~5-month-old hAPP mice show increased c-Fos⁺ cell density (Figure 4A). Hyperactivity may emerge independently in these brain regions or may arise through their functional connectedness with another hyperactive region. To test whether functional connectedness could contribute to hyperactivity, we next investigated whether connection strength to the primary visual cortex under nonpathological conditions is predictive of regional hyperactivity and hyperconnectivity across the brain in amyloidosis. We observed a positive brain-wide correlation between regional connection strength (measured as Pearson's r) to the primary visual cortex in the WT network and regional hyperactivity effect size in the hAPP network (Figure 4B, left). Consistently, regions with statistically significant functional connections to the primary visual cortex in WT mice displayed a higher mean effect size of hyperactivity in hAPP (Figure 4B, right). Likewise, functional connectivity strength to the primary visual cortex in the WT network trended towards positive correlation with node degrees in hAPP mice (Figure 4C, left). Consistently, regions with strong functional connections to the primary visual cortex on average formed 1.5-fold more functional connections across the brain than regions with weak or no functional connections to it (Figure 4C, right). These results indicate that functional connectivity under nonpathological conditions to a brain region that would become hyperactive in amyloid pathology partially determines their hyperactivity and hyperconnectivity phenotype in amyloidosis.

Hyperactivity of a brain region in amyloidosis may also be proportional to the number of functional connections under nonpathological conditions. Therefore, we next asked whether regions that have a higher degree of resting state functional connectivity under nonpathological conditions, both within the visual network and across the brain, are generally more at risk of becoming hyperactive in amyloidosis. To test this, we correlated the resting state node degree of each region in WT mice with the effect size of hyperactivity of the same regions in hAPP mice, both within the visual network and across all brain regions (Figure 4D). Under both conditions, we observed a significant positive correlation between node degree in the WT network and hyperactivity effect size in hAPP mice.

DISCUSSION

Here we characterize brain-wide hyperactivity at the cellular level based on immediate early gene expression and identify that visual network hyperactivity in amyloidosis stems partly from functional connectedness under nonpathological conditions. We also found that VGluT1, but not VGluT2 or VGAT expressing synapses, are reduced in both hyperactive and non-hyperactive areas of the visual network, which exhibits broad cortical hyperactivity, but not the non-hyperactive auditory cortex, which lies outside of the visual network.

Using *in vivo* imaging of excitatory and inhibitory postsynaptic structures in the visual cortex of hAPP mice, we recently found an increased ratio of excitatory to inhibitory synapses, indicating that structural synaptic changes favor visual cortex hyperactivity[1]. Therefore, we expected an increase in excitatory presynaptic structures as well. Surprisingly, we found that presynaptic structures harboring VGluT1 are reduced in the visual cortex of hAPP mice. This finding is consistent with a recent study showing reduced bouton density but unaltered postsynaptic spine density in the barrel cortex of the same mouse model[93]. Furthermore,

presynaptic terminals are more vulnerable at the initial stages of amyloid accumulation[94-101].

A reduction in bouton density but normal or elevated postsynaptic structures indicates that each presynaptic structure may be associated with multiple postsynaptic structures. Thus, early stages of amyloidosis could be associated with an increase in polysynaptic boutons. Polysynaptic boutons could reduce neuronal stimulus specificity and lead to memory interference.

Consistently, we found that stimulus specificity is reduced in hAPP mice resulting in disrupted visual recognition memory due to interference[1]. Hippocampal-dependent memory interference is also observed in a different amyloid mouse model[102].

The reduction in excitatory presynaptic density could be due to the synaptotoxic effects of amyloid[103-108]. Inhibitory synapses have also been shown to be vulnerable to amyloid toxicity, but the results are not consistent[3, 25, 109-112]. Within the excitatory synapses, we found VGluT1 to be more vulnerable than VGluT2 in amyloid pathology. One possible cause could be the higher amyloid accumulation in VGluT1-containing boutons than in VGluT2-containing boutons[113]. An alternative possibility is that VGluT1 predominantly reflects presynaptic terminals from cortical neurons[90, 91], which are hyperactive, whereas VGluT2 in the visual cortex arises from the lateral geniculate nucleus[90-92, 114, 115], which is not hyperactive. Hyperactivity alters calcium dynamics in presynaptic structures and may lead to synaptotoxicity[5, 24, 26, 27, 116-119]. Consistent with this possibility, the auditory cortex, which does not show significant hyperactivity in hAPP mice, likewise did not show VGluT1 reduction.

A reduction in VGluT1 density in the non-hyperactive lateral geniculate nucleus and normal VGluT2 density in the hyperactive primary visual cortex suggests that hyperactivity at the source of these presynaptic terminals rather than at their target may lead to synapse loss.

Therefore, we speculate that cell-intrinsic mechanisms, such as altered presynaptic calcium dynamics[5, 24, 120-123], rather than cell-extrinsic mechanisms, such as microglia-mediated synapse removal[123-127], may be involved in the hyperactivity-associated presynaptic loss. A loss in presynaptic terminals would serve to counteract hyperactivity. Consistently, hyperactive regions tend to become more hypoactive with disease progression[22, 46, 82]. Hyperactivity-induced synapse loss is consistent with the observation that functional abnormalities precede structural abnormalities in AD[128-134].

