Neuronal heterogeneity in the medial septum and diagonal band of Broca: classes and continua

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SUMMARY

The medial septum and diagonal band of Broca is known for its diverse populations of cholinergic, GABAergic, and glutamatergic neurons and their behaviorally relevant functions. Behavioral studies and cell-specific manipulations within this region have underscored its involvement in a diverse array of mouse behaviors, implying the presence of a more intricate and complex cellular landscape than previously acknowledged. In this study, we employed single-cell RNA sequencing to thoroughly characterize the heterogeneity of septal neurons. Our findings confirmed previously known neuronal classes and uncovered previously undescribed subclasses, as well as expression gradients. We identified transcriptomic identities of molecularly defined cell populations and validated the expression of cell type-specific marker genes using spatial transcriptomic datasets, mapping distinct patterns of cell distribution. Taken together, our analyses provide a comprehensive description of MSDB cell type diversity and novel marker genes to investigate the intricate neuronal composition of the medial septal region.

Keywords: medial septum, diagonal band of Broca, scRNA-Seq, MERFISH, spatial transcriptomics, basal forebrain, cell types

INTRODUCTION

Located in the medial-ventral portion of the basal forebrain, the medial septum and diagonal band of Broca (MSDB) is a part of the limbic system highly interconnected with the hippocampal formation and the hypothalamus[1]. Functional studies on this brain region trace back to the early 1950s[2,3] revealing a multifaceted role of the septal area. Functions include the regulation of food and water intake[4,5], navigation and memory[6,7] and the support of reinforcing behaviours[3,8]. As more sophisticated techniques for identifying, recording, and manipulating specific neuronal types within defined brain regions have emerged, our understanding of the MSDB's influence on behavior, as well as the contribution of its various neuronal populations, has become increasingly complex.

Despite a broad consensus regarding the presence of three primary cell types[9–11]- cholinergic, GABAergic, and glutamatergic neurons – molecular, electrophysiological, and functional studies suggest a broader heterogeneity. Initially, the MSDB GABAergic population was thought to be characterized by the expression of the calcium-binding protein parvalbumin (*Pvalb*)[12]. However, further investigation revealed diverse firing patterns among the GABAergic population[13,14], suggesting the existence of at least two different subclusters. Additionally, some MSDB neurons positive for calretinin, a marker for GABAergic neurons in the hippocampal formation[15], do not colocalize with *Pvalb*[16]. Currently the difficulty to record from multiple identified GABAergic subclusters in-vivo still limits our understanding of their functional diversity.

Genetic mouse lines targeting cholinergic (Chat-Cre), glutamatergic (VGluT2-Cre), and GABAergic (VGAT-Cre, Gad2-Cre, PV-Cre and SST-Cre) neurons within the MSDB for *in vivo* studies have highlighted the limitation of the traditional tripartite classification of septal cell types[11,17,18]. Notably, a recent study revealed that two subsets of cholinergic neurons within the MSDB exist, can be differentiated based on their expression of calbindin (*Calb1*), and play distinct roles in behavior[17]. Additionally, manipulation of the MSDB glutamatergic population targeting specific projections resulted in diverse behavioral outcomes, including aversion[19], feeding[20], reinforcement and exploration[21,22].

While projection target specificity may account for some of the behavioral variability, the number of MSDB neuron subpopulations and their full molecular profiles remain unclear. By employing single cell RNA sequencing (scRNA-Seq) and spatial transcriptomics, we aimed at describing the molecular profile and spatial distribution of the MSDB neurons. Our analyses not only confirm the existence of three major classes of cholinergic, GABAergic, and glutamatergic populations, but also identify previously undescribed subclusters and novel markers to interrogate molecularly defined MSDB neurons.

RESULTS

Transcriptomic profiling of the mouse medial septal area

To study the diverse neuronal population of the MSDB we performed single cell RNA sequencing (scRNA-Seq). The region of interest was microdissected based on anatomical landmarks and the cells were manually dissociated (*n* = 4 mice). After the exclusion of non-neuronal cell types and low-quality cells, our dataset comprised a total of 903 MSDB neurons (median number of features per cell: 5563 – interquartile range (IQR): 4477-6947; median RNA count per cell: 154711 - IQR: 89072-273657; median percentage of mitochondrial genes: 2.7% - IQR: 2.26-3.35 %, Figures S1A-B).

To identify the main neuronal classes, we clustered the data using the Leiden algorithm[23]. The most informative resolution was determined using a co-dependency index (CDI)-based differential expression analysis[24] (Figures S1D-F). Four transcriptionally distinct classes emerged from the clustering which constitute four separate groups on a Unifold Manifold Approximation and Projection (UMAP) on a two-dimensional plane (Figure 1A). Since the MSDB is populated by cholinergic, glutamatergic, and GABAergic neurons[10,11,25], we examined the expression of commonly used genetic markers for each of these cell classes (Figure 1B). We identified one cholinergic class characterized by the expression of the neurotransmitter-synthesizing enzyme choline acetyltransferase (*Chat*) as well as the choline transporter (*Slc5a7*); one glutamatergic class selectively expressing the gene *Slc17a6* for the vesicular glutamate transporter type 2 (VGluT2); and two GABAergic classes with high expression levels of the gene *Slc32a1* coding for the vesicular GABA transporter (VGAT). Despite the broad use of glutamate decarboxylase 1 (*Gad1*) and glutamate decarboxylase 2 (*Gad2*) Cre mouse lines to target MSDB GABAergic neurons[26–29], we found that both markers were not specific. Instead, *Gad1* was broadly expressed also in the cholinergic class, while *Gad2* expression spanned across all neurons.

To differentiate between the two GABA classes, we conducted a differential expression analysis using Wilcoxon rank sum test. The analysis revealed that *Zic1* and *Lhx6*, two transcription factors involved in the septal region development[30,31], are mutually exclusive in the two GABAergic classes (Figures 1C-D). Building upon this analysis, we named the four neuron classes ChAT, VGluT2, GABA_Lhx6 and GABA_Zic1, respectively. To provide a detailed overview of gene expression differences across all neuron classes, we identified the ten most significant differentially expressed genes (DEGs) for each of the four neuron classes (Figure 1E).

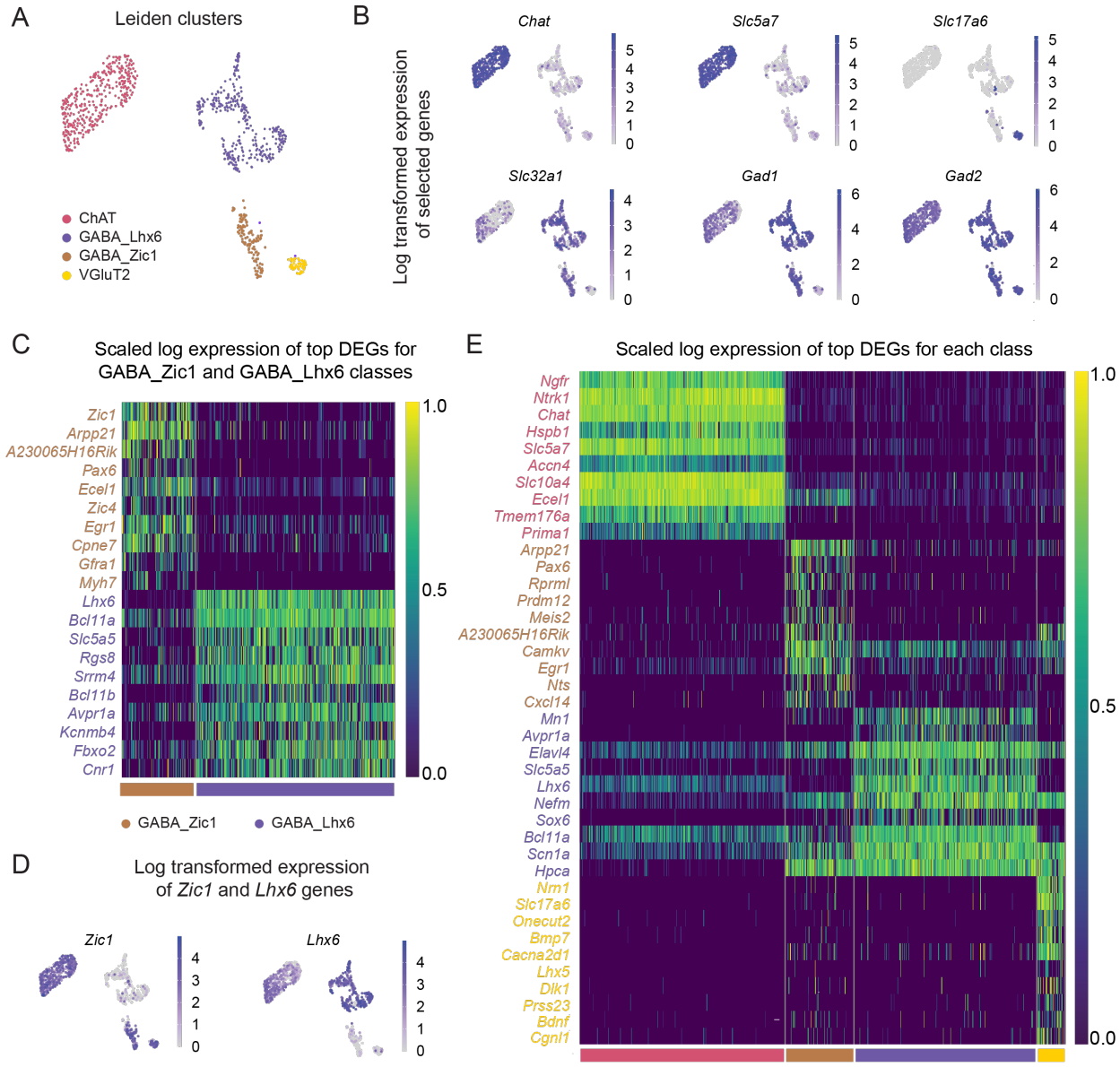

Figure 1. scRNA-Seq analysis of the mouse septal area.
A) Leiden clusters with resolution of 0.1. B) Feature plots showing the log-transformed expression of cholinergic (*Chat, Slc5a7*), GABAergic (*Slc32a1, Gad1, Gad2*), and glutamatergic (*Slc17a6*) markers. C) Heat map representing the scaled log-transformed expression of DEGs between GABA_Zic1 and GABA_Lhx6 clusters sorted by false discovery rate (FDR-) corrected p-value (Wilcoxon rank sum test). D) Feature plots of log transformed expression of *Zic1* and *Lhx6* genes. E) Heat map representing the scaled log-transformed expression of the top 10 DEGs for each cluster sorted by FDR-corrected (Wilcoxon rank sum test). Only genes with a $\log_2$ fold-change expression (log2FC) higher than 1.5 and that had a fraction of expression of at least 0.3 higher in the cell class of interest than in the rest of the population were considered as DEGs in Figure 1C and 1E. Classes color code throughout the figure: ChAT in pink, GABA_Lhx6 in purple, GABA_Zic1 in brown, VGluT2 in yellow.

MSDB scRNA-Seq integration with MERFISH ABCA datasets

While scRNA-Seq is the state-of-the-art method for identifying and classifying neuronal subpopulations within a specific region, it cannot capture the cells' spatial distribution and often exhibits bias in the relative proportions of different cell types[32]. To quantify the abundance of the neuronal populations and investigate their localization in the MSDB, we combined our scRNA-Seq analysis with the analysis of publicly available spatial transcriptomic datasets obtained using Multiplexed Error-Robust Fluorescence *In Situ* Hybridization (MERFISH). Specifically, we used the Zhuang-ABCA-1 and Zhuang-ABCA-2[33] datasets, which comprise mouse brain coronal sections targeting 1,122 genes, available from the Allen Brain Cell Atlas (ABCA) (Figure S2A). For our study, we analyzed one hemisphere for each coronal section and defined a region of interest comprising both $MSDB^+$ and nearby $MSDB^-$ neurons. To identify $MSDB^+$ neurons, we refined the segmentation provided with the Zhuang datasets in Allen Mouse Brain Common Coordinate Framework version 3 (CCF) coordinates [34] with a custom-written tool (see Methods). Our further analysis focused only on neurons, excluding glial, immune, and vascular cells.

