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## Lateral mammillary body neurons in mouse brain are disproportionately vulnerable in Alzheimer's disease

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### Abstract

The neural circuits governing the induction and progression of neurodegeneration and memory impairment in Alzheimer's disease (AD) are incompletely understood. The mammillary body (MB), a subcortical node of the medial limbic circuit, is one of the first brain regions to exhibit amyloid deposition in the 5xFAD mouse model of AD. Amyloid burden in the MB correlates with pathological diagnosis of AD in human postmortem brain tissue. Whether and how MB neuronal circuitry contributes to neurodegeneration and memory deficits in AD is unknown. Using 5xFAD mice and postmortem MB samples from individuals with varying degrees of AD pathology, we identified two neuronal cell types in the MB harboring distinct electrophysiological properties and long-range projections: lateral neurons and medial neurons. Lateral MB neurons harbored aberrant hyperactivity and exhibited early neurodegeneration in 5xFAD mice compared to lateral MB neurons in wildtype littermates. Inducing hyperactivity in lateral MB neurons in

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**Author Contributions:** WCH and L-HT conceived the study. WCH, MHM, and ZP designed the study and collected the data. LL performed and analyzed the slice electrophysiological data. WCH performed experiments with help from MC, ZP, XJ, HM, MHM, and FA. WCH analyzed mouse single-cell RNA sequencing data with help from HM, XJ, and FG. WCH and JDV analyzed human single-nucleus RNA sequencing data with help from XJ, AN, and HM. DAB provided human postmortem brain tissue samples with clinical and pathologic data and critically reviewed the manuscript. MK and L-HT supervised the study. WCH, MHM, ZP, and L-HT wrote the paper with critical input from all the authors.

**Competing interests:** All authors declare that they have no competing interests.

**Data and materials availability:** All data are present in the main paper or supplementary materials. Mouse MB sequencing data can be found in GEO with accession code: GSE224647. Human MB sequencing data can be found in Synapse at <https://www.synapse.org/#!/Synapse:syn50670858> using the SynID syn50670858.

wildtype mice impaired performance on memory tasks, whereas attenuating aberrant hyperactivity in lateral MB neurons ameliorated memory deficits in 5xFAD mice. Our findings suggest that neurodegeneration may be a result of genetically distinct, projection-specific cellular dysfunction, and that dysregulated lateral MB neurons may be causally linked to memory deficits in AD.

### **Accessible Summary:**

The constellation of circuit dysfunction, pathological insults, and neurodegeneration driving memory deficits in Alzheimer's disease remains poorly understood. The mammillary body, a subregion of the hypothalamus, exhibits early amyloid deposition in 5xFAD mice, which we hypothesized offered a tractable system to interrogate mechanisms of cell-type specific dysfunction regulating memory loss in Alzheimer's. Using a combination of single cell RNA-seq of mouse and post-mortem mammillary body, combined with slice electrophysiology and bidirectional circuit manipulation, we identify functional characteristics that confer disproportionate AD related vulnerability to select neurons. These results shed insight on the circuit and molecular logic of neurodegeneration.

### **One sentence summary:**

Lateral mammillary body neurons in mouse brain are disproportionately vulnerable in Alzheimer's disease and may be involved in memory loss.

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## **INTRODUCTION**

Neurodegeneration is a major cause of memory loss and cognitive impairment, but the mechanisms driving susceptibility to cell death in individual neurons of the degenerating brain are incompletely understood. Alzheimer's disease (AD) is a memory disorder pathologically characterized by extracellular deposits of amyloid plaques and neurofibrillary tangles(1–3), and evidence from human and animal studies indicates that AD impairs circuit connectivity and network function (1, 4–7). Neuronal hyperactivity, including non-convulsive seizure activity in the cortical and hippocampal networks (8–10), is evident in early stages of AD (4, 5, 11) even before amyloid plaque deposition (11, 12). Whereas neuronal hyperactivity and neurodegeneration in the cortical-hippocampal networks are associated with AD, memory systems are distributed throughout the brain (13–16), and contributions to AD dementia from deep brain regions are only vaguely characterized (17). Identifying new brain regions and cell types uniquely vulnerable to hyperexcitability, memory deficits, and neurodegeneration in AD may provide new therapeutic targets for disease-modifying treatments.

We recently examined the sequence of amyloid deposition in 5xFAD mice (18), a mouse model harboring five familial AD mutations that recapitulates AD-related cognitive and cellular dysfunctions (19). We found that the mammillary body (MB) exhibits the highest density of amyloid deposition (18). The MB is a subcortical node of the medial limbic circuit that plays a key role in memory retrieval (20, 21), and lesions in the MB result in anterograde amnesia and memory deficits (22–28). MB volume correlates with episodic memory recall in patients who underwent surgical removal of colloid cysts (25), in which

the extent of MB atrophy differs among individuals. The critical role played by the MB in memory recall is recapitulated in lesion studies in monkeys (29–31), rats (32–40) and mice (41–44). Post-mortem brain studies report amyloid deposition and neurofibrillary tangles in the MB of individuals with AD (45–47), and suggest increased MB amyloid is associated with increased likelihood of pathological AD (18). Moreover, MB synaptic alterations are observed before amyloid and neurofibrillary tangle pathology emerge (48), indicating MB synaptic deficits may be an early event leading to disease progression. Reduction of MB volume is also reported in individuals with mild AD (49). Together, these findings suggest a potential role of MB dysfunction in early stages of AD, but whether and how MB circuit dysfunction is related to AD-related cognitive decline is unclear. Here, using single cell transcriptomic profiling of mouse and human MB postmortem tissue, combined with multiple interventions in the 5xFAD mouse model of AD, we provide evidence that a class of MB neurons may be critically involved in AD memory loss.

## RESULTS

### Single cell transcriptomic profiling of mouse MB brain tissue

To define cell types in the MB of 5xFAD mouse brain, we dissected the hypothalamus, which includes the MB, for single cell RNA-seq (scRNA-seq) (fig. S1A). We pooled hypothalamus tissue from nine female C57BL/6 mice (two months old) into two samples to reduce the variability of the dissected brain regions between samples. We included 7,754 single cells for analysis, which we classified into astrocytes (expressing *Slc6a11*, *Agt*, *Slc4a4*), microglia (*Aif1*, *Csf1r*, *Cx3cr1*), neurons (*Snap25*, *Nrsn2*, *Syt4*), mature oligodendrocytes (*Mag*, *Mal*, *Mog*), oligodendrocyte precursor cells (*Pdgfra*, *Matn4*, *C1ql1*), newly formed oligodendrocytes (*Fyn*, *Gpr17*, *Bfsp2*), tanycytes (*Col23a1*, *Crym*, *Rax*), ependymal cells (*Ccdc153*, *Tmem212*, *Foxj1*), endothelial cells (*Cldn5*, *Itm2a*, *Ly6c1*), and mural cells (*Vtn*, *Higd1b*, *Ndufa4l2*) (fig. S1B, C). All major cell types included cells derived from both samples (fig. S1D). Unsupervised clustering analysis of neurons ( $n=1,382$  cells) revealed twelve clusters (Fig. 1A). We classified neurons into glutamatergic and GABAergic neurons based on the expression of genes necessary for the synthesis and packaging of glutamate and GABA (Fig. 1B) (50). To evaluate which neuronal clusters represented MB neurons, we first determined whether MB neurons are glutamatergic or GABAergic using RNA in situ hybridization of *Slc17a6* and *Slc32a1*. We found expression of *Slc17a6* and the absence of *Slc32a1* in the mouse MB (Fig. 1C), indicating that the MB is composed of glutamatergic neurons, consistent with previous observations in rats (51, 52). Among the five glutamatergic neuronal clusters, the top marker genes for clusters 4 and 11 were detected in the MB (Fig. 1D), but the other clusters were not (fig. S2A), suggesting that clusters 4 ( $n=154$  cells) and 11 ( $n=47$  cells) represented two separate neuronal cell types in the MB. We found the top marker genes for these two clusters (*Rprm* and *Tac2*) labeled neurons in anatomically discrete MB subregions, the medial MB and lateral MB (Fig. 1D). The expression profiles of lateral and medial MB clusters revealed multiple discriminatory marker genes: medial MB marker genes included *Rprm*, *Cck*, *Cartpt*, *Lhx1os*, and *Foxb1*, whereas lateral MB marker genes included *Tac2*, *Prlr*, *Esr1*, *Nr4a2*, and *Pdyn* (Fig. 1E). To interrogate the functional differences between these two types of neurons, we performed Gene Ontology (GO) enrichment analysis. The top GO terms for medial MB neurons

were associated with ion channel activity (fig. S2B), whereas those for lateral MB neurons included structural constituents of ribosomes (fig. S2C). These observations suggest the two types of MB neurons may feature different electrophysiological properties and require specific metabolic demands. To confirm the transcriptional subtype of MB neurons, we micro-dissected the MB and repeated scRNA-seq in wildtype (WT) and 6-month-old 5xFAD mice (fig. S3). We again found consistent evidence for lateral and medial MB neurons in the microdissected MB dataset in both WT and 5xFAD mice (fig. S3). Collectively, these findings indicate that neurons of the MB harbor two distinct neuronal subtypes.