An imbalance in excitation and inhibition triggers hyperactivity. However, there is considerable heterogeneity among brain regions in disrupting these synapse types[109-111, 135-137]. The interconnected nature of brain networks allows hyperactivity to spread to multiple brain regions without requiring local synaptic disruption. Therefore, excitatory-inhibitory disruption occurring in a hub brain region, which influences the activity of many brain structures, is likely to be more consequential in the spread of hyperactivity[28, 138-142]. In AD patients, hyperconnectivity and hyperactivity are observed in resting-state functional networks[4, 45, 128, 138, 143-145]. Furthermore, hub regions are more vulnerable to amyloid accumulation and neurodegeneration[138, 139, 143, 144, 146-150]. However, when both hyperactivity and hyperconnectivity occur, it is difficult to delineate whether increased connectivity precedes hyperactivity or vice versa, though the selective vulnerability of hub regions indicates that increased connectivity predisposes circuits to a pathological state. Once a brain region becomes hyperactive, activity-dependent amyloid production could further exacerbate hyperactivity leading to hyperconnectivity [17, 151, 152], and the vicious cycle that ensues would lead to synaptic and neurotoxicity. Consistently, we found that brain regions that are highly functionally connected under nonpathological conditions tend to become more hyperactive in amyloid

pathology, indicating that high connectivity favors the spread of hyperactivity. Functional connectivity to an impaired hub region could lead to hyperactivity in a brain region even if it lacks a direct structural connection with the hub. With multiple brain regions targeted by the same hub, coactivated activity flow could occur through multiple pathways, thus increasing the likelihood of hyperactivity. The association of higher functional connectivity with hyperactivity and subsequent accumulation of amyloid and synaptic failure indicates that randomly generated transient hyperactivity in hub regions may contribute to idiopathic AD when stabilized by the aforementioned vicious cycle.

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CONFLICT OF INTEREST

The authors have no conflict of interest to report.

DATA AVAILABILITY STATEMENT

The data supporting the findings of this study are available on request from the corresponding author.

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FIGURE LEGENDS

Figure 1: Amyloidosis-associated neuronal hyperactivity emerges in cortical areas of the visual network. **A)** Representative images of 24 evenly spaced landmark slices used for brain-wide c-Fos⁺ cell density quantification. **B)** Representative image of Allen CCFv3 brain region overlay following semiautomated slice registration. **C)** Representative images of c-Fos fluorescence in the primary visual cortex of J20-hAPP mice (right) and WT littermate controls (left). The blue box is magnified below. Blue circles indicate c-Fos⁺ cells identified by automatic cell detection. Scale bar: 1mm (top), 100 μ m (bottom). **D)** c-Fos⁺ cell density across subcortical (left) and cortical (right) regions of the visual network. Data are presented as mean \pm SEM, multiple *t*-tests with Benjamini-Hochberg FDR correction for all regions combined, **q*-value < 0.05. *n* = 8 wild type (WT), 9 J20-hAPP mice.

Figure 2: Excitatory cortical synapse loss is associated with hyperactivity **A)** Representative images of synaptic immunohistochemistry labeling VGluT1 (top left), VGluT2 (top right), VGAT (bottom left), and merged channels (bottom right) in the primary visual cortex, layer 2/3. Circles indicate puncta identified by automated synapse detection. Scale bar: 5 μ m. **B-D)** Density of VGluT1 (B), VGluT2 (C), and VGAT (D) in primary visual cortex (VISp), dorsal lateral geniculate nucleus (LGD), and primary auditory cortex (AUD). **E)** Representative images of amyloid- β immunofluorescence with 6E10 antibody in the primary visual cortex (left) and auditory cortex (right). Scale bar: 100 μ m. **F)** hAPP-wild type (WT) ratio of the densities of VGluT1 and VGluT2 puncta. Data are presented as mean \pm SEM, student's *t*-tests, **p*-value < 0.05, # *p*-values between 0.05 and 0.1 displayed. *n* = 14 WT, 12 hAPP mice (primary visual cortex and auditory cortex). *n* = 13 WT, 11 hAPP mice (dorsal part of the lateral geniculate nucleus)

Figure 3: Amyloidosis increases functional hyperconnectivity across the brain and within the visual network. (A-B) Resting state functional connectivity matrices showing pairwise correlation (Pearson's r) of c-Fos⁺ activity between regions across (A) the brain and (B) the visual network for wild type (WT; left) and hAPP mice (right). Region label color indicates anatomical brain area. (C-D) Resting state functional connections (p -value < 0.05) across (C) the brain and (D) the visual network in WT (left) and hAPP mice (right). Node color indicates anatomical brain area, node size indicates degree rank. E) Node degrees of selected brain regions across the brain (left) and visual network (right). Paired t -tests, *** p -value < 0.001, **** p -value < 0.0001. $n = 8$ WT, 9 hAPP mice.

Figure 4: Brain-wide WT resting state connectivity patterns predict regional amyloidosis-induced hyperactivity and hyperconnectivity A) Effect size (Cohen's d) of hyperactivity across the brain in hAPP mice. Dotted lines at $d = 0.8$ and -0.8 . B) Correlation of each region's functional connection strength (Pearson's r) to the visual cortex from regions across the brain in the wild type (WT) network with effect size of hyperactivity in hAPP mice (left). Linear regression with 95% confidence intervals shown. Hyperactivity effect sizes of regions that are (VIS connection⁺) or are not (VIS connection⁻) functionally connected (p -value < 0.05) to the visual cortex in the WT network (right). Data presented as mean \pm SEM, Welch's t -test. C) Correlation between functional connection strength to the visual cortex in the WT network and node degrees in the hAPP network (left). Linear regression with 95% confidence intervals shown. Regions that are functionally connected to the visual cortex in the WT network show higher node degree in the hAPP network compared to regions that are not (right). Data presented as mean \pm SEM, Welch's t -test. D) Correlation between each region's node degree in WT mice and the regional effect size of hyperactivity in hAPP mice within the visual network (left) and

across the brain (right). Linear regression with 95% confidence intervals shown. *p-value < 0.05,

***p-value < 0.001, n = 8 WT, 9 hAPP mice.