Using Canonical Correlation Analysis (CCA)[35], we predicted the identity of MERFISH neurons in the region of interest using the scRNA-Seq dataset as a reference. To quantify the likelihood of a MERFISH neuron to belong to a scRNA-Seq class, CCA calculates a prediction score ranging from 0 to 1. MERFISH neurons with a prediction score above 0.9 were assigned to their predicted class. We further compared marker gene expression profiles of individual classes between scRNA-Seq and MERFISH datasets, ensuring consistency (Figure S2B).

Next, we mapped all the neurons with a prediction score above 0.9 in the spatial domain and marked each cell with the corresponding class-based color. For the visualization of the cell position, we used four representative slices along the anterior-posterior extent of the MSDB in both Zhuang datasets (Figures 2A, S3A). Consistent with previous studies, the GABA_Lhx6 population was localized in the MSDB[25], while GABA_Zic1 neurons were mostly distributed in the lateral septum (LS)[36,37]. We concluded that the scRNA-Seq *Zic1*$^+$ neurons belong to the transition area between MSDB and LS, given the lack of distinct anatomical demarcations between the two[38]. Thus, we focused our analysis of MSDB GABAergic neurons on the GABA_Lhx6 class, only.

ScRNA-Seq analysis may not capture all the cell types in a given brain region, due to biological and technical limitations[39]. To confirm that the scRNA-Seq data included all MSDB neuronal classes present in the MERFISH dataset, we projected the cells of both MERFISH and scRNA-Seq datasets on a UMAP in a joint feature space (jFS) and quantified the number of neurons for each class in both datasets (Figures 2B - scRNA-Seq, 2C - MERFISH, S2C - all batches). We found that 90% of the MERFISH neurons are assigned to one of the four scRNA-Seq classes with a prediction score above 0.9. Thus, there is a high correspondence between the two datasets in regards of $MSDB^+$ neuronal classes. Moreover, the 10% MERFISH neurons with a prediction score lower than 0.9 did not segregate into a separate group in the UMAP visualization. This indicates that our scRNA-Seq analysis reliably captured all main cell classes in the MSDB,

suggesting that the lower prediction scores were likely due to imperfect single-cell segmentation or cell overlap in the MERFISH data rather than the presence of unrecognized neuronal classes.

Leveraging the spatial resolution provided by the MERFISH datasets, we employed a shuffling approach to detect significant spatial clustering of the MSDB classes along the anterior-posterior axis. The analysis revealed that GABA neurons are homogeneously distributed, ChAT neurons are more prominent in the anterior sections, and VGluT2 neurons populate more abundantly the posterior part (Figures 2D, S3B). Furthermore, we examined whether there was significant spatial clustering along the dorsoventral and mediolateral axes by investigating spatial trends in individual coronal sections (Figures 2D, S3B). We found that VGluT2 neurons are significantly enriched in the dorso-lateral regions of the MSDB, while the ChAT population is significantly enriched in the more ventral region of the posterior MSDB, mostly occupying the diagonal band of Broca.

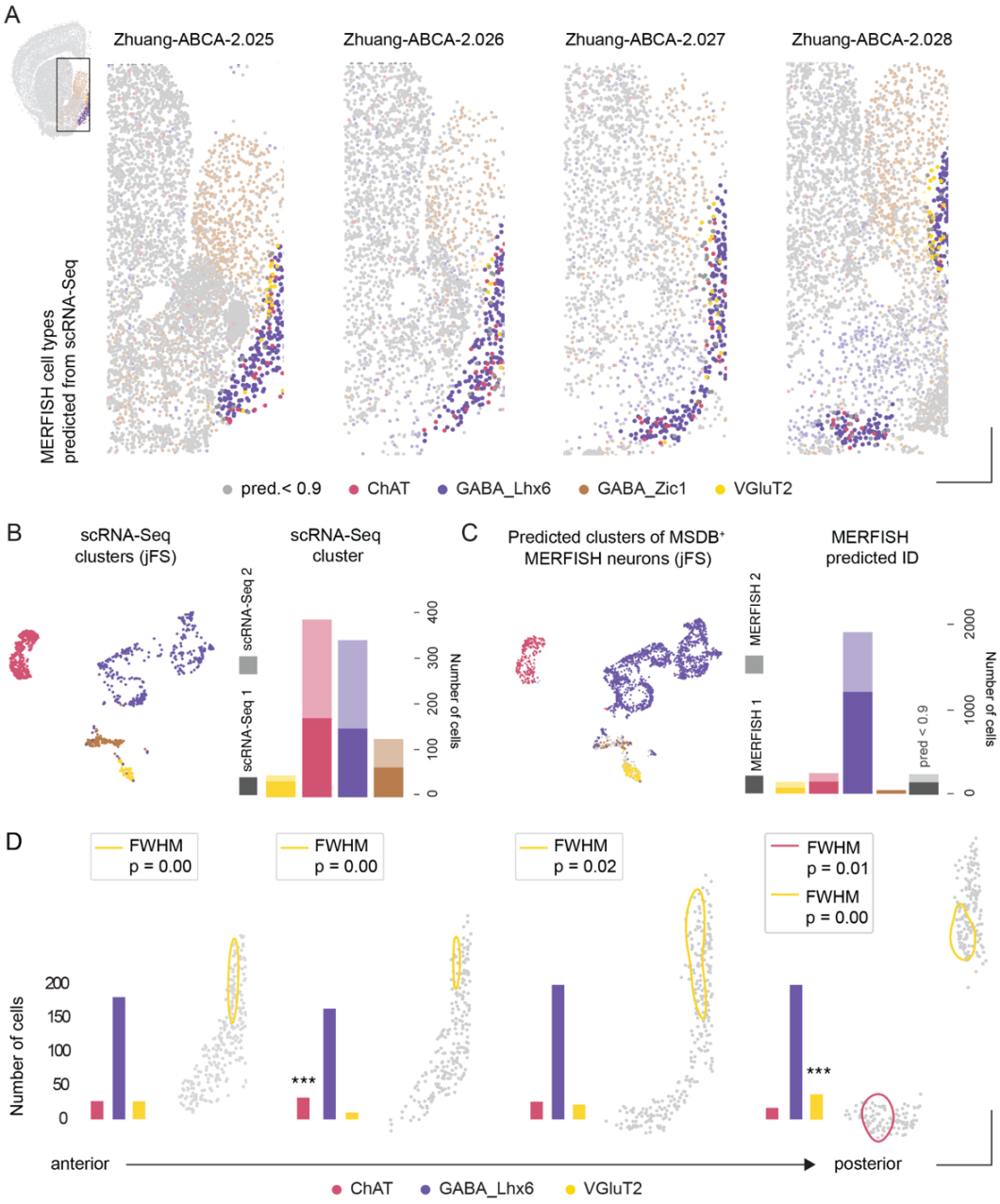

Figure 2. Integration of the scRNA-Seq and the MERFISH ABCA datasets revealed four neuronal clusters. A) Coronal slices of the Zhuang-ABCA-2 MERFISH dataset (slices 025, 026, 027, and 028) with cells color-coded based on the predicted identity from the scRNA-Seq dataset (MSDB+ neurons in bold colors, MSDB- neurons in pale colors). Scale bars correspond to 5 CCF units for both axes. B) UMAP in jFS with scRNA-Seq neurons color-coded by cluster identity (left panel) and the proportion of neurons assigned to each cluster from each batch (right panel). C) UMAP in jFS with MERFISH neurons color-coded by predicted identity (left panel) and the proportion of neurons assigned to each cluster including neurons with a prediction score < 0.9 (right panel). D) FWHM of the maximum-likelihood kernel density estimate (ml-KDE) for cell types that are significantly spatially localized inside the respective slice. P-values correspond to the permutation test with 500 shuffles (see Methods). Bar plots represent the number of neurons per cluster for each coronal slice. Stars represent significant enrichment of the respective cluster on the respective slice (* p<0.05, ** p<0.01, *** p< 0.001). Scale bars correspond to 5 CCF units for both axes. Classes color code throughout the figure: ChAT in pink, GABA_Lhx6 in purple, GABA_Zic1 in brown, VGluT2 in yellow, MERFISH neurons with prediction scores < 0.9 in gray.

Cholinergic neurons in the MSDB are organized in a transcriptomically continuous cluster with two distinct endpoints.

For many decades MSDB cholinergic neurons have been studied as the main source of acetylcholine to the hippocampus[10], involved in memory[40], attention[41], and type II theta oscillations[42]. However, further studies showed cholinergic subpopulations co-expressing other neurotransmitters[43], projection targets outside the hippocampal formation[44], and multiplex behavioral outcomes[17], suggesting a broader heterogeneity than previously acknowledged.

Thus, using Leiden clustering, we aimed to explore whether MSDB cholinergic neurons form molecularly distinct clusters. A CDI-based criterion determined the optimal clustering resolution of 0.4, resulting in two subcluster (Figures 3A, S4A-C). To explore the transcriptional features distinguishing the two subclusters, we conducted differential gene expression analysis (Figure 3B). *Gal* and *Amigo2* appeared among the most significant DEGs between the two ChAT clusters, thus we named the clusters ChAT_Gal and ChAT_Amigo2, respectively.

To investigate if these two clusters represent individual classes or are part of a transcriptomic continuum, we utilized the gap c statistic[45] which relies on two metrics: the diffusion pseudotime metric[46], where cells with a similar transcriptomic profile lie closer on a pseudotime axis compared to cells with more distinct profiles; and the relative cluster connectivity metric, which describes how confident a cell can be assigned to one of two different clusters. We calculated the diffusion pseudotime for the MSDB ChAT neurons along the direction of highest variance between the two subclusters within the ChAT class (Figure 3C). Our analysis revealed no significant gaps on either the pseudotime axis or the axis for relative cluster connectivity (Figure 3D). Additionally, we examined cumulative differential expression scores[45] of DEGs between the two clusters, sorted according to their rank on the pseudotime axis. Notably, we observed no significant gap in the cumulative expression scores either (Figure 3E). Taken together, these findings suggest that ChAT neurons in the MSDB are organized in a transcriptomic continuum with two distinct endpoints.

To further characterize the ChAT continuum, we plotted the expression profiles of a selection of significant DEGs for each endpoint along the diffusion pseudotime axis (Figure 3F). We discovered that ChAT_Amigo2 neurons highly express genes related to the synthesis and transport of the neurotransmitter GABA (*Slc6a1*, *Gad1*, *Slc32a1*), while ChAT_Gal neurons are more closely linked to neuromodulators as demonstrated by the presence of the neuropeptide galanin (*Gal*) and the vesicular monoamine transporter 2 (*Slc18a2* – VMAT2) that facilitate dopamine and serotonin loading into synaptic vesicles. These results align with recent evidence of a ChAT-GABA co-releasing population in the MSDB[43,47,48] and opens new avenues to study the impact of neuromodulators in the basal forebrain. In line with the notion of a continuum, the expression profile of the DEGs does not show a clear gap between the two ChAT subclusters, as expression ranges of individual genes vary along the diffusion pseudotime axis.

Gene ontology analysis represents a possible tool to disentangle the two endpoints of the ChAT continuum based on their molecular functions (Figure 3G) and biological processes (Figure 3H; details in Methods). The molecular function analysis revealed that ChAT_Amigo2 neurons are enriched in cell adhesion molecule encoding genes, particularly of the cadherins family (*Cadh4, Cadh8*), while ChAT_Gal neurons are abundant in transcripts related to calcium ion binding and calcium homeostasis (*ESyt3, Efcab6, Clstn2*) (Figure 3G).