### Two MB neuron subtypes are distinguished by morphology, projection targets, and neuronal activity patterns

Given that the two types of MB neurons were located in anatomically defined subregions, we characterized their morphology, projections, and neuronal activity patterns. To quantify neuronal morphology, we retro-orbitally injected AAV-PHP.eB-CAG-tdTomato (53) into female 2 month-old C57BL/6 mice to sparsely label MB neurons. We found that the soma of lateral MB neurons was significantly ( $p = 0.0016$ ) larger than that of medial MB neurons (Fig. 2A, B). Given that metabolic activity is associated with cell size (54, 55), this observation was consistent with our finding that lateral MB neurons harbored elevated expression of genes associated with metabolic activity and protein synthesis compared to medial MB neurons (fig. S2C).

Given the differences in lateral and medial MB neuronal soma size, we wondered whether these neuronal types harbored different electrophysiological properties. Using cell-attached patch-clamp recordings, we found that medial MB neurons fired more action potentials than did lateral MB neurons (Fig. 2C). The spontaneous firing rate was ~11 Hz for medial MB neurons and ~0.2 Hz for lateral MB neurons (Fig. 2D). The action potential threshold was much lower and the width of action potentials was much shorter in medial MB neurons compared to lateral MB neurons, whereas input resistance, resting membrane potential, and overshoot were not different between the two cell types (Fig. 2E). Action potentials are tightly regulated by sodium and potassium ion channels (56), and many genes encoding these channels, including subunits of sodium channels (*Scn1a*, *Scn1b*) and potassium channels (*Kcna2*), were enriched in medial MB neurons compared to lateral MB neurons (Table S1). Transcripts related to ion channels may therefore be responsible for the increased firing rate of medial compared to lateral MB neurons.

To examine the projection patterns of medial and lateral MB neurons, we began by using anterograde tracing. After injecting AAV8-CAMKII-eGFP into female 2 month-old C57BL/6 mice MB (Fig. 2F), we found abundant axonal eGFP signals in the anterior thalamus (Fig. 2G) and the tegmental nuclei of Gudden (Fig. 2H and I), consistent with previous neural tracing studies in rats and monkeys (51, 52, 57–59). To evaluate whether lateral and medial MB neurons project to distinct brain regions, we performed retrograde tracing using cholera toxin subunit b (CTB), a recombinant protein that binds to ganglioside GM1 and mediates retrograde axonal transport, thereby labeling presynaptic neurons (60). Fluorophore conjugated-CTB injected into the medial and ventral (but not dorsal) regions of the anterior thalamus labeled presynaptic neurons in the medial (but not lateral)

mouse MB (Fig. 2J and K). In contrast, CTB injected into the anterior dorsal thalamic nucleus (one hemisphere), labeled presynaptic neurons located in the lateral MB in both hemispheres (Fig. 2L and M), suggesting that lateral MB neurons project both ipsilaterally and contralaterally to the anterior dorsal thalamic nucleus. We also found medial and lateral MB neurons project to distinct nuclei within the tegmental nuclei of Gudden (fig. S4). These observations indicate that medial and lateral MB neurons project to distinct brain regions.

### **Lateral MB neurons in 5xFAD mice are more vulnerable to neurodegeneration compared to medial MB neurons**

Based on our observations that lateral and medial MB neurons are distinct from one another across multiple dimensions, we hypothesized they may be asymmetrically affected by AD. To explore this possibility, we used scRNA-seq from female 6-month-old 5xFAD mice and WT littermates, a time point when these mice suffer memory impairments (19). We pooled posterior hypothalamus from four mice into one sample as one replicate and collected a total of three replicates per genotype (5xFAD and WT). We annotated 16,213 cells into major brain cell types (fig. S4C and D), which were represented across biological replicates (fig. S5E) and genotype (fig. 3C, fig. S6). We confirmed our observation that lateral and medial MB neurons harbor distinct markers (Fig. 3A), including *Tac2* as a lateral MB neuronal marker and *Rprm* as a medial MB neuronal marker (Fig. 3B).

To explore if medial and lateral MB neurons are differentially vulnerable to degeneration in 5xFAD mice, we performed in situ hybridization for MB marker genes in 6-month-old 5xFAD mice and WT control littermates. The density of *Tac2* neurons, a marker of lateral MB neurons, was reduced in 5xFAD mice (Fig. 3D and E), whereas the density of *Rprm* neurons, a marker of medial MB neurons, was not altered between genotypes (Fig. 3F and G). We also found reduced expression of the NeuN marker in lateral but not medial MB neurons of 6-month-old 5xFAD mice compared to WT littermates using immunohistochemistry (fig. S7). Furthermore, using stereological techniques and markers for lateral and medial MB neurons (*Tac2* and *Rprm*, respectively), we found reduced lateral MB neuronal density in 6-month-old 5xFAD mice compared to age-matched WT littermates (fig. S8). Collectively, these results suggest lateral MB neurons may be differentially vulnerable to neurodegeneration compared to medial MB neurons in 6-month-old 5xFAD mice.

To gain insights into the potential mechanisms underlying differential degeneration of lateral MB neurons, we compared the transcriptomes of lateral MB neurons between WT and 5xFAD mice. Enriched GO terms for genes upregulated in 5xFAD lateral MB neurons were related to neuronal death (including positive regulation of neuron death, neuron apoptotic process, and regulation of programmed cell death) and synaptic activity (including regulation of synaptic transmission, regulation of neurotransmitter concentrations, and synaptic signaling) (Fig. 3H). We found these terms were not enriched in medial MB neurons (fig. S9). To determine whether lateral MB neuronal dysfunction was unique to MB or shared with other brain regions, we analyzed a previously published snRNA-seq dataset from 7-month old mouse 5xFAD hippocampus (61). We found that genes expressed in the lateral MB neurons were not differentially expressed in the 7-month-old 5xFAD

hippocampus (fig. S10), potentially suggesting lateral MB neurodegeneration is associated with a unique transcriptomic state that is not necessarily associated with a brain-wide signature of neurodegeneration associated with the 5xFAD genotype.

### Single-nucleus RNA profiling of human postmortem MB samples

To explore whether MB neuron subtypes we identified in mice are conserved in humans, we performed snRNA-seq of postmortem MB samples from 32 individuals in the Religious Order Study or the Rush Memory and Aging Project (ROSMAP), two longitudinal cohort studies of aging and dementia. Information collected in ROSMAP cohorts included clinical data, detailed postmortem pathological evaluations, and multi-omics tissue profiling (62). We selected 13 individuals with AD pathology (8 females and 5 males) (fig. S11A) based on multiple consensus metrics of pathology and 19 individuals as non-AD controls (11 females and 8 males). We did not observe differences in education, age of death, sex, post-mortem interval, fixation interval, and co-morbidities between groups (fig. S11C–H). We confirmed the major differences between the two groups were amyloid burden (fig. S11I) and neurofibrillary tangles (fig. S11J) based on consensus metrics quantifying pathology across multiple brain regions, including hippocampus and multiple cortical regions. Although we cannot rule out the possibility that other pathologies may have influenced our results, these findings suggest that the major differences between the pathologies of our snRNA-seq cohort were due to tau and amyloid. In total, we analyzed 136,636 nuclei in MB samples from 32 individuals, which stratified into major brain cell types, including neurons (expressing *SYT1*, *SNAP25*, *SYP*), astrocytes (*GFAP*, *AQP4*, *GJA1*), microglia (*CSF1R*, *CD74*, *C3*), oligodendrocytes (*MOBP*, *MOG*, *CNDP1*), oligodendrocyte precursor cells (*VCAN*, *MEGF11*, *PDGFRA*), and vascular cells (*FLT1*, *CLDN5*, *PDGFRB*) (fig. S12A).