The biological processes analysis revealed an increase in gene expression linked to pre- and post- synaptic remodeling and plasticity in ChAT_Amigo2 enriched cells, with high levels of reelin (*Reln*), synaptotagmin (*Syt7*), and Munc13 (*Unc13c*). ChAT_Gal neurons also appear to be related to learning and memory processes; of interest is the increase in several genes related to neuromodulators such as the rate-limiting enzyme of catecholamine synthesis, tyrosine hydroxylase (*Th*), the neurotensin receptor 1 (*Ntsr1*), and the histamine receptor H1 (*Hrh1*) (Figure 3H). Overall, MSDB ChAT neurons seem to be strongly linked to synaptic plasticity, learning, and memory.

Next, we studied the spatial distribution of the MSDB$^+$ ChAT neurons and investigated whether they share similar features with the nearby MSDB$^-$ ChAT neurons from a common selection window. First, we plotted the scRNA-Seq and the MERFISH datasets of the ChAT MSDB$^+$ neurons on a UMAP in jFS and predicted the subcluster identity of the MERFISH cells using CCA (Figures 4A, S4D). Then, we performed a second round of integration including all ChAT neurons inside the selection window, i.e. incorporating both MSDB$^+$ and MSDB$^-$ ChAT MERFISH cells. We found that MSDB$^-$ ChAT neurons constitute a transcriptionally distinct cluster mostly populating the striatum. Thus, we named this group ChAT_Striatum (Figure 4B). The fact that the ChAT neurons from the scRNA-Seq dataset co-localize with ChAT_Gal and ChAT_Amigo2 neurons in the jFS, instead of ChAT_Striatum neurons further validates our integration strategy. In line with previous literature, differential expression analysis revealed that ChAT_Striatum neurons have higher expression of the dopamine receptor *Drd2*[49], the homeodomain transcription factor *Gbx2*[50], and the protein phosphatase *Ppp1r1b*[51], further validating our analysis and cell-type classification (Figure 4C).

Finally, we investigated if the two endpoints of the MSDB ChAT continuum are spatially segregated along the anterior-posterior and dorsal-ventral/medio-lateral axes. Although our analysis uncovered significant enrichment along the dorsal-ventral axis for some slices in both Zhuang datasets (Figures 4D, S4E), these findings did not converge to indicate a consistent spatial distribution.

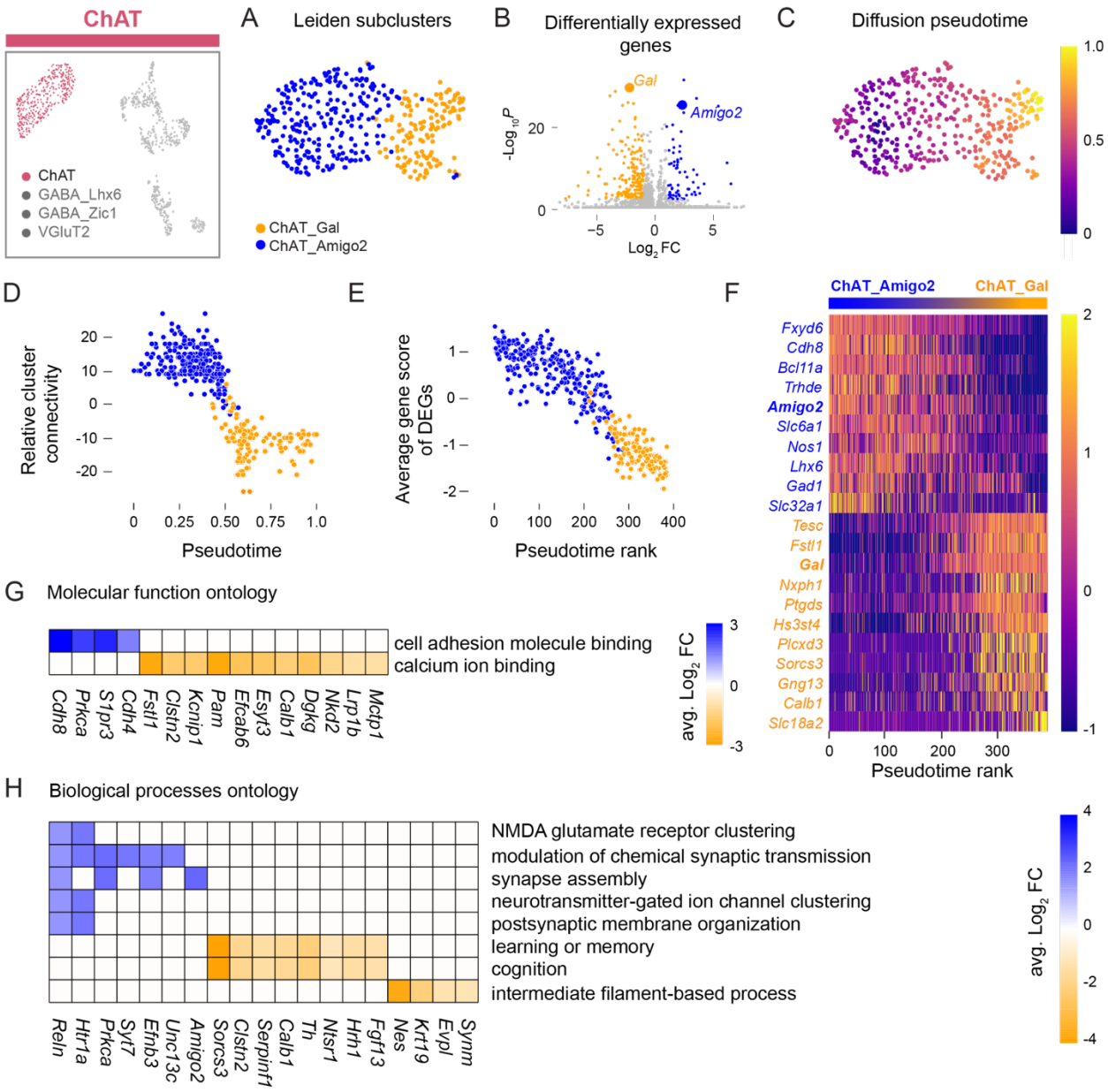

Figure 3. Characterization of the MSDB cholinergic cluster.
A) UMAP of cholinergic subclusters (ChAT_Gal in orange and ChAT_Amigo2 in blue) from Leiden sub-clustering with resolution 0.4. B) Volcano plot of differentially expressed genes between the two subclusters. Gray dots have either an absolute log2FC value below 1 or a FDR-corrected p-value below 0.001 (bold dots indicate Gal (orange) and Amigo2 (blue); total number of genes = 12256; total number of genes above thresholds = 840). C) UMAP showing the diffusion pseudotime along the direction of highest variance. D) Relative cluster connectivity of neurons as a function of diffusion pseudotime. E) Average gene score of significant DEGs (FDR corrected p-value < 0.01) ordered by diffusion pseudotime rank. F) Heatmap showing the scaled expression value of selected DEGs ordered by diffusion pseudotime rank. G) Marker genes for molecular function ontology that are differentially expressed along the cholinergic continuum. H) Marker genes for biological process ontology that are differentially expressed along the cholinergic continuum. For marker selection thresholds in G and H, see Methods.

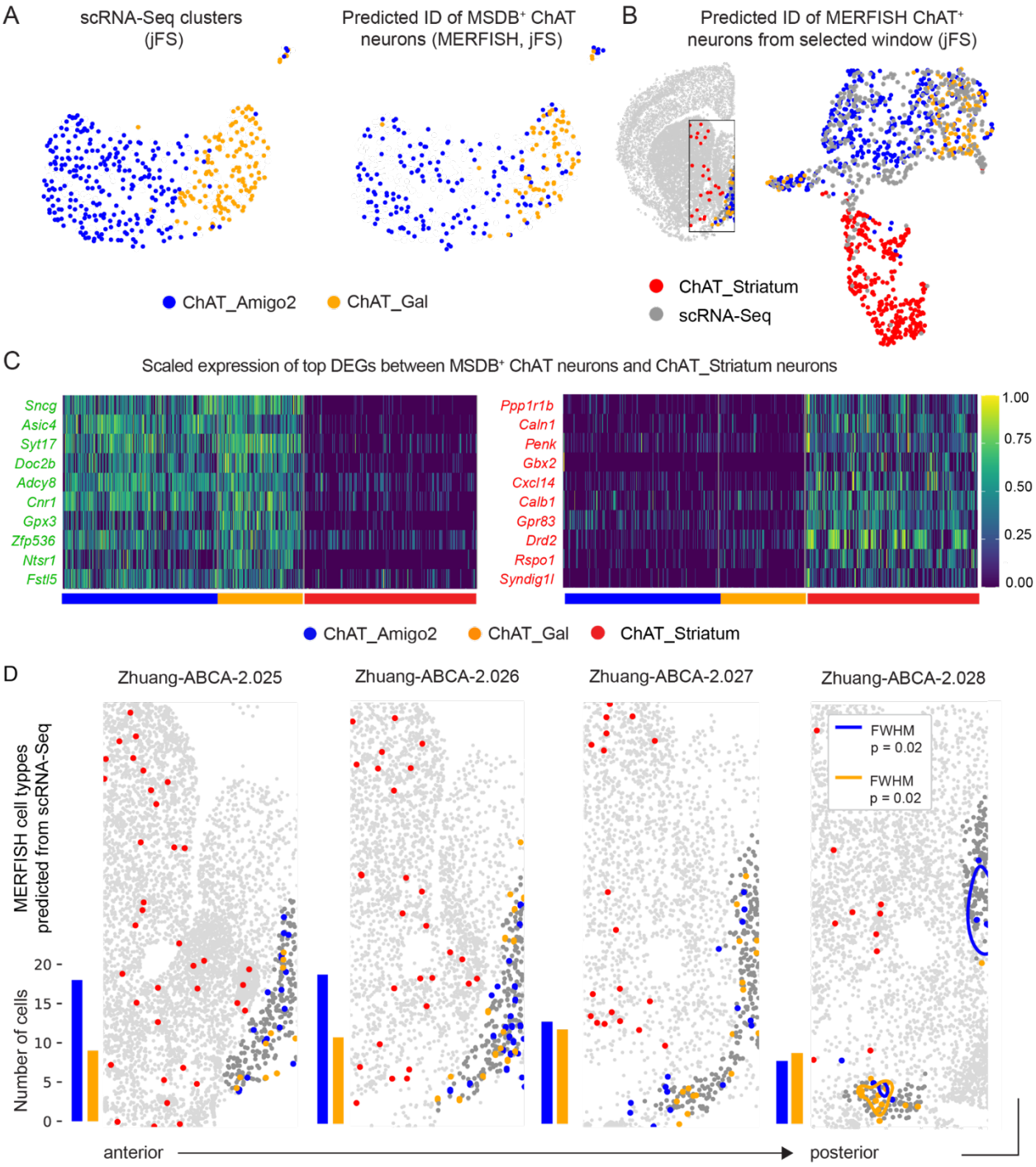

Figure 4. Spatial distribution of cholinergic MSDB neurons and their relation to striatal ChAT neurons. A) UMAPs in jFS of ChAT$^+$ scRNA-Seq and MERFISH neurons (left panel: scRNA-Seq, right panel: MERFISH) color coded by Leiden clusters (scRNA-Seq) and predicted cluster identities (MERFISH). B) UMAP of ChAT$^+$ neurons from MSDB scRNA-Seq analysis and ChAT$^+$ MERFISH neurons from the selection window in jFS. C) Heat map of selected DEGs of ChAT MSDB$^+$ neurons and ChAT_Striatum neurons. D) Spatial distribution of the ChAT clusters along the anterior-posterior axis. (ChAT_Amigo2 in blue, ChAT_Gal in orange, ChAT_Striatum in red). Bar plots represent the abundance of the two MSDB$^+$ ChAT neuronal populations in each slice. FWHM of ml-KDE indicates significantly spatial clustered abundance. Scale bars correspond to 5 CCF units for both axes.

Heterogeneity of MSDB Lhx6 GABAergic cluster

GABAergic neurons in the MSDB have been extensively studied due to their dense projections to the hippocampal formation[12]. In particular, it was found that MSDB *Pvalb* interneurons expressing the hyperpolarization-activated, cyclic nucleotide-gated non-selective cation (HCN) channel exert pacemaking activity, capable of synchronizing both the local network and the hippocampal formation during theta oscillations[14,52–54]. However, these neurons represent only a fraction of the GABAergic cell population in the MSDB, and there is no clear consensus on the overall number of distinct GABAergic clusters and their characteristics.

To address this issue, we sub-clustered the GABA_Lhx6 class. Using Leiden clustering with a resolution of 1.2 as determined by the CDI-based method, we delineated six distinct subclusters (Figures 5A, S5A-D). To investigate whether these subclusters are transcriptionally distinct or part of a continuum, we used the gap c statistics and found that the GABA_Lhx6 sub-clusters blend into each other continuously (Figures 5B, S5E).

To characterize genetic profiles for the GABAergic subclusters, we identified the 10 most significant DEGs of each subcluster using the Wilcoxon rank sum test (Figure 5C). We further identified marker genes with high specificity based on the CDI method including well-known genes associated with MSDB cell types or common Cre-lines (Figure 5D). Based on these genes, we named the subclusters as follows: GABA_Lhx6_Calb2, characterized by high expression levels of the calcium-binding protein calretinin (*Calb2*); GABA_Lhx6_Tcerg1l, expressing the transcriptional regulator *Tcerg1l*; GABA_Lhx6_Nts, marked by the presence of the endogenous neuropeptide neurotensin (*Nts*); GABA_Lhx6_Pvalb, coding for the calcium binding protein parvalbumin (*Pvalb*); GABA_Lhx6_Npas1, identified by the expression of the transcription factor *Npas1*; and GABA_Lhx6_Adra1a, characterized by the adrenergic receptor alpha 1A (*Adra1a*).

Finally, since MSDB *Pvalb* neurons play a key role in hippocampal theta rhythm, and given the extensive *in vivo* and *in vitro* recordings studying their features[14,44,46], we explored potential correlations between gene expression and electrophysiological properties in GABA_Lhx6_Pvalb^{+} and GABA_Lhx6_Pvalb^{-} neurons. For this reason, we compared differentially expressed genes in the GABA_Lhx6_Pvalb subcluster with electrophysiological properties significantly linked to these genes. Our analysis is based on a publicly available database by Bomkamp and colleagues[55] correlating gene expression gradients of inhibitory neurons with their firing properties (Figure 5E). We found that the GABA_Lhx6_Pvalb^{+} subcluster is enriched in genes associated with high firing frequency, high rheobase, low input resistance, and narrow action potential width (Figure 5E). Indeed, these electrophysiological features are classically associated with MSDB *Pvalb* neurons activity[56], further validating the results of our analysis.

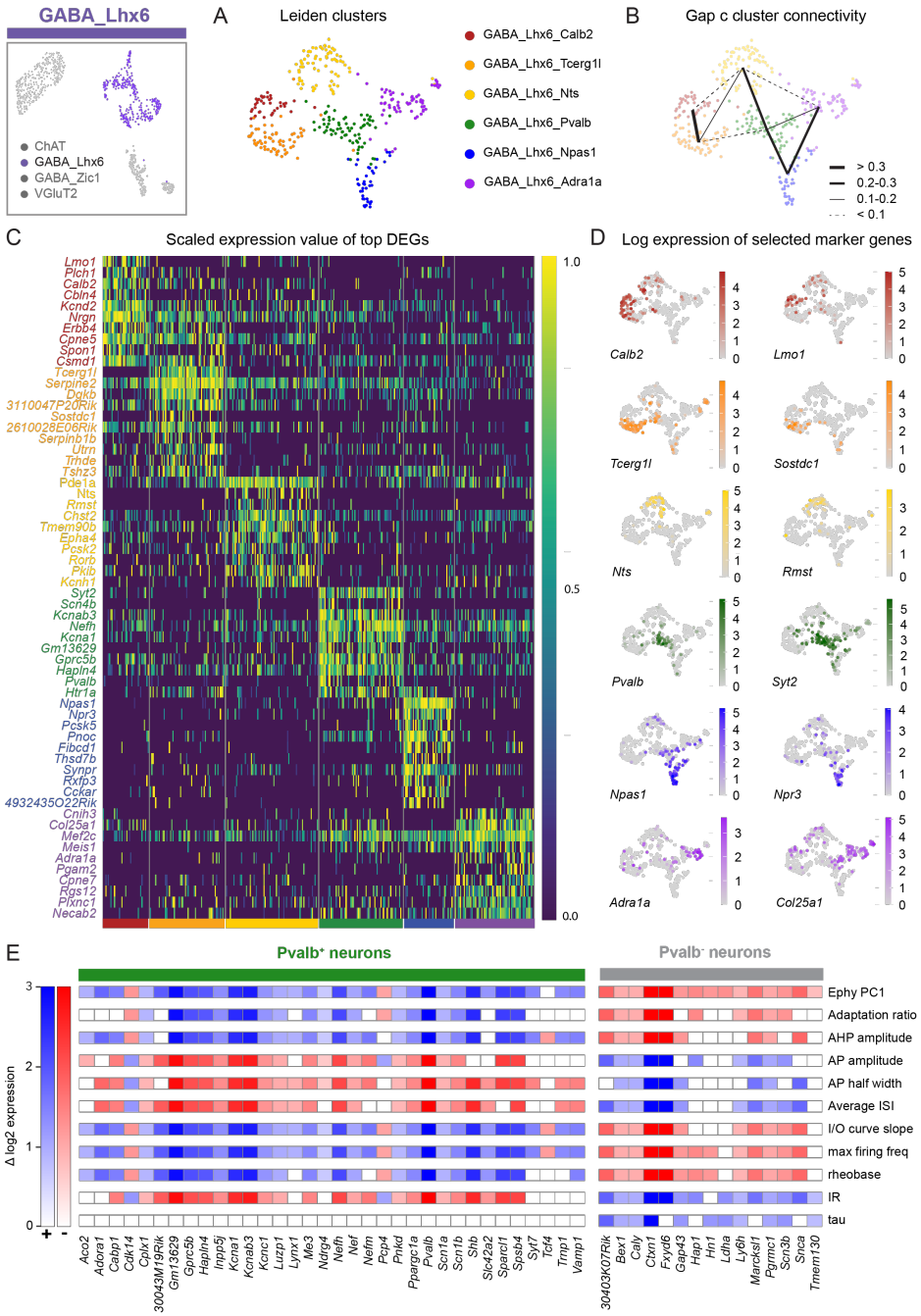

Figure 5. Transcriptomic profile of MSDB GABAergic Lhx6 continuum.
A) UMAP of GABAergic Lhx6 subclusters from Leiden sub-clustering with resolution 1.2. B) Strength of cluster connectivity based on gap c statistic. C) Heatmap showing the scaled expression value of top DEGs per Leiden subcluster ranked by FDR-corrected p-value (Wilcoxon rank sum test). Only genes with log2FC value higher than 1.5 and that had a fraction of expression which was 30 percent higher in the subcluster of interest compared to the rest of the population were considered as DEGs D) Feature plots showing the expression of selected marker genes per Leiden subcluster. E) Log transformed differential expression of positive (green) and negative (gray) marker genes of the GABA_Lhx6_Pvalb subcluster which are negatively (red) or positively (blue) correlated with identified electrophysiological properties based on the Bomkamp et al. database[55].

Next, we integrated MERFISH and scRNA-Seq neurons of the GABA_Lhx6 class using CCA-based integration. By predicting the subcluster identity of GABAergic MERFISH neurons and mapping the prediction scores onto a UMAP in jFS (Figure 6A), we observed high prediction scores, except for neurons situated between two clusters. This occurrence reflects the concept of continuous clusters: neurons positioned between two endpoints of a continuum are equally assigned to both clusters, resulting in a prediction score of 0.5. For further analysis of the GABA_Lhx6 class, we included all MERFISH neurons with maximum prediction scores equal or above 0.5. To confirm the alignment between scRNA-Seq clusters and MERFISH GABAergic clusters we also projected $MSDB^+$ scRNA-Seq neurons from the GABA_Lhx6 class onto the UMAP in jFS (Figure 6B). We additionally subpartitioned the MERFISH neurons only using Leiden Clustering and projected the clusters in the jFS UMAP (Figure 6C). We found each MERFISH subcluster region on the jFS UMAPs to be mainly populated by one specific scRNA-Seq subcluster. This suggested a robust alignment between the transcriptomic profile of GABAergic MERFISH and scRNA-Seq neurons. Additionally, we confirmed that selected marker genes for GABAergic subclusters in the scRNA-Seq data exhibit consistent expression patterns with the corresponding subclusters in the MERFISH data (Figure S6A).

In order to determine spatial trends within each coronal slice and along the anterior-posterior axis of the MSDB, we mirrored the analysis previously employed for the main MSDB neuronal classes and for the ChAT neurons, this time shuffling across GABAergic neurons only. Our analysis unveiled that GABA_Lhx6_Pvalb neurons predominantly occupy the midline of the MSDB, GABA_Lhx6_Tcerg1l neurons being slightly more lateral, and GABA_Lhx6_Nts neurons often extending into the surrounding areas. In the most posterior slice, GABA_Lhx6_Calb2 and GABA_Lhx6_Adra1a preferentially occupy the diagonal band of Broca with GABA_Lhx6_Adra1a also extending further into the surroundings of the diagonal Band (Figures 6D, S6B). Additionally, we observed that GABA_Lhx6_Nts and GABA_Lhx6_Tcerg1l are significantly more abundant in the anterior portions of the MSDB, GABA_Lhx6_Adra1a in the middle, and GABA_Lhx6_Pvalb in the more posterior region (Figures 6E, S6C).