Within neurons, we identified three major neuronal cell types, of which two expressed glutamatergic markers (*SLC17A6*) and one expressed GABAergic markers (*SLC32A1*, *GAD1*, and *GAD2*) (Fig. 4A and B). To test whether specific neuronal clusters corresponded to the lateral and medial MB neurons we found in mice, we calculated the enrichment score from the aggregation of the top 15 marker genes identified in the mouse lateral and medial MB neuron clusters (fig. S13A). We found distinct neuronal clusters corresponded to the mouse lateral MB (Fig. 4C, fig. S13C–E) and medial MB (Fig. 4D). RNAscope of the human postmortem MB samples revealed that the mouse lateral MB neuron marker gene *KCNC2* was expressed exclusively in lateral MB neurons in human tissue, and the mouse medial MB neuron marker gene *FOXBI* was expressed exclusively in medial MB neurons in human tissue, indicating that mouse medial and lateral MB neuronal marker genes are conserved in humans (fig. S14). We also identified a neuronal cell type marked by *RELN* expression, which we confirmed using in situ hybridization (fig. S12B), that we did not observe in mouse, potentially representing a rare MB neuronal subtype that may be unique to human MB compared to mouse MB.

Mouse lateral and medial MB neurons generated distinct firing patterns in our slice electrophysiology experiments, which was reflected by their differential expression of ion channel transcripts. Enriched GO terms for differentially expressed genes (DEGs) between human lateral and medial MB neurons were also associated with ion channel activity (Fig.

4E). As expected, compared to human lateral MB neurons, human medial MB neurons harbored higher expression of the genes encoding the subunits of ion channels, including *SCN1A*, *SCN1B*, *KCNA2*, and *HCN1* (Fig. 4F and G), potentially suggesting that distinct spiking properties of medial and lateral MB neurons might be conserved across mice and humans.

To determine whether human lateral MB neurons also upregulate genes associated with synaptic activity in individuals with AD as we observed in 5xFAD mice, we performed DEG analysis between MB samples from individuals with AD pathology and non-AD controls. Individuals with AD pathology showed upregulation of genes related to synaptic activity in human lateral MB neurons (Fig. 4H), such as *SCN7A* (voltage-gated sodium channel), *NSG1* (neuronal vesicle trafficking protein), *ATPIA2* (a ATPase Na<sup>+</sup>/K<sup>+</sup> transporter subunit), *SYT4* and *SYT11* (synaptotagmins), *CACNA1E* (voltage-gated calcium channel), *GRID1* (glutamate ionotropic receptor), and *GRM8* (glutamate metabotropic receptor), *NPTXR* (neuronal pentraxin receptor), *VDAC1* and *VDAC3* (voltage dependent anion channels), *CALY* (calcyon neuron-specific vesicular protein), *SV2A* (a synaptic vesicle glycoprotein), *SLC17A6* (vesicular glutamate transporter) (Fig. 4I). This observation suggests lateral MB neurons may become more active in individuals with AD compared to non-AD controls.

To further resolve transcriptomic responses to AD in human MB samples, we identified sub-clusters within medial and lateral MB neurons (Fig. 4J). Lateral MB neurons clustered into two subpopulations (Fig. 4J), one of which showed enrichment for GO terms associated with cellular stress responses (including unfolded protein binding, ubiquitin protein ligase binding, and electron transfer activity) (Fig. 4K–L). Overrepresentation analysis revealed that individuals with AD pathology were overrepresented in this cluster (Fig. 4M). Together, these findings suggest that human lateral MB neurons mount a unique stress-associated transcriptional response to AD compared to medial MB neurons. In situ hybridization of human MB samples further confirmed that individuals with AD pathology harbored increased expression of *CALY* (Calcyon Neuron Specific Vesicular Protein) (fig. S15) and *SYT11* (Synaptotagmin-11) (fig. S16) in the lateral MB compared to individuals with no AD pathology. These results suggest the lateral MB neurons in AD individuals and 6-month-old 5xFAD mice harbored similar gene expression signatures related to neuronal hyperexcitability and cellular stress (64–66). To directly test whether lateral MB neurons degenerate in individuals with AD, we performed RNA in situ hybridization of the lateral MB marker gene *TAC3*, the human homologue of the rodent *Tac2*, and quantified *TAC3* cells in the postmortem MB samples of individuals with AD pathology. We found that the number of *TAC3* cells in the MB was reduced in individuals with AD pathology compared to no pathology (Fig. 4 N and O). These findings suggest lateral MB neurons exhibit degeneration in individuals with AD, similar to our observations in the 5xFAD mice.

### **LM neurons of 5xFAD mice become hyperactive in an age-dependent manner**

Our transcriptional findings in both mice and humans suggested that lateral MB neurons increase neuronal firing in AD compared to medial MB neurons. To directly test this hypothesis, we used electrophysiology and recorded lateral and medial MB neurons in





fear conditioning. Training comprised five tone-interval-shock sequences (15s tone + 30s interval + 1s shock) and fear memory recall was tested 24 hours later. Gq-expressing mice showed reduced freezing compared to control mice during the recall tests (Fig. 6E). The effect of chemogenetic inhibition on memory performance was not confounded by changes in anxiety or motor activity measures because we found no difference in freezing behavior in the pre-tone habituation period (fig. S18). Although we cannot rule out the possibility that non-lateral MB neurons may have been affected by our viral strategy and contributed to memory deficits, these observations suggest that lateral MB neuronal hyperactivity may be sufficient to induce memory deficits.

Next, we tested whether reducing activity in lateral MB neurons of 5xFAD mice could ameliorate memory deficits. We used the anti-epileptic drug levetiracetam to attenuate the increased activity of lateral MB neurons in female 6-month-old 5xFAD mice. Levetiracetam is known to treat seizures by reducing neuronal activity in part by binding to SV2A, a synaptic vesicle glycoprotein (69–72). We found that the expression of *SV2A* was elevated in individuals with AD pathology as well as in 5xFAD mice in the corresponding human and mouse lateral MB neuronal clusters (Fig. 6F, G). In situ hybridization of *Sv2a* and *Tac2* further revealed that the intensity of *Sv2a* puncta in *Tac2* neurons in the lateral MB was increased in 6-month-old 5xFAD mice (Fig. 6H, I). Bath application of 1 $\mu$ M levetiracetam to 5xFAD mouse brain slices reduced lateral MB neuronal spiking activity 5xFAD (Fig. 6J), as the frequency of spontaneous action potentials was decreased after the application of levetiracetam (Fig. 6K). To test if reducing lateral MB neuronal activity rescued memory deficits in female 6-month-old 5xFAD mice, we delivered levetiracetam specifically into the lateral MB via a bilateral cannula (Fig. 6L). We infused levetiracetam daily for 7 days before behavioral testing, and on the day of behavioral testing, levetiracetam was infused 1 hour before the tests. We again used spontaneous alternation in the Y maze task and trace fear conditioning tests in which 5xFAD mice show deficits by 6 months of age (19, 73). In the Y maze task, we found that while 5xFAD mice receiving vehicle alternated in ~51% of the trials, less than WT control littermates receiving vehicle (~72%), 5xFAD mice receiving levetiracetam alternated in ~69% of the trials (Fig. 6M). In the trace fear conditioning tests, the freezing percentage of 5xFAD mice receiving vehicle was reduced compared to that of WT control littermates receiving vehicle, and levetiracetam rescued this deficit (Fig. 6N). Additionally, we found levetiracetam attenuated the intensity of *Sv2a* puncta in *Tac2* neurons in the lateral MB neurons to WT levels, suggesting the transcriptional signature relating to neuronal hyperactivity was also alleviated by levetiracetam (fig. S19). Although we cannot rule out effects of levetiracetam on other cell types, we found levetiracetam had no effect on the firing activity of medial MB neurons (fig. S20), suggesting the effect of levetiracetam on memory within the MB was due to changes in lateral MB neurons. Together, these observations provide evidence that hyperactivity of lateral MB neurons contributes to memory deficits, and that manipulating lateral MB neuronal activity may represent a therapeutic strategy to improve cognition in AD.

## DISCUSSION

The mechanisms predisposing individual neuronal circuits to degeneration in the AD brain are poorly understood. One possibility is that aging neurons die in a stochastic,

erratic manner. A competing possibility—one with critical therapeutic implications—is that specific neurons become vulnerable to degeneration in a predictable manner based on a convergence of genetic identity, anatomic connectivity, and cellular milieu. Here, we found that the MB contains two neuronal cell types with distinct molecular markers, neuronal morphology, long-range projection targets, and electrophysiological properties. The transcriptional profiles of the two types of MB neurons were conserved across mice and humans. Lateral MB neurons upregulated genes associated with neuronal activity in both an AD mouse model and postmortem human brain tissue with AD pathology compared to non-AD controls. Lateral MB neurons—but not medial MB neurons—exhibited age-dependent progression of neuronal hyperactivity in 5xFAD mice. Increasing spiking activity in lateral MB neurons of WT mice impaired performance in two tests of memory, and selectively reducing lateral MB neuronal hyperactivity in 5xFAD mice rescued memory deficits, suggesting that lateral MB neuronal hyperactivity is both necessary and sufficient to drive memory deficits.