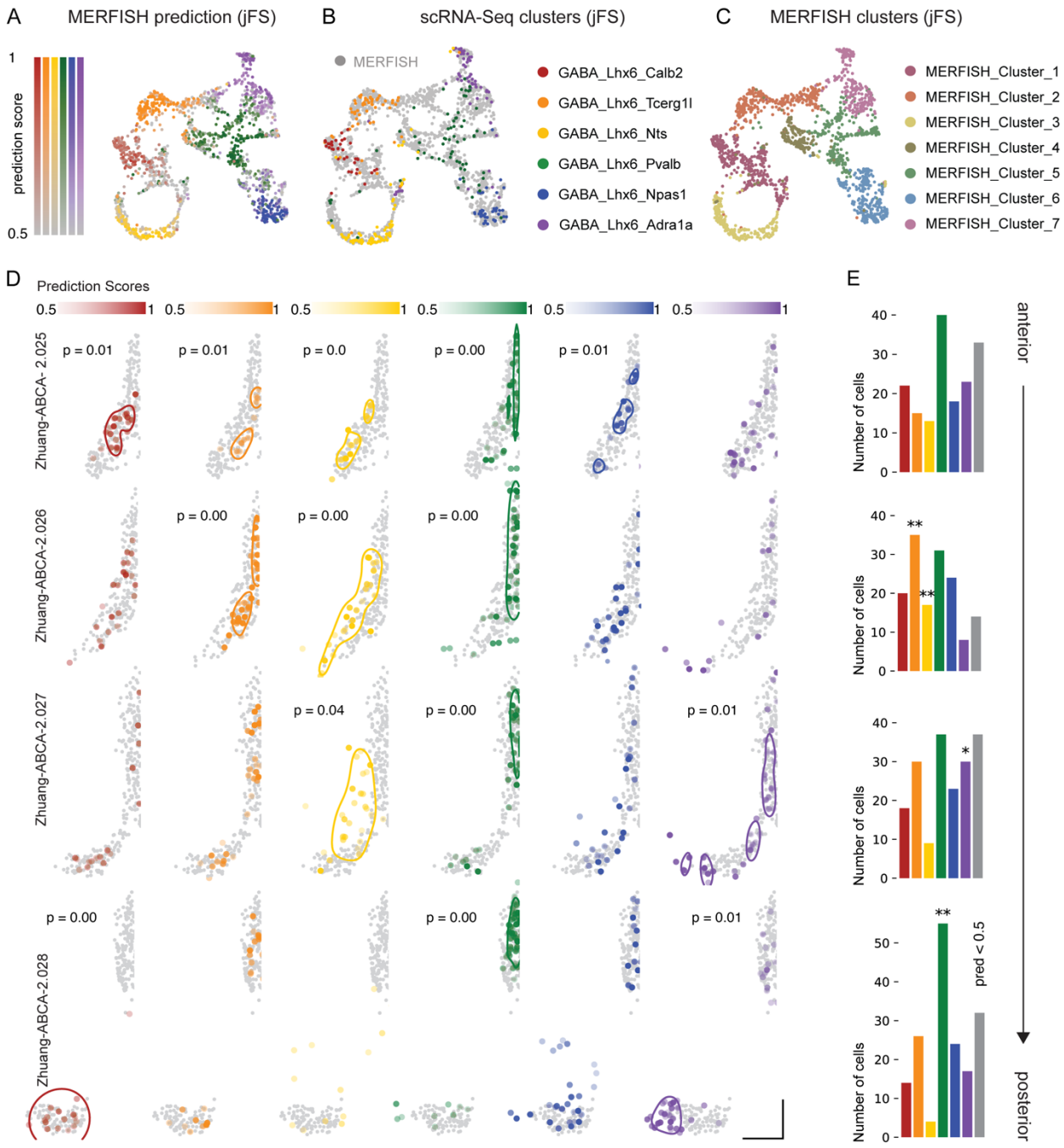

Figure 6. Spatial distribution of GABA_Lhx6 subclusters.
A) UMAP in jFS of scRNA-Seq and MERFISH GABA_Lhx6 neurons with MERFISH neurons color-coded by prediction identity and prediction score. B) UMAP in jFS of the GABA_Lhx6 cluster with scRNA-Seq neurons color-coded by subcluster identity and MERFISH neurons in gray. C) UMAPs in jFS of MERFISH neurons color coded by MERFISH subcluster identity, (Leiden resolution = 0.3). D) Spatial expression patterns of predicted MERFISH subclusters color-coded by prediction score in the Zhuang-ABCA-2 dataset. Significant clustering is represented by FWHM of the respective ml-KDE. Scale bars correspond to 5 CCF units for both axes. E) Number of neurons per cluster for each coronal slice. Stars represent significant enrichment of the respective cluster on the respective slice (* p<0.05, ** p<0.01, *** p< 0.001).

MSDB$^+$ VGluT2 neurons are transcriptomically distinct

Accounting for a quarter of MSDB neurons, VGluT2 cells have been found to form the smallest neuronal subset in this brain region[9]. Our scRNA-Seq data reflects this, capturing only a limited number of VGluT2$^+$ neurons in the MSDB. Although the VGluT2 class in the scRNA-Seq dataset appeared to be homogeneous, its size was insufficient for a representative sub-clustering analysis, like the one conducted for the GABA and ChAT classes. Nonetheless, we aimed to further characterize this cell class given the recent interest in its functional role[11,21,22,57,58]. Therefore, we investigated how the MSDB VGluT2 neurons identified in our scRNA-Seq dataset differ from other VGluT2 cells in the septal surroundings. To achieve this, we used Leiden clustering on the different MERFISH VGluT2 neurons within a defined selection window. Our analysis revealed four main VGluT2 clusters (Figure 7A).

When observing the spatial distribution of the VGluT2 clusters (Figures 7B, S7A), only one of them was overlapping with the septal area, thus we named it VGluT2_Septum. Another group of VGluT2$^+$ neurons appeared very dense in the ventral portion of the more caudal septal slices and overlapped with the medial preoptic area (VGluT2_MPO). Similarly, a smaller population was distributed on the more lateral aspects of the posterior septal region, above the MPO, and could be assigned to the lateral preoptic area (VGluT2_LPO). Finally, a fourth group of VGluT2 neurons was located laterally, and for this reason we assigned it to the ventral pallidum (VGluT2_VP). Next, we investigated the DEGs for each of these MERFISH VGluT2 clusters and compared the expression profiles of their most significant DEGs with their expression profiles in scRNA-Seq VGluT2$^+$ neurons (Figure 7C). This approach confirmed that the VGluT2 neurons in our scRNA-Seq dataset share their transcriptomic profile with the VGluT2_Septum MERFISH cluster, expressing the transcription factor *Onecut2* and the proto-oncogene *Ret*[59,60], among the others. In line with previous studies, we detected high levels of the transcription regulators *Tcf7l2* and *Skor1* in the VGluT2_VP neurons[61,62], *Lhx1* in the VGluT2_LPO neurons[63], as well as specific expression of the prolactin receptor (*Prlr*) in the VGluT2_MPO neurons[64]. Notably, VGluT2_Septum neurons are situated dorsally within the septum, occupying an area that, based on the expression of the GABA_Lhx6 and GABA_Zic1 clusters, overlaps with both the medial and lateral septum. Moreover, VGluT2 neuron clusters increasingly intermingle with one another along the anterior-posterior axis, with VGluT2_VP cells almost completely overlapping with the diagonal band of Broca in the more posterior parts of the MSDB (Figures 7B, S7A).

Finally, we investigated the expression of broadly studied marker genes across all MSDB subclusters (Figure 7D). We confirmed previous observations, such as the co-expression of *Hcn1* with *Pvalb*[14], and *Slc5a7* with *Gal*[65]. We also found *Calb2* expression in VGluT2 neurons and *Calb1* in both VGluT2 and ChAT neurons, although both genes were previously attributed exclusively to the GABAergic population. This highlights how our study provides new insights into the transcriptomic landscape of the MSDB and paves the way for future investigations of the functional and behavioral roles of each MSDB subcluster.

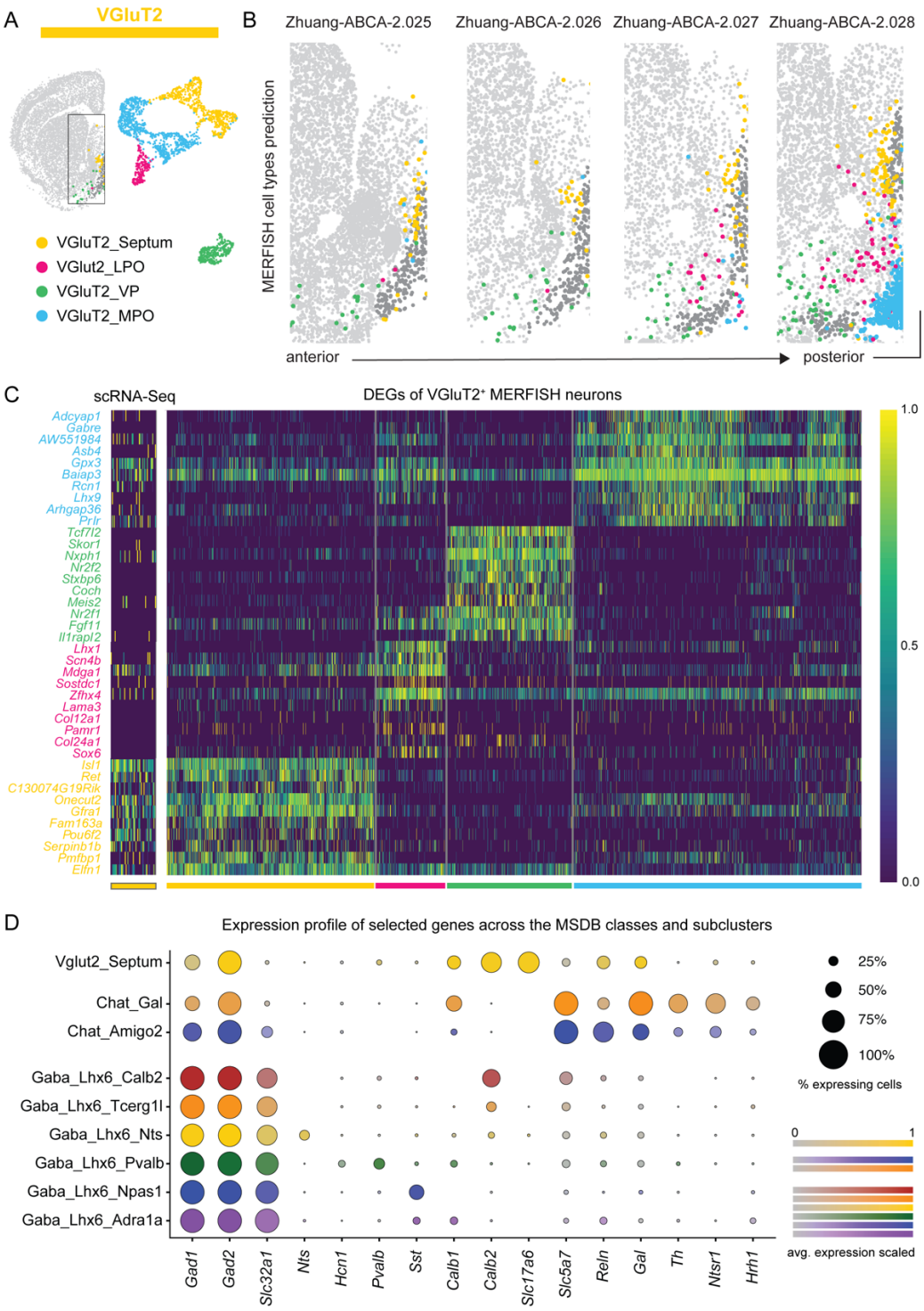

Figure 7. Transcriptomic profile of MSDB⁺ and MSDB⁻ VGluT2 neurons and selected genes expression.
A) Selection window and UMAP displaying the clusters of VGluT2⁺ neurons from the two MERFISH datasets. B) Spatial distribution of VGluT2 neurons in the selection window along the anterior-posterior axis of the Zhuang-ABCA-2 dataset. Scale bars correspond to 5 CCF units for both axes. C) Heatmap of DEGs for each MERFISH VGluT2 cluster and corresponding expression in the scRNA-Seq VGluT2 neurons. D) Expression profile of selected scRNA-Seq genes of interest across all MSDB subclusters. Percentage of cells expressing each gene indicated by dot size, average scaled expression indicated by the color bar.

DISCUSSION

The cellular landscape of the MSDB has been extensively studied, yet a consensus on the number and characteristics of its neuronal populations has remained elusive. Combining scRNA-Seq and MERFISH datasets, our study provides a comprehensive analysis of the transcriptomic profile and spatial distribution of the MSDB neurons. First, we confirmed the presence of distinct classes for cholinergic, GABAergic, and glutamatergic neurons (Figures 1 and 2). Then, we sub-clustered these classes and identified their genetic expression profiles. Finally, we analyzed the spatial distribution of the classes and their subclusters within each coronal slice and along the MSDB anterior-posterior axis.

We found that the MSDB cholinergic class is organized along a transcriptional continuum with two distinct endpoints: one exhibiting co-expression of GABAergic markers (ChAT_Amigo2), and the other associated with neuromodulators such as galanin and neurotensin (ChAT_Gal) (Figure 3). The GABAergic population is best described by six subclusters, which blend into each other, highlighting a complex and overlapping landscape (Figure 5). As indicated by their transcriptomic identities, the GABA_Lhx6_cluster is consistent with the well-documented rhythmically firing *Pvalb*$^{+}$ neurons[14,52]. Furthermore, we found the septal VGlut2 population (VGluT2_Septum) to be transcriptomically distinct from other basal forebrain (VGluT2_VP) and hypothalamic (VGluT2_MPO and VGluT2_LPO) glutamatergic populations (Figure 7).

Spatial transcriptomic analysis revealed that the cholinergic neurons show the highest density in the anterior-middle sections (Figure 4). GABAergic subclusters display specific localization patterns, with GABA_Lhx6_Pvalb neurons concentrated along the midline and GABA_Lhx6_Nts neurons being the most lateralized (Figure 6). VGluT2_Septum neurons are predominantly localized in the dorsal medial septum and increase in density towards the caudal region (Figure 7).

Transcription factor expression in the adult MSDB

The development of the septum follows what has been described as an “onion skin-like” structure[66]. This laminated structure is given by different streams of neurons that during embryonic days E10.5 to E14.5 migrate to their final location occupying first the medial and then the lateral portion of the septal area[37,66].

Transcription factors play a crucial role to regulate the neurons’ migration into their final location[67]. Having access to the full transcriptomic profile of the adult septal neurons gave us valuable information about the different populations’ identity and origin. In particular, we could distinguish between lateral and medial septum GABAergic neurons based on the exclusive expression of *Lhx6* and *Zic1*, with the GABA_Lhx6 class populating the MSDB and the GABA_Zic1 class the LS. These findings align with embryonic studies showing the specificity of *Lhx6* and *Sox6* for MSDB neurons and *Zic* family genes together with *Pax6* for LS GABAergic neurons[25,30].

Our data further confirmed *Zic1* expression in the MS ChAT population[31] even in the adult mouse brain, suggesting that MSDB ChAT neurons and LS GABAergic neurons may derive from a common progenitor or are migrating at similar time points. Indeed, recent data highlighted that nearly all cholinergic neurons in the basal forebrain express the vesicular GABA transporter (*Slc32a1)* at some point in development[43]. Additionally, we found that a strong negative marker for MSDB cholinergic neurons is the transcription factor *Gbx2,* which is exclusively expressed in the ChAT_Striatum population and completely absent in the MSDB ChAT neurons. Finally, our data show that the transcription factor *Onecut2* represents a specific signature of VGluT2_Septum neurons.

Recent studies have highlighted that the *Pvalb*$^+$ MSDB neurons are generated at E.10.5, being the earliest in the development of MSDB neurons, and thus occupying the most medial portion of the septum[24]. Indeed, our spatial analysis revealed a significant increase of GABA_Lhx6_Pvalb cells around the midline of the MSDB. Interestingly, we found that the more lateralized GABA_Lhx6 population, GABA_Lhx6_Nts, expresses *Nts,* a gene that is classically associated with LS GABAergic neurons. Our spatial analysis also revealed that the boundary between the MSDB and LS significantly depends on the markers chosen to define it. This suggests that studies using *Pvalb* to identify the MSDB may have excluded more lateral parts, particularly areas populated by VGluT2 neurons.

Septal cholinergic neurons

Being one of the most prominent cholinergic areas in the basal forebrain[68], and given its direct inputs to the hippocampal formation[69], multiple lines of research have focused on the properties of MSDB cholinergic neurons. So far, no categorization between subtypes of cholinergic neurons in the MSDB exists. While our data confirm that classical markers like *Chat* and *Slc5a7* reliably target the whole MSDB cholinergic population, we demonstrated that these neurons span through a continuum of gene expression.

On one end of the continuum resides the ChAT_Gal population, characterized by high expression levels of galanin (ChAT_Gal). Previous studies described a subpopulation of septal cholinergic neurons expressing this neuropeptide[44,70] and projecting to the hippocampal formation[65]. Interestingly, it was reported that galanin injection in the MSDB reduces theta amplitude, impairs working memory in the rat dorsal hippocampus[71], and increases acetylcholine release in the ventral hippocampus[72]. In the latter, it is suggested that galanin has a permissive effect on acetylcholine release, but an excessive release driven by galanin impairs working memory performances[72]. This observation raised some interest for its possible implications in Alzheimer disease (AD): AD patients were shown to have high levels of galanin in the basal forebrain[73,74] but it remains unclear to which extent galanin has a neuroprotective or toxic effect on the pathological septohippocampal system[75–77]. This might be further complicated by the fact that galanin is expressed, albeit at lower levels, in the glutamatergic and GABAergic neurons of the MSDB (Figure 7D). Currently no fluorescence-based reporters are available to study galanin release. Given its potential implication in AD and a so far underexplored role in the regulation of septohippocampal activity during learning and memory processes, the development of galanin

sensors could strongly advance our understanding of neuropeptide release by the Chat_Gal population. This, in turn, would shed light on both the physiological and pathological effects of galanin on the activity of the MSDB and the hippocampal formation.

On the other end of the continuum the ChAT_Amigo2 population shows high co-expression of GABAergic markers such as *Gad1* (Gad 67), *Gad2* (Gad65), *Slc32a1* (VGat) and *Slc6a1* (Gat1). While we observed that *Gad2* is present in all the MSDB neuronal types, the expression of transporters that are usually located in the presynaptic terminals of GABAergic neurons (Gat1)[78], or in the GABA containing vesicles (VGat)[79] suggests that this population is capable of co-releasing GABA and acetylcholine, as previously reported in functional[47,48,80] and developmental[43] studies. Notably, we found that the ChAT_Amigo2 neurons are expressing high levels of reelin (*Reln*), a glycoprotein studied for its role in neurodevelopment[81], synaptic plasticity[82], learning[83,84], and AD[85]. While previous studies have shown reelin positive neurons in the MSDB during development[86] and in adult mice[87]; and despite the broad interest for reelin and the MSDB in relation to AD[88–90], no studies to our knowledge have reported its expression in cholinergic neurons or have investigated the functional role of reelin in the MSDB.

The diversity of MSDB GABAergic neurons

The complexity of the GABAergic cell types in both cortical and subcortical circuits has been widely recognized[91–94]. The GABAergic MSDB neurons have been initially studied in relation to the hippocampal formation and *Pvalb* was recognized as a key marker for septohippocampal GABAergic projections[12]. Other populations were then described based on the observation that some MSDB neurons express GABAergic markers but are not *Pvalb*$^{+}$[16]. In particular, *Calb1*[95], *Calb2*[16], and *Slc32a1* (VGat)[96], were used as GABAergic markers in the MSDB. However, so far there is still limited knowledge about the degree of overlap between these markers and the total number of distinct GABAergic populations in the MSDB.

Our analysis revealed that MSDB GABAergic neurons can be best described by six sub-clusters blending into each other. Surprisingly, we found that two classical GABAergic markers, *Gad1* and *Gad2,* are not specific for GABAergic septal neurons. Thus, using Cre dependent lines with these promoters in the MSDB may lead to targeting a broader and less specific population of neurons than anticipated.

We identified that the GABA_Lhx6_Pvalb subcluster of GABAergic neurons expresses *Pvalb*. Further analysis of the transcriptomic profile of this subcluster revealed that its neurons also exhibit the highest expression of *Hcn1* (Figure 7D), the hyperpolarization-activated, cyclic nucleotide-gated (HCN) channel. *Hcn1* is known for its role in the pacemaking activity widely reported in MSDB *Pvalb* neurons, which is crucial for the synchronization of hippocampal theta activity[14,52]. Additionally, our findings show that the genes expressed in the GABA_Lhx6_Pvalb cluster strongly correlate with the electrophysiological features of *Pvalb*$^{+}$ neurons, further validating our transcriptomic analysis.

We further characterized a subcluster, GABA_Lhx6_Npas1, with the highest expression of somatostatin (*Sst*) (Figure 7D). *Sst* is a well-characterized marker for GABAergic neurons in the cortex and in the hippocampal formation[97]. While earlier studies reported only scattered *Sst* expression in the MSDB[98], recent research demonstrated a role of these neurons in appetitive learning[99] and spatial working memory[100] highlighting that scattered and sparse expression does not per se preclude a behavioral relevance. Notably, these GABA_Lhx6_Npas1 neurons also express the Neuronal PAS domain 1 (*Npas1*) gene, which is known to limit interneuron proliferation and is linked to the formation of *Sst* neurons during cortical development[101]. *Npas1*$^+$ GABAergic neurons have been extensively studied in the nearby ventral pallidum, where they are implicated in anxiety[102] and sleep regulation[103]. This observation suggests that a deeper experimental investigation into the relevance of these *Npas1*$^+$/*Sst*$^+$ population in the MSDB could lead to important insights.

Furthermore, we identified neurotensin (*Nts)* in the GABA_Lhx6_Nts subcluster. *Nts* has been so far studied in relation to feeding behavior in the hypothalamus and LS[104,105]. Although a few studies have reported the presence of *Nts*$^+$ neurons in the MSDB[98,106], no functional studies have yet been conducted on this neuronal population. This gap of knowledge could be partially due to the subcluster's spatial distribution, which is quite lateralized in the mid- and posterior- MSDB coronal slices. Notably, ChAT_Gal neurons express the neurotensin receptor 1 (*Ntsr1*). *In vitro* studies in guinea pigs have shown that neurotensin increases the excitability of MSDB cholinergic neurons, potentially impacting hippocampal theta activity[107] and hippocampal learning and memory processes[44,107]. Future research on the mechanisms by which the GABA_Lhx6_Nts population interacts with hippocampal rhythmogenesis and plasticity via neurotensin release may hold promise to shed new light on non-canonical ways of neuronal communication in the septo-hippocampal system.

Finally, we detected a subcluster expressing high levels of the calcium binding protein calretinin (*Calb2*), GABA_Lhx6_Calb2. Notably, we observed comparable expression levels of *Calb2* in the VGluT2_Septum population (Figure 7D). This finding is in line with developmental studies indicating that at E17.5 the VGluT2 MSDB neuron distribution pattern overlaps with *Calb2* but not with *Gad1*[108]. Additionally, the VGluT2 and ChAT_Gal subclusters exhibited higher levels of the calcium binding protein calbindin (*Calb1*) compared to any other of the identified GABAergic groups.

In summary, we uncovered a previously undescribed diversity within the MSDB GABAergic population. The data underscore the importance of carefully selecting marker genes to accurately target GABAergic subclusters selectively. This also applies to the selection of driver-lines for specific targeting and manipulation of neuronal activity. A special consideration should be given to MSDB neuronal populations co-expressing cholinergic and GABAergic markers, as evidence for specific functional relevance of synaptic co-transmission of different neurotransmitter molecules emerges[43,47]. Our data also imply that markers typically associated with inhibitory neuronal transmission in the MSDB may also be present in excitatory and neuromodulatory septal neurons. This finding underscores the importance of designing experimental strategies that account for this complexity.