Previous studies suggest that neurodegeneration in the cerebral cortex and subiculum is not observed before 9 months of age in 5xFAD mice (19, 74). Our findings suggest lateral MB neurons degenerate as early as 6 months of age in 5xFAD mice, potentially one of the earliest brain regions to degenerate in this AD mouse model 5xFAD. These findings more broadly suggest some neuronal types may harbor distinct cellular properties, including circuit connectivity and cell-autonomous properties, that increase their risk for dysfunction and degeneration. The asymmetric reduction of neurons in the MB may induce desynchronized circuit assembly and brain-wide network dysfunction. Loss of lateral MB neurons may also redirect MB presynaptic inputs to the remaining lateral MB neurons, leading to excessive synaptic connections and neuronal hyperactivity. Indeed, our data indicate that lateral MB neurons increased spontaneous firing frequency in 5xFAD mice, suggesting lateral MB neurons might receive more excitatory presynaptic inputs in 5xFAD mice compared to control littermates. Given that behavioral deficits in 5xFAD mice do not emerge until ~6 months of age (19), lateral MB neuronal hyperactivity may critically induce memory deficits. Reducing lateral MB neuronal hyperexcitability in 6-month-old 5xFAD mice using levetiracetam rescued memory deficits. Of note, levetiracetam reduced neuronal hyperactivity in lateral MB neurons, but did not affect the firing of medial MB neurons, suggesting that levetiracetam may correct pathological hyperactivity without affecting physiological neuronal firing, making it a potential approach to treat AD associated with neuronal hyperactivity (75–77).

Our study has several limitations. We acknowledge that some of our behavioral data had broad overlap between groups and therefore the subtle changes observed should be interpreted with caution. However, transcriptomic overlap between mouse and human MB neuronal populations suggest increased neuronal activity in lateral MB neurons may represent an inflection point in the progressive loss of memory in AD. We found upregulation of neuronal activity in 5xFAD LM neurons at 2 months and 6 months of age compared to age-matched wildtype littermates, and we also found upregulation of LM neuronal activity in Tau P301S mice at 9 months of age compared to age-matched wildtype littermates, and additional models may be helpful to further test the effect of age, genotype, and AD pathology on neuronal activity in MB neurons. Additionally, while

the primary goal of our study was to explore contributions of MB neuronal heterogeneity to AD pathology and memory dysfunction, we did not elucidate the cellular mechanisms linking neuronal hyperactivity to cell death. Hyperactivity may be associated with DNA damage and a cellular state leading to neuronal senescence (78). Furthermore, pinpointing how subtypes of MB neurons are coordinated within broader medial limbic memory circuits might contribute to additional insight into memory impairments in AD. Further defining hypothalamic neurons (79–83) might help to unravel the complex physiology of hypothalamic contributions to memory deficits in AD, particularly given that lesion studies suggest the MB governs spatial working memory, navigational memory, and episodic memory (35). Future studies using transgenic mouse lines to specifically label distinct MB neuronal subtypes will enable the exploration of functional contributions of each subtype to particular aspects of learning, memory, and cognition. For example, previous studies have found head-direction and angular-velocity cells in the LM (84, 85), and our study provides a strategy to test their functional contributions to specific memory processes. Collectively, our data suggest that subcortical contributions to memory may play important roles in AD and neurodegeneration.

## MATERIALS AND METHODS

### Study design

The goal of this study was to define the cellular heterogeneity of the mammillary body (MB) in mouse brain and its possible roles in regulating memory in AD. We used scRNA-seq to define the cell types of the MB in WT mice. 5XFAD (Tg 6799) breeding pairs were acquired from the Mutant Mouse Resource and Research Center (MMRRC) (Stock No. 034848-JAX). 5XFAD mice were crossed with WT mice to generate offspring for this study. All animal experiments were conducted in accordance with NIH guidelines and were approved by The Committee for Animal Care of the Division of Comparative Medicine at the Massachusetts Institute of Technology. Female mice were used in the study, unless otherwise specified. Two-month-old WT (C57BL/6: JAX Stock No. 000664) mice were used for initial single cell RNA sequencing (scRNAseq). Six-month-old 5XFAD and littermate control mice were further used for scRNAseq and the subsequent validation experiments. Mice for slice electrophysiology contains both 2-month-old and 6-month-old 5XFAD and littermate control. To compare differences in MB neurons in AD, we performed scRNAseq of 6-month-old 5xFAD mice versus WT littermates and snRNA-seq in postmortem MB samples from individuals with varying stages of AD pathology. For human sequencing experiments, postmortem samples were processed in batches that included both AD and non AD pathology in case of batch effects. Our human mammillary body single nuclei RNA sequencing dataset contained a total of 32 individuals from the Religious Order Study (ROS) or the Rush Memory and Aging Project (MAP), two longitudinal cohort studies of aging and dementia. The studies include clinical data collected annually, detailed postmortem pathological evaluation, and extensive genetic, epigenetic, transcriptomic, proteomic, and metabolomic bulk-tissue profiling (62). ROSMAP data and biospecimens can be requested at [www.radc.rush.edu](http://www.radc.rush.edu). Details of the clinical and pathological data collection methods has been previously reported (87–91). Informed consent was obtained from each subject, and the ROSMAP were approved by an Institutional Review Board (IRB) of Rush University

Medical Center. Further, all participants signed a repository consent to allow their data and biospecimens to be repurposed. NIA-Regan pathologic diagnosis of intermediate- or high-likelihood was used to dichotomize individuals pathologic AD or not pathologic AD. This study contains 13 individuals with AD-pathology (8 females and 5 males) and 19 individuals with no-pathology (11 females and 8 males). AD-pathology and no-pathology groups were balanced for years of education and age of death. Inclusion criteria for AD diagnosis included multiple metrics of AD pathology.

We characterized distinct neuronal populations of the MB in mouse and human brain using histology. Based on our observation that lateral MB neurons are associated with hyperactivity in AD using slice electrophysiology and single cell transcriptomic profiling, we manipulated lateral MB neurons in WT and 5xFAD mice. For all studies, mice were controlled by age and sex across groups. For sequencing, immunohistochemistry, and RNAscope, all groups were processed, stained, and imaged at the same time. Imaging quantification was carried out in a blinded fashion by a researcher who did not perform the imaging, and no mice were excluded from analysis.

### Statistical analysis

Prior studies using similar experiments or power analysis were used to determine sample size. Student t-tests (two-sided) were used for comparison between two groups (e.g., lateral versus medial MB; WT versus 5xFAD). One-way analysis of variance (ANOVA) was used in experiments containing more than two groups. Tukey's post hoc tests were used where appropriate. Two-way analyses of variance (ANOVAs) were used in experiments containing two variables (genotypes and ages). All statistics, except single cell RNA sequencing analysis, which was performed using R, were performed using GraphPad Prism, with significance set at  $p < 0.05$ . Throughout the paper, values represent means; error bars indicate SEMs; N refers to biological replicates. Only positive statistics were reported. All measurements and testing were performed blind to the genotypes or experimental manipulations.

### Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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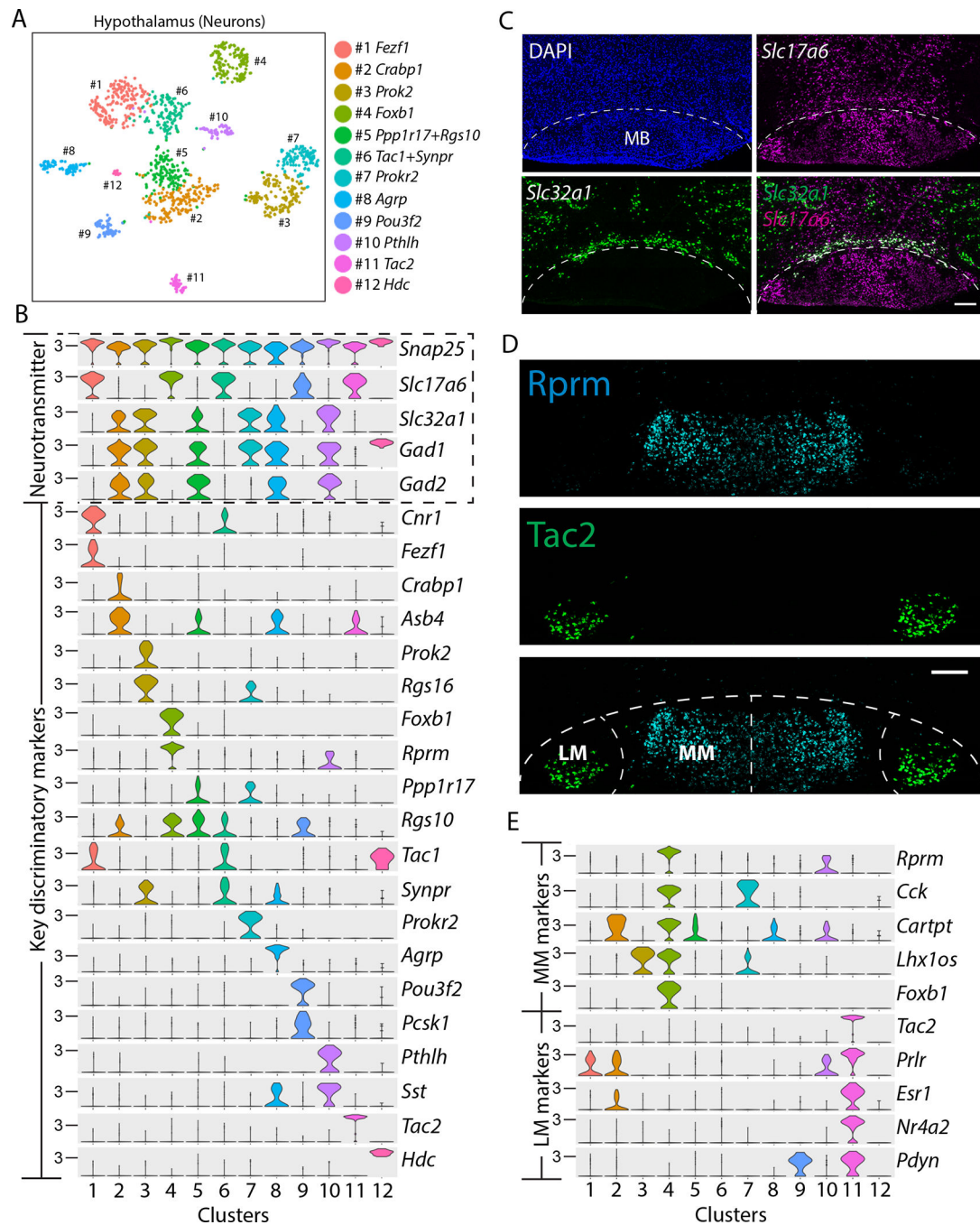
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**Figure 1. Single cell transcriptomic analysis reveals two anatomically distinct neuronal cell types in the MB.**

(A) A tSNE plot shows 12 clusters of neuronal subtypes in the hypothalamus of C57BL/6 mice. (B) Violin plots demonstrate the expression of the pan-neuronal gene (*Snap25*), glutamatergic marker gene (*Slc17a6*), GABAergic marker genes (*Slc32a1*, *Gad1*, and *Gad2*), and the key discriminatory genes in each neuronal cluster. (C) Confocal images of WT mouse brain show in situ hybridization of *Slc17a6* (vesicular glutamate transporter 2; magenta) and *Slc32a1* (vesicular GABA transporter; green) in the mammillary body (MB), with DAPI nuclear stain (blue). The dotted line outlines the boundary of the MB. Scale bar:

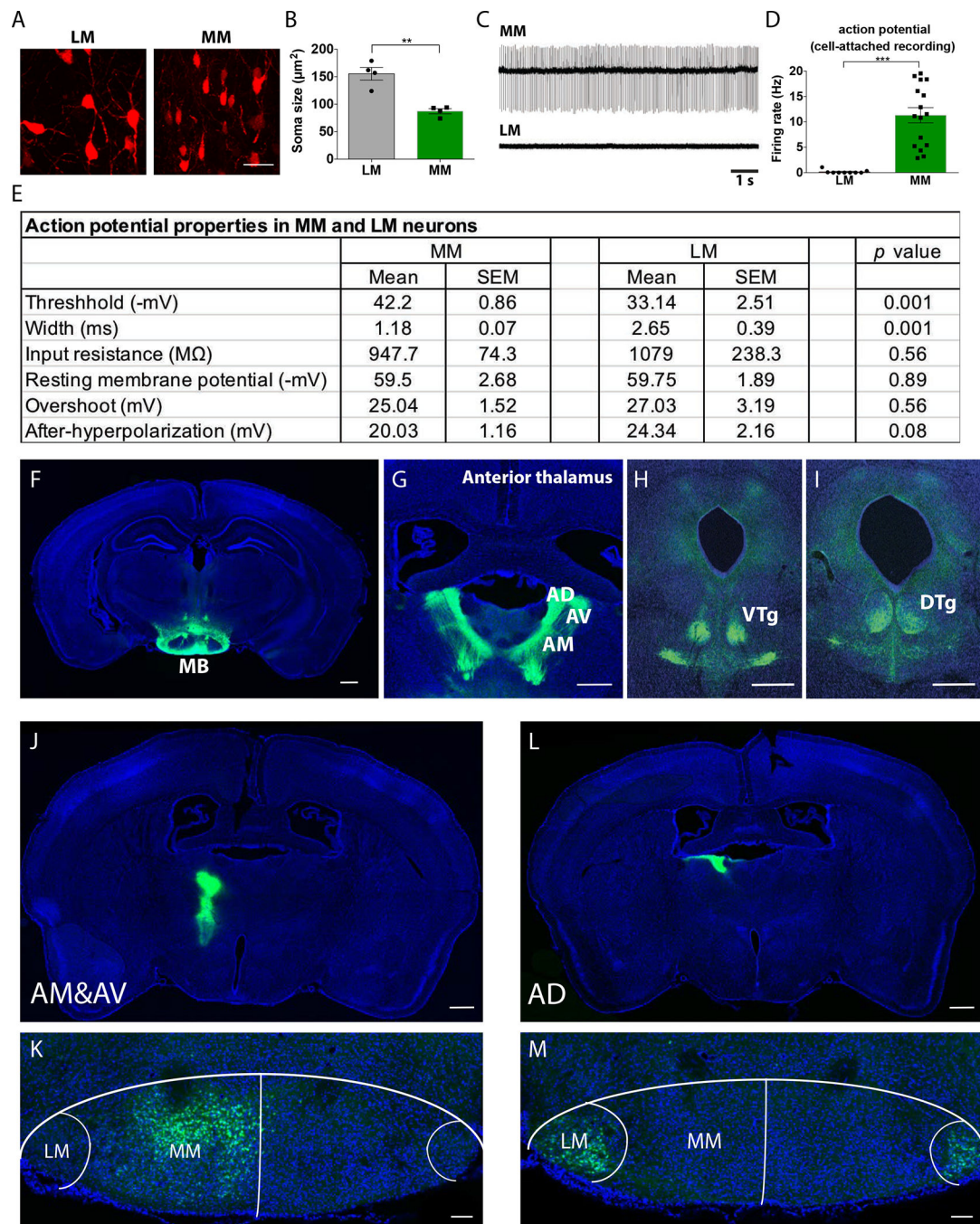
200 $\mu$ m. (D) Confocal image of in situ hybridization of *Tac2* (green) and *Rprm* (cyan) in the MB of WT mice. The dotted line outlines the boundary of the lateral MB (LM) and medial MB (MM). Scale bar: 200 $\mu$ m. (E) Violin plots show the expression of top marker genes for MM (cluster 4) and LM (cluster 11).