Limitations and future research

It is important to point out, that transcriptomic studies have intrinsic methodological limitations. First, some cell types may be particularly sensitive to the mechanical procedures required for scRNA-Seq, leading to underrepresentation in the sequencing data as shown by the different proportion of scRNA-Seq and MERFISH cell count for cholinergic and GABAergic neurons. Additionally, MERFISH data acquisition necessitates the a priori selection of a panel of genes of interest. When using publicly available datasets, this requirement can constrain the depth of analysis, as it depends heavily on the initially selected genes. For instance, many genes of interest highlighted in our dot plot analysis are absent from the MERFISH dataset, limiting our ability to explore their spatial localization. Lastly, transcriptomic analysis provides only a snapshot of the genes expressed at the time of tissue collection. While these data are valuable for planning future experiments, they need to be further corroborated by protein expression analysis.
Despite these potential limitations, we presented a solid framework for studying the MSDB and its diverse cell populations in the future. The discovery that both ChAT and GABAergic neurons are organized in a continuum of clusters underscores the cellular complexity of the MSDB which is comparable to those observed in other subcortical and cortical regions[45,109,110].This so far unaccounted complexity necessitates the development of new approaches, such as intersectional gene targeting and multi-omics assays, to fully understand the functional roles of these neurons within the network. By combining our results with novel techniques, future research will provide deeper insights into the interactions and contributions of the various cell types within the MSDB in guiding rodent behavior.

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AUTHOR CONTRIBUTIONS
Conceptualization: S.P., M.S.C., and S.R.; Software & Formal analysis: F.K.; Resources: M.S.C.; Writing - Original Draft: P.M., F.K.; Visualization: F.K., P.M.; Funding acquisition: S.R.

DECLARATION OF INTERESTS
The authors declare no competing interests.

CODE AND DATA AVAILABILITY
Code and data will be made available upon final publication.

METHODS

Key resources table

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Deposited data		
ScRNA-Seq data	This paper	GEO: GSE163476
Single-cell spatial transcriptomics data	Zhang et al.[33]	
Experimental models: Organisms/strains		
C57BL/6 mice	Jackson Laboratory	RRID: IMSR_JAX:000664
Software and algorithms		
R	R Development Core Team[111]	RRID:SCR_001905
Seurat	Satija et al.[112]	RRID:SCR_007322
Python 3	van Rossum et al.[113]	RRID:SCR_008394
scanpy	Wolf et al.[114]	RRID:SCR_018139
statsmodels	Seabold et al.[115]	RRID:SCR_016074
PySal-esda	Rey et al.[116]	
scMiko	Mikolajewicz et al.[24]	
Code	This paper	

EXPERIMENTAL MODEL

Animals

Experiments used 4 male wild-type C57BL/6 mice between 2-4 months of age, with mice individually housed and maintained on a 12-h light-dark cycle with *ad libitum* access to food and water, with tissue harvested during the light phase. All experimental procedures were approved by the Janelia Research Campus Institutional Animal Care and Use Committee.

METHOD DETAILS

scRNA-Seq data acquisition

Single-cell RNA sequencing datasets were generated according to a previously published protocol[117]. In total, four mature C57BL/6 WT male mice were used to construct datasets. From each mouse, coronal brain sections were cut, and the medial septum and nucleus of the diagonal band micro-dissected and dissociated. For manual purification of individual cells[118], cells were aspirated in capillary needles in approximately 0.1-0.5 mL ACSF cocktail and placed into 8-well strips containing 3 µL of cell collection buffer (0.1% Triton X-100, 0.2 U/µL RNAse inhibitor (Lucigen, Middleton, WI), and generally processed according to published methodology[119].

In brief, each strip of cells was flash frozen on dry ice, then stored at -80°C until cDNA synthesis. Cells were lysed by adding 1 µL lysis mix (50 mM Tris pH 8.0, 5 mM EDTA pH 8.0, 10 mM DTT, 1% Tween-20, 1% Triton X-100, 0.1 g/L Proteinase K (Roche), 2.5 mM dNTPs

(Takara), and ERCC Mix 1 (Thermo Fisher) diluted to 1e-6) and 1 µL 10 µM barcoded RT primer (E3V6NEXT primer from [121], modified to add a 1 bp spacer before the barcode, extending the barcode length from 6bp to 8bp, and designing the 384 barcodes to tolerate 1 mismatch error correction). The samples were incubated for 5 minutes at 50°C to lyse the cells, followed by 20 minutes at 80°C to inactivate the Proteinase K. Reverse transcription master mix (2 µL 5× buffer (Thermo Fisher Scientific), 2 µL 5M Betaine (Sigma-Aldrich, St. Louis, MO), 0.2 µL 50 µM E5V6NEXT template switch oligo (Integrated DNA Technologies, Coralville, IA), 0.1 µL 200 U/µL Maxima H- RT (Thermo Fisher Scientific), 0.1 µL 40 U/µL RNasin (Lucigen), and 0.6 µL nuclease-free water (Thermo Fisher Scientific) was added to the approximately 5.5 µL lysis reaction and incubated at 42°C for 1.5 hour, followed by 10 minutes at 75°C to inactivate reverse transcriptase. PCR was performed by adding 10 µL 2× HiFi PCR mix (Kapa Biosystems) and 0.5 µl 60 µM SINGV6 primer with the following conditions: 98°C for 3 minutes, 20 cycles of 98°C for 20 seconds, 64°C for 15 seconds, 72°C for 4 minutes, with a final extension step of 5 minutes at 72°C. Samples were pooled across the plate to yield approximately 2 mL pooled PCR reaction. From this, 500 µL was purified with 300 µL Ampure XP beads (0.6× ratio; Beckman Coulter, Brea, CA), washed twice with 75% ethanol, and eluted in 20 µL nuclease-free water. The cDNA concentration was determined using Qubit High-Sensitivity DNA kit (Thermo Fisher Scientific).

Twelve plates were analyzed in total, with six hundred pg cDNA from each plate of cells used in a modified Nextera XT (Illumina, San Diego, CA) library preparation with 5 µM P5NEXTPT5 primer [66]. The resulting libraries were purified according to the Nextera XT protocol (0.6× ratio) and quantified by qPCR using Kapa Library Quantification (Kapa Biosystems). Plates were pooled on a NextSeq 550 high-output flowcell with 26 bases in read 1, 8 bases for the i7 index, and 50 bases for read 2. Alignment and count-based quantification of single-cell data was performed by removing adapters, tagging transcript reads to barcodes and UMIs, and aligned to the mouse genome via STAR [123].

Data preprocessing and batch integration of scRNA-Seq data

For the computational analysis of the scRNA-Seq data the R package Seurat (v.5.1.0)[120] was used. All functions mentioned hereafter are from the Seurat package with default parameters unless stated otherwise. A Seurat Object for each batch was created separately from the raw count data using the *CreateSeuratObject* function. Only high-quality neurons, which expressed at least 2500 features, at least 10,000 RNAs, and had a count for the neuronal marker *Snap25* of at least 10, were considered. To normalize the data, scale the data, find variable features per cell, and remove confounding sources of variation, the *SCTransform* function was applied to each batch separately. After that, 4000 integration features were determined using the function *FindIntegrationFeatures*, based on which the integration of both datasets was conducted using Canonical correlation analysis (CCA)[35] with the *PrepSCTIntegration*, *FindIntegrationAnchors* and *IntegrateData* functions.

Dimensionality reduction and (sub-)clustering of scRNA-Seq data

To cluster the data into coarse neuron classes, the dimensionality of the integrated Seurat object was reduced to thirteen dimensions by running principal component analysis (PCA). Thirteen dimensions in principal component (PC) space were selected for clustering based on *ElbowPlot* inspection. The number of dimensions was chosen to be on the higher end because *SCTransform* allows for the identification of more nuanced biological differences and variations across different cell types while maintaining low sensitivity to technical noise and the selected number of dimensions. Then the data was clustered in the dimensionality reduced space with the *FindNeighbors* (dims = 1:13) and *FindClusters* (resolution = 0.1) functions, using the Leiden algorithm[23]. The clustering's insensitivity to the number of dimensions was demonstrated by reclustering the data using 20 dimensions without change in cell class assignments across all neurons. The resolution for the Leiden clustering of 0.1 was determined using the *multiCluster* function followed by the *multiSpecificity* function of the Seurat-based package *scMiko*[24]. This function clusters the data over a wide range of resolutions, and calculates an aggregate score for marker gene specificity for each resolution, based on the co-dependency index (CDI) metric. The optimal resolution was chosen as the one with the highest aggregate score. The identification of glutamatergic, GABAergic and cholinergic clusters was based on the expression profiles of the cholinergic marker gene Chat, the gene for the glutamate transporter vGluT2 (*Slc17a6*) and the gene for the vesicular GABA transporter vGAT (*Slc32a1*). To visualize the clustering results we projected the data points from the reduced feature space on a two dimensional plane using Unifold Manifold Approximation and Projection (UMAP)[122] with *RunUmap* (dims=1:13).
For subclustering of the GABA_Lhx6 and the ChAT cell class, neurons belonging to the specific class of interest were batch-integrated anew. This new batch integration was performed to disregard effects from non-related neuron classes. For the integration, 2000 integration features were used. Subclustering followed the same procedure as clustering for main cell classes. Both the ChAT class and the GABA_Lhx6 class were subclustered in the first 10 dimensions after PCA using resolutions of 0.4 and 1.2, respectively.

Differential expression analysis and identification of marker genes

To identify the top differentially expressed genes (DEGs) for all four coarse cell classes, the Seurat object's SCT assay was used. Initially, the *PrepSCTFindMarkers* function was run, followed by the Wilcoxon rank sum test for DEG identification using *FindMarkers* (*min.diff.pct* = 0.3, *logfc.threshold* = 1.5, *only.pos* = TRUE). The test compared the expression of each gene in a certain class to its expression in all other classes combined. This was also done for DEG identification of ChAT and GABA_Lhx6 subclusters, only that here the test compared gene expression in the respective subcluster with its expression in all other subclusters of the respective class combined. The min-max scaled log-expression of the 10 DEGs with the lowest FDR-corrected p-values (using Bonferroni correction) per cluster was visualized on heatmaps using the *DoHeatmap* function. Cells of the ChAT subclusters were additionally sorted according to their rank on the diffusion pseudotime axis before being plotted on the heatmap. The *R* package *EnhancedVolcano*[124] was employed to display DEG expression between the ChAT_Amigo2 and ChAT_Gal subclusters in a Volcano plot.

Exclusive marker genes for subclusters were identified by calculating CDI and CDI based p-values for each gene using the *findCDIMarkers* function of the *scMiko* package. The function was run on the Seurat object's SCT assay after running *PrepSCTFindMarkers*. For the suffixes of the subclusters we used genes which were previously mentioned in the literature in association with MSDB cell types or common Cre-lines if they had a normalized CDI of at least 0.2 and a p-value below 1e-6 (*Amigo2* for ChAT_Amigo2 - Jackson Strain #:030215; *Gal* for ChAT_Gal; *Nts*[107] for GABA_Lhx6_Nts - Jackson Strain #:017525; *Calb2*[16] for GABA_Lhx6_Calb2 - Jackson Strain #:010774; *Pvalb*[56] for GABA_Lhx6_Pvalb, Jackson Strain #:017320). If no previous association was apparent with any of the top marker genes, we named the subclusters by using genes with the lowest p-value that had a normalized CDI of at least 0.2 as suffixes (*Tcerg1l* for GABA_Lhx6_Tcerg1l, *Npas1* for GABA_Lhx6_Npas1 and *Col25a1* for GABA_Lhx6_Col25a1).

Subcluster discreteness analysis

To evaluate the discreteness of GABA_Lhx6 and ChAT subclusters, a method introduced by Stanley and colleagues[45] was employed to examine gaps in diffusion pseudotime and relative cluster connectivity. Diffusion pseudotime, which places cells on an axis reflecting the highest variance between two clusters[46], and relative cluster connectivity, which measures a cell's similarity to cells within the same cluster compared to those in different clusters, were both calculated. Discrete clusters exhibit a larger gap in diffusion pseudotime compared to continuous ones. This gap was quantified using the gap c statistic. For the analysis of ChAT and GABA_Lhx6 subclusters diffusion pseudotime, relative cluster connectivity, and the gap c statistic were calculated using customized code from Stanley et al.[45] which is based on the *scanpy* package[114].