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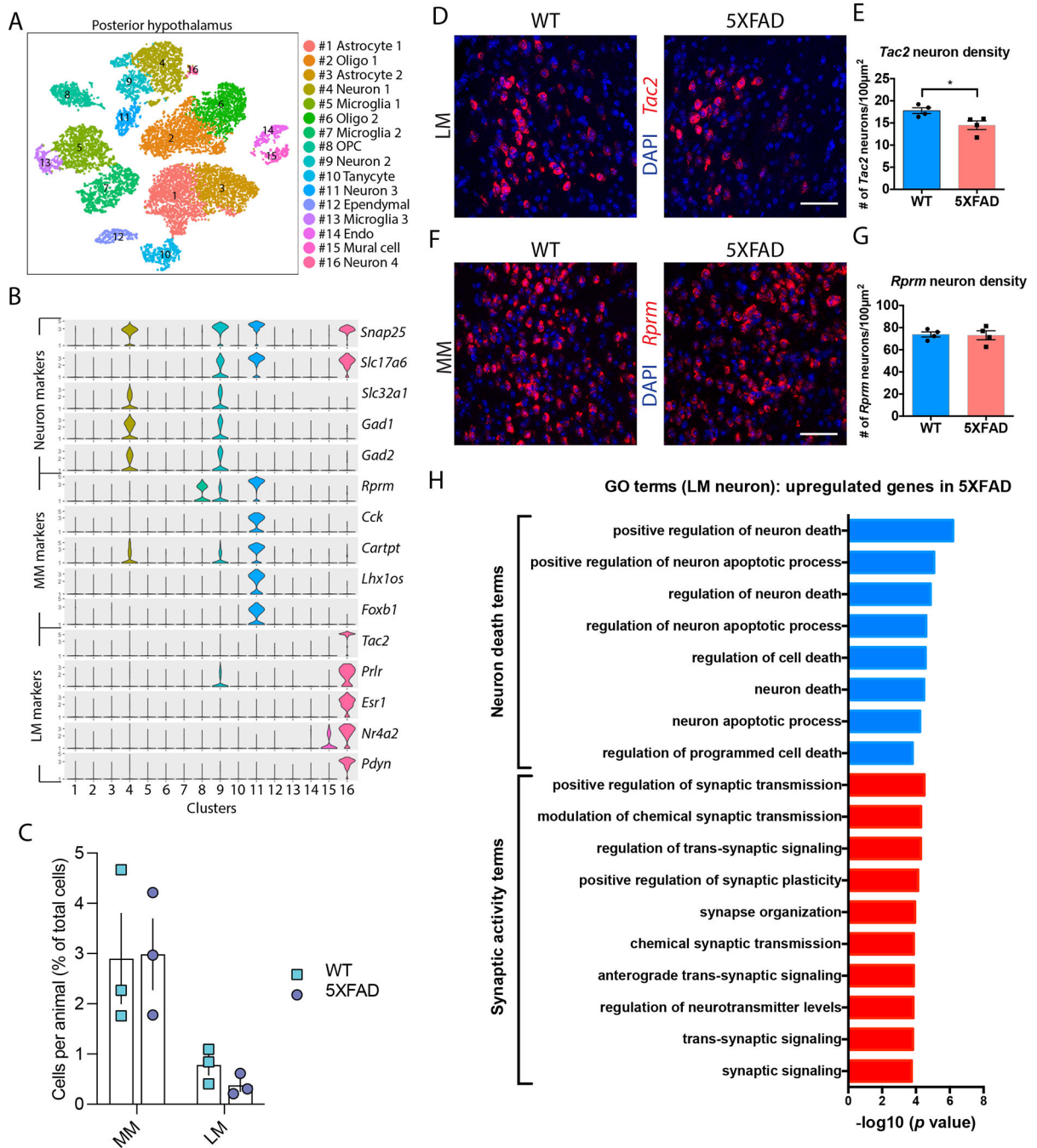
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**Figure 2. Lateral and medial MB neurons exhibit distinct morphology, electrophysiological properties, and projection targets.**

(A) Confocal images of mCherry labelled neurons (red) in the lateral mammillary body (LM) and the medial mammillary body (MM) are shown. Scale bar: 25μm. (B) Cell soma size for neurons in the LM and MM was measured.  $t(6)=5.506$ ,  $p=0.0015$ .  $**p<0.01$  (Unpaired t-test).  $n=4$  mice per group. (C) Representative action potential traces of neurons located in the MM or LM of WT mice. (D) Action potential firing rate for medial MB neurons (MM) and lateral MB neurons (LM) was quantified.  $t(23)=5.490$ ,  $p<0.0001$ ,  $***p<0.0001$  (unpaired t-test).  $n=9$  for LM and  $n=16$  for MM neurons. (E) Action potential

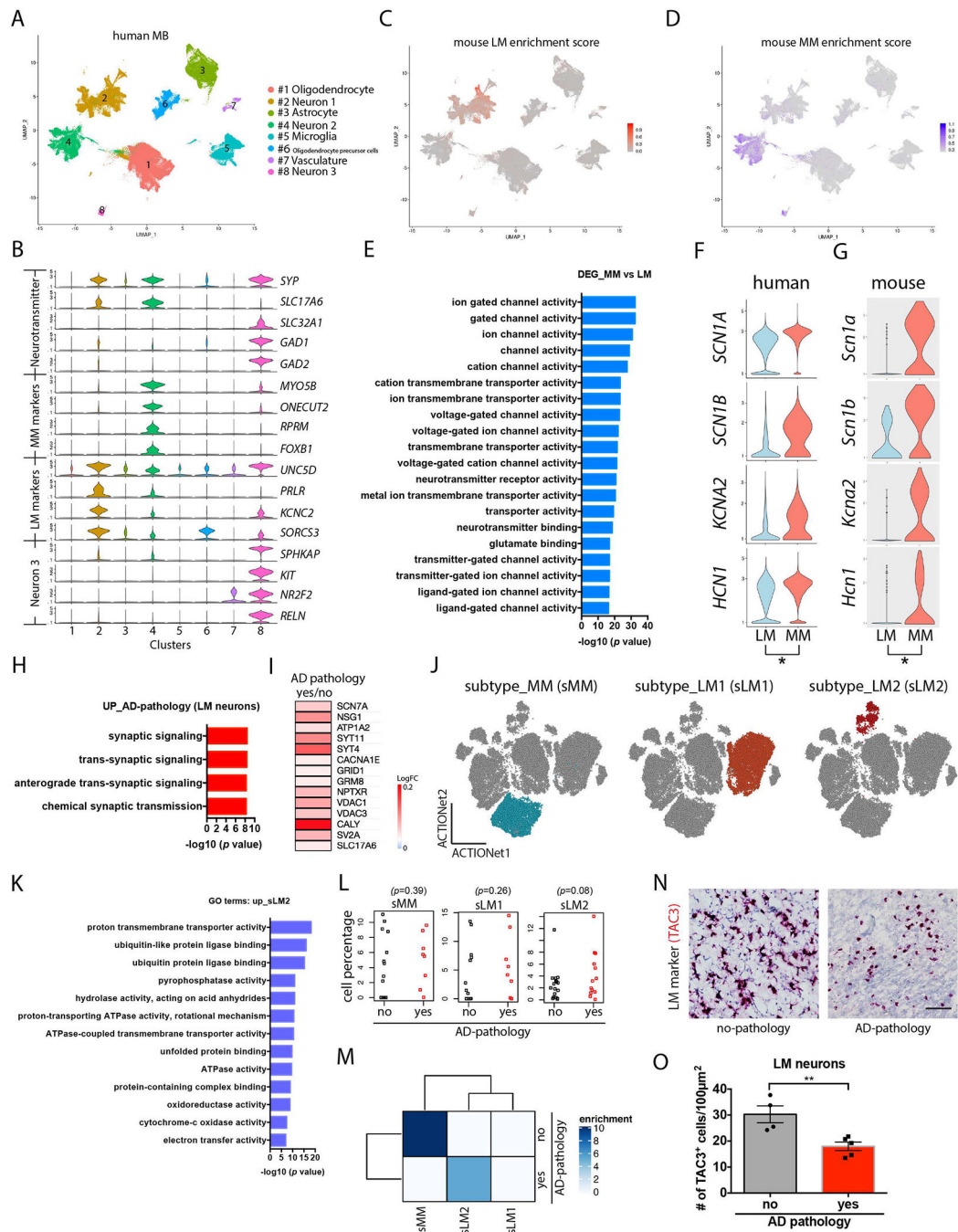
properties of MM and LM neurons are shown. n=10–12 cells per group (p values are shown; unpaired t-test). (F-I) Mouse brain images show (F) the mammillary body (MB) projecting to (G) the anterior thalamus, including the anterior dorsal (AD), anterior medial (AM), and anterior ventral (AV) thalamic nuclei, (H) ventral tegmental nuclei (VTg), and (I) dorsal tegmental nuclei (DTg) following AAV8-CAMKII-eGFP injection to MB. DAPI stain (blue), and eGFP (green). Scale bar: 500 $\mu$ m. (J-M) Alexa 488 (green) conjugated cholera toxin B (CTB) was injected into (J) anterior medial (AM) and anterior ventral (AV) thalamic nuclei and (L) anterior dorsal (AD) thalamic nuclei of WT mouse brain. CTB labeled neurons (green) were located in (K) the medial MB (MM) and (M) the lateral MB LM of mouse brain slices. Hoechst stain, blue. For panels J and L, scale bar: 500 $\mu$ m; for panels K and M, scale bar: 100 $\mu$ m.



**Figure 3. Lateral MB neurons are vulnerable to neurodegeneration in 5xFAD mice.** (A) A tSNE plot shows 16 cell clusters composed of cells derived from the posterior hypothalamus of brains from WT and 5xFAD mice. (B) Violin plots show markers for glutamatergic and GABAergic neurons and markers for medial MB neurons (MM) and lateral MB neurons (LM). Cluster 11 and cluster 16 show enrichment for MM and LM markers, respectively. (C) Number of cells per hypothalamus as a percent of total cells recovered (n=3 mice per group; two-way ANOVA). (D) Confocal images show in situ hybridization of *Tac2* (red) in the lateral MB of WT and 5xFAD mice at 6 months of age;

DAPI stain (blue). Scale bar: 50 $\mu$ m. (E) Quantification of *Tac2* positive cells in the lateral MB (LM) of 6-month-old WT and 5xFAD mice.  $t(6)=2.81$ ,  $p=0.0308$ ,  $*p<0.05$  (unpaired t test).  $n=4$  mice per genotype. (F) Confocal images show in situ hybridization of *Rprm* (red) in the medial MB of WT and 5xFAD mice at 6 months of age; DAPI stain (blue). Scale bar: 50 $\mu$ m. (G) Quantification of *Rprm* positive cells in the medial MB (MM) of 6-month-old WT and 5xFAD mice.  $n=4$  mice per genotype. (H) Gene Ontology (GO) term enrichment for genes upregulated in 5xFAD compared to wildtype mouse brain lateral MB neurons (LM, cluster 16).

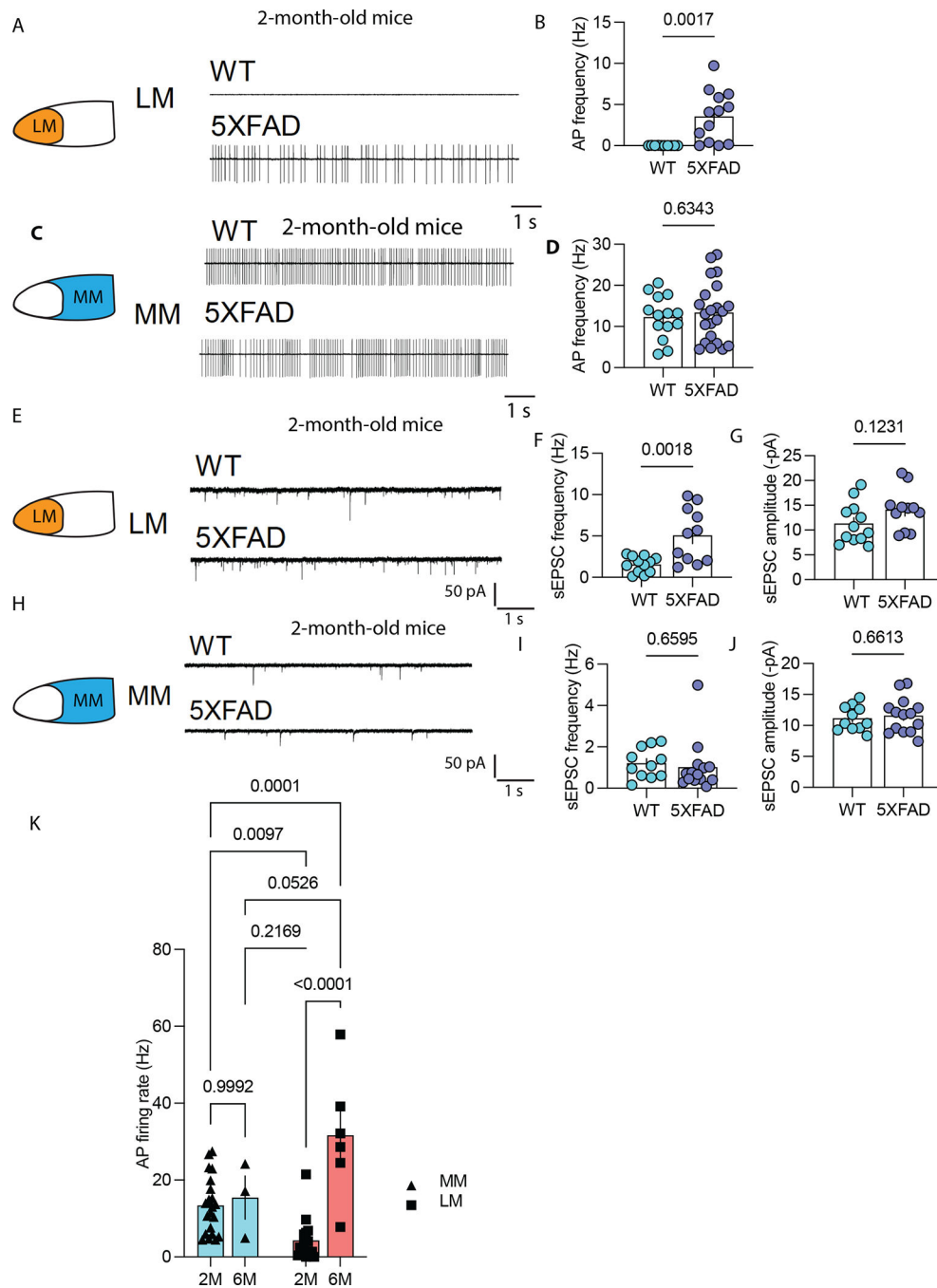




**Figure 4. Single nuclei transcriptomic analysis of human postmortem MB samples reveals lateral and medial MB neurons.**

(A) Shown is a Uniform Manifold Approximation and Projection (UMAP) of single nuclei transcriptomes in postmortem MB samples from individuals with and without AD pathology. (B) Violin plots of markers for glutamatergic and GABAergic neurons and markers for the 3 neuronal cell types. (C). Enrichment score analysis of human MB with mouse lateral MB neurons. (LM) (D) Enrichment score analysis of human MB with mouse lateral MB neuron markers. (E) Enriched GO terms for differentially expressed genes (DEG) between human medial and lateral MB neurons. (F, G) Violin plots showing medial

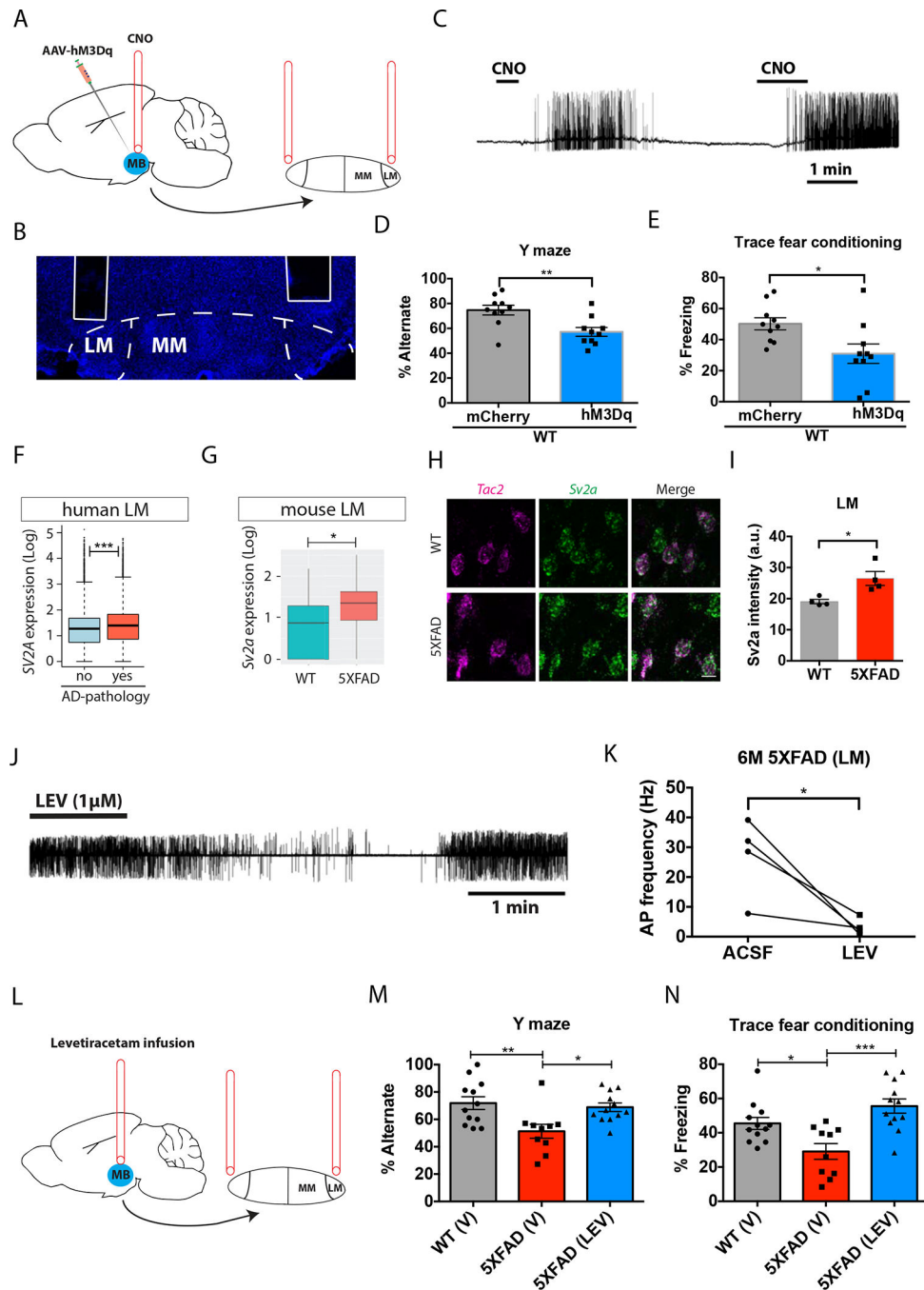
and lateral MB neuron expression of subunits of sodium and potassium ion channels and hyperpolarization-activated cyclic nucleotide-gated channels in MB samples from human (F) and mouse (G). (H) Selection of GO terms for genes upregulated in human LM neurons in postmortem MB samples from individuals with AD pathology. (I) A heatmap showing a selection of upregulated synaptic genes in human lateral MB neurons in postmortem MB samples from individuals with AD pathology. (J) Shown are dimension plots indicating subtypes of human medial and lateral MB neurons that have the most transcriptional similarity to mouse medial and lateral MB neurons. (K) Enriched GO terms are presented for genes upregulated in a lateral MB neuron sub cluster (sLM2, stressed lateral MB cluster 2). (L) Shown is the percentage of cells in human medial MB (sMM, stressed medial MB) and in two lateral MB clusters (sLM1, stressed lateral MB cluster 1, and sLM2, stressed lateral MB neuron cluster 2) for postmortem MB samples from individuals with or without AD pathology. Wilcoxon tests were used to compare cell percentage between AD pathology and no AD pathology. (M) Overrepresentation analysis for subtypes of human medial and lateral MB neurons (sMM, sLM1, sLM2). Color scale indicates the significance of overrepresentation. (N) Example images of immunohistochemical staining of human postmortem MB sections from individuals with and without AD pathology showing RNA in situ hybridization of *TAC3* (red), a lateral MB neuron marker gene. Scale bar: 50 $\mu$ m. (O) Quantification of *TAC3*<sup>+</sup> lateral MB neurons (LM) in postmortem MB samples from individuals with and without AD pathology.  $t(7)=3.614$ .  $p=0.0086$ . \*\* $p<0.01$  by unpaired t-test.



**Figure 5. Lateral MB neurons of 5xFAD mice are hyperactive.**

(A) Shown are representative action potential (AP) traces of the lateral MB neurons (LM) of a 2-month-old 5xFAD mouse and a WT littermate control using slice electrophysiology. (B) Shown is the summary of the firing frequency of LM neurons in a 2-month-old 5xFAD mouse and a WT littermate control using slice electrophysiology.  $t(20)=3.403$ ,  $p=0.0017$ . \*\* $p<0.01$  (unpaired t test).  $n=9$  in WT group and  $n=13$  in 5xFAD mouse group. (C) Shown are representative action potential traces from the medial MB neurons (MM) of a 2-month 5xFAD and a WT littermate control. (D) Shown is the summary of the firing frequency of

medial MB neurons in a 2-month 5xFAD mouse and a WT littermate control.  $n=14$  in the WT group and  $n=22$  in 5xFAD group. (E) Shown are representative traces of spontaneous excitatory postsynaptic currents (sEPSC) in the lateral MB neurons of a 2-month 5xFAD mouse and a WT littermate control. (F, G) Quantification of sEPSC frequency (F) and amplitude (G) in the lateral MB neurons of a 2-month-old 5xFAD mouse and a WT littermate control.  $t(21)=3.57$ ,  $p=0.0018$  (F) (unpaired t-test).  $n=12$  in WT group and  $n=11$  in 5xFAD group. (H) Shown are representative traces of sEPSCs of medial MB neurons (MM) from a two-month-old 5xFAD mouse and a WT littermate control. (I, J) Quantification of sEPSC frequency (I) and amplitude (J) in the medial MB neurons of a 2-month-old 5xFAD mouse and a WT littermate control.  $n=11$  in WT group and  $n=13$  in 5xFAD group. (K) Quantification of action potential frequency in the lateral and medial MB neurons of 2-month-old and 6-month-old 5xFAD mice is shown. Two-way ANOVA with Sidak's *post hoc* test  $F(1,14)=6.64$ ,  $p=0.022$  (interaction).



**Figure 6. Lateral MB neuronal hyperactivity contributes memory deficits in mice.**

(A) Experimental design for increasing neuronal activity specifically in neurons located in the lateral mammillary body (LM) of mice. An AAV vector carrying the DREADD hM3Dq (Gq) was injected into the mammillary body (MB) and a cannula was implanted above the LM, allowing the delivery of clozapine-N-oxide (CNO) into the mouse LM. (B) A confocal image shows the location of the cannula just above the LM in mouse brain. (C) Shown is an action potential trace induced by mouse LM neurons expressing the hM3Dq DREADD in response to 10  $\mu$ M CNO. (D) WT mice expressing hM3Dq showed

reduced performance in the Y maze task compared to control mice (expressing mCherry).  $t(18)=3.319$ ,  $p=0.0038$  (unpaired t-test).  $n=10$  mice per group. (E) WT mice expressing hM3Dq showed reduced freezing time in the trace fear conditioning test compared to control mice (expressing mCherry).  $t(18)=2.612$ ,  $p=0.0176$  (unpaired t-test).  $n=10$  mice per group. (F, G) *SV2A* expression in (F) human lateral MB neurons (LM) and (G) mouse LM neurons. (H) In situ hybridization of *Tac2* (magenta) and *Sv2a* (green) in brain sections from the lateral MB of a 6-month-old 5xFAD mouse and a WT littermate control. Scale bar: 10 $\mu$ m. (I) Quantification of *Sv2a* intensity in *Tac2*<sup>+</sup> LM neurons in a 6-month-old 5xFAD mouse and a WT littermate control.  $t(6)=3.161$ ,  $p=0.0195$ . \* $p<0.05$  (unpaired t-test).  $n=4$  mice per group. (J) A representative trace of spontaneous action potentials acquired using cell-attached patch-clamp recording in LM neurons of 5xFAD mice at 6 months of age before, during, and after bath application of levetiracetam (1 $\mu$ M). (K) Quantification of action potential (AP) frequency in LM neurons from 6 month-old 5xFAD mice before and after bath application of levetiracetam (LEV) or artificial cerebrospinal fluid (ACSF) as control.  $t(3)=3.286$ ,  $p=0.0462$  (paired t-test).  $n=4$  neurons from 3 mice. (L) Experimental design for levetiracetam infusion specifically into the lateral MB of 6 month-old 5xFAD mice. (M) Percentage of spontaneous alternation in the Y maze task in WT mice treated with vehicle (V), and 6-month old 5xFAD mice treated with vehicle or levetiracetam (LEV).  $F(2, 31)=6.238$ ,  $p=0.0053$  (One-way ANOVA with Tukey's *post hoc* test).  $n=12$  mice in WT (V) group, 10 mice in 5xFAD (V) group, and 12 mice in 5xFAD (LEV) group. (N) Percentage of freezing responses during the cued trace fear conditioning test in WT mice treated with vehicle (V), and 6-month old 5xFAD mice treated with vehicle or levetiracetam (LEV).  $F(2, 31)=10.35$ ,  $p=0.0004$  (One-way ANOVA with Tukey's *post hoc* test;  $N=12$  mice in WT (V) group, 10 mice in 5xFAD (V) group, and 12 mice in 5xFAD (LEV) group. \* $p<0.05$ , \*\* $p<0.01$ , \*\*\* $p<0.001$ ).