As an additional assessment of ChAT subcluster discreteness, the relative gene score of each cell was plotted as a function of pseudotime rank. To calculate the relative gene score for each ChAT cell, positive DEGs for both subclusters were first calculated using the Wilcoxon rank sum test. The z-scored gene expression of positive DEGs for the ChAT_Amigo2 subcluster was added, and the z-scored gene expression of positive DEGs for the ChAT_Gal subcluster was subtracted for each cell individually. Only genes with a Bonferroni-corrected p-value below 1e-6 were included in this calculation.

Gene ontology analysis and correlation with electrophysiological properties

Gene ontology (GO) analysis for both ChAT subclusters was done using the R package *clusterProfiler*[125]. First, a list of DEGs between the two subclusters was calculated using the Seurat function *FindMarkers* (*min.diff.pct* = 0.3, *logfc_threshold* = 1, *min.pct* = 0.5). This list was then subsetted to include only genes with a Bonferroni-corrected p-value below 5e-4. Subsequently, clusterProfiler's *compareCluster* function was applied to the Molecular Function ontology and the Biological Process ontology. The embedded *enrichGO* function, with a q-value cutoff of 0.01, was used to identify significant correlations between clusters and GO terms based on the marker genes. For the Biological Process ontology, only brain-related terms were considered, excluding e.g. terms such as bone development.

To identify how differentially expressed genes (DEGs) of the GABA_Pvalb subcluster correlate with electrophysiological properties, positive DEGs for GABA_Pvalb neurons compared to all other neurons of the GABA_Lhx6 class were calculated using Wilcoxon rank sum test with *FindMarkers* (*min.pct* = 0.3 and *logfc.threshold* = 0.5). The database and demo code from Bomkamp and colleagues[55] were then utilized to identify DEGs which had significant correlations (either positive or negative) with electrophysiological properties in inhibitory neurons. A significance threshold of *FDR_gene_inh_only* < 0.1 was applied. Next, a heatmap was constructed showing the log2 fold-change expression of significantly upregulated DEGs of the GABA_Lhx6_Pvalb cluster which also had a significant correlation with electrophysiological properties. Electrophysiological properties were included in the heatmap only if they had either four times as many positively correlated genes as negatively correlated genes, or four times as many negatively correlated genes as positively correlated genes. For GABA_Lhx6 neurons not belonging to the GABA_Lhx6_Pvalb subcluster, the same analysis was performed with negative DEGs of the GABA_Lhx6_Pvalb subcluster (i.e., genes significantly downregulated in GABA_Lhx6_Pvalb).

MERFISH data integration and analysis

For the spatial transcriptomics analyses, two coronal MERFISH datasets, Zhuang-ABCA-1 and Zhuang-ABCA-2[33], from the Allen Brain Cell Atlas (ABCA) were utilized. Both datasets included 1122 genes. The segmentation of mRNA spots into single cells was already given by the Zhuang-ABCA datasets and adopted. The segmentation of the MSDB was based on alignment with the Allen Mouse Brain Common Coordinate Framework version 3 (CCF)[34], which was also provided with the Zhuang-ABCA datasets. The MSDB segmentation was further refined and cropped to include only the left hemisphere using a custom-made tool. This refinement was done to avoid any bias in cell quantification due to the incomplete representation of the right hemisphere in both Zhuang datasets. Both Zhuang datasets were further subset to include only neurons. For each dataset a separate Seurat object was created and the *SCTransform* function was applied to both Seurat objects separately. Subsequently, CCA-based integration of both objects was performed using the *FindIntegrationAnchors* and *IntegrateData* functions.

MERFISH cell-type prediction and validation

To predict the class identity of MERFISH neurons based on the scRNA-Seq analysis, CCA-based prediction scores were calculated for all MERFISH neurons using Seurat's *FindTransferAnchors* (dims = 1:13) and *TransferData* (dims = 1:13) functions. The integrated MERFISH dataset served as the query, while the cell class identities of the integrated scRNA-Seq neurons served as reference. Only neurons with a maximum prediction score above 0.9 were assigned class labels. To explore the spatial distribution of cell types in the periphery of the MSDB, this analysis was repeated, also including cells from a selection window over all slices spanning from $CCF_z = 4$ to the brain midline and from $CCF_y = 3$ to $CCF_y = 7$, with CCF_z and CCF_y being the coordinates in the CCF framework spanning coronal slices. For all the analyses mentioned hereafter, the selection window refers to the window described here.

To validate the predicted class identity of the MERFISH neurons, marker genes for the predicted MERFISH cell classes were identified with *scMiko*'s *findCDIMarkers* function. Gene expression profiles displaying the min-max scaled log-expression of the top 10 marker genes which had the lowest p-value, a normalized CDI score of at least 0.2 and which were present in both scRNA-Seq and MERFISH datasets were confirmed for similarity between scRNA-Seq and MERFISH datasets.

To ensure that no major cell class was overlooked in the scRNA-Seq dataset, an integrated Seurat object of $MSDB^+$ neurons from both MERFISH datasets and both scRNA-Seq batches was created using the *FindIntegrationAnchors* (dims = 1:13) and *IntegrateData* (dims = 1:13) functions. A UMAP was then computed in the integrated dataset's feature space (dims = 1:13), referred to as joint feature space (jFS). The similar distribution pattern of both MERFISH and scRNA-Seq neurons on the UMAP indicated that no major neuron class was missed in the scRNA-Seq dataset.

For the prediction and integration of MERFISH ChAT subclusters, the same analysis as for the main neuron classes was employed with a few differences: only MERFISH neurons previously predicted as ChAT neurons were used for prediction and integration; both prediction and integration were conducted in the first 10, instead of the first 13 dimensions of PC space; and the threshold for prediction scores was lowered to 0.5. This adjustment ensured that cells lying in the middle of the continuum between both ChAT subclusters were not disregarded. The analysis was repeated, including MERFISH ChAT neurons from both MSDB and Striatum by selecting cells from the selection window. After subclustering the integrated dataset of MSDB and Striatal ChAT MERFISH neurons (following the previously described subclustering workflow - here with dims = 1:13 and a Leiden resolution of 0.05), it was found that Striatal ChAT neurons formed a distinct cluster compared to $MSDB^+$ ChAT neurons. Therefore, subcluster identities from scRNA-Seq ChAT subclusters were only predicted for MERFISH ChAT neurons belonging to the cluster populated with $MSDB^+$ cells. Neurons from the other cluster were assigned the label ChAT_Striatum.

The subcluster identities of $MSDB^+$ MERFISH neurons of the GABA_Lhx6 class were determined using the same methods as for the ChAT class. Prediction scores for MERFISH GABA_Lhx6 neurons, as well as the subcluster identities of GABA_Lhx6 scRNA-Seq neurons, were visualized on a UMAP in jFS. Since some regions of the jFS were only sparsely populated by scRNA-Seq neurons, but densely by MERFISH neurons, it was checked if the MERFISH neurons in this region constitute separate subclusters that were not represented in the scRNA-Seq dataset. Therefore, the GABA_Lhx6 neurons from both MERFISH datasets were additionally integrated without the scRNA-Seq neurons and subclustered using the same functions for integration and subclustering as for the GABA_Lhx6 scRNA-Seq data; here with a Leiden resolution of 0.3. The MERFISH subcluster assignments were also visualized in the jFS. The areas of the jFS which were densely populated by MERFISH neurons and sparsely by scRNA-Seq cells did not constitute separate MERFISH clusters, indicating that the scRNA-Seq data covered the spectrum of GABA_Lhx6 subclusters well.

To further validate the prediction for the MERFISH GABA_Lhx6 subclusters, the top marker genes for the predicted subclusters of MERFISH GABA_Lhx6 neurons were identified with *scMiko*'s *findCDIMarkers* function. Heatmaps displaying the min-max scaled expression of the top 10 marker genes which had the lowest p-value, a normalized CDI score of at least 0.2 and which were present in both scRNA-Seq and MERFISH datasets were plotted for both MERFISH and scRNA-Seq neurons and confirmed for similarity. For the spatial analysis (described later in the Methods section), prediction and integration were additionally conducted for neurons in the selection window, also including neurons outside of the MSDB borders. For this all functions and parameters were the same as for the prediction and integration of MSDB+ neurons only.

Clustering analysis of VGluT2 cells in MERFISH datasets

Neurons from inside the selection window were chosen from both MERFISH datasets and further subsetted for glutamatergic neurons using the neurotransmitter labels given by the ABCA. The selected neurons of both MERFISH datasets were integrated and subclustered as described for the GABA_Lhx6 MERFISH neurons, only that here the first 6 dimensions in PC space and a Leiden resolution of 0.05 was chosen after inspection of the *ElbowPlot*. The relatively low number of PCs and the relatively low resolution focuses the analysis on the most significant sources of variation, minimizing the effects of a potential bias that could have been introduced by the pre-selected and limited MERFISH gene set.
Since the cell number of scRNA-Seq neurons was relatively small and thus not optimal for CCA-based integration with the MERFISH dataset, CDI-based markers were calculated for the glutamatergic MERFISH clusters using *scMiko*'s *findCDIMarkers* function on the integrated dataset. The min-max scaled log-transformed expression of the marker genes with the lowest p-values, which had a normalized CDI score of at least 0.2, were plotted in a heatmap. Additionally, the min-max scaled log-expression of the same genes was plotted for all scRNA-Seq neurons of the VGluT2 class, showing that the expression profile of the scRNA-Seq VGluT2 neurons corresponds with the expression profile of the VGluT2_Septum class.

Spatial analysis

To show the spatial distribution of MERFISH cell classes and subclusters, cells inside of the selection window were plotted in CCF-coordinates color coded by the specific classes or subclusters of interest. Significant spatial trends were investigated among $MSDB^+$ neurons inside of each MERFISH slice, as well as along an anterior-posterior axis across slices.
Significant spatial trends of MSDB+ neurons across the anterior-posterior axis were determined by shuffling class or subcluster labels of MSDB+ neurons across all $MSDB^+$ slices 1,000 times. A neuron class or subcluster was determined to be significantly enriched in a slice along the anterior-posterior axis if it was abundant more often than in 95 percent of the shuffles. For anterior-posterior trends of neuron classes the shuffling was performed across all neurons; for Chat subclusters and GABA_Lhx6 subclusters, shuffling was performed among ChAT and GABA_Lhx6 neurons only.

Spatial trends of MSDB$^+$ neurons along the mediolateral and dorsoventral axes were investigated for each individual slice separately. First, a k-nearest neighbors' graph was constructed using euclidean distance. To account for the differences in cell densities, a k of 15 was used for main cell classes, a k of 10 was used for GABAergic subclusters and a k of 5 was used for ChAT subclusters. Each edge of the graph that connected two cells of the respective class or subcluster of interest was given a weight of 1; all other edges were given a weight of 0. The graph was then used to calculate global Moran's I[126] on it, which is a metric that quantifies the spatial clustering of the data. Moran's I was calculated using the *moran.Moran* function of the Python package *PySal-esda*[116]. To determine if the spatial clustering observed on the respective slice was significantly above chance, class/subcluster labels of the neurons of interest were shuffled 1,000 times and global Moran's I was calculated for each of the shuffles. Spatial clustering was determined to be significant if the rank of the actual global Moran's I was above the 95th percentile ($p < 0.05$) of all shuffles. For the main neuron classes, all MSDB$^+$ neurons of the respective MERISH slice were used for shuffling; for ChAT subclusters, only ChAT neurons were used, and for the GABA_Lhx6 subclusters, only GABA_Lhx6 neurons were used. The procedure was repeated for each class/subcluster separately.

For neuron classes/subclusters that showed significant spatial clustering inside MSDB on individual slices, a two-dimensional maximum-likelihood kernel density estimation (ml-KDE) was calculated using the *KDEMultivariate* function of the Python package *statsmodels*[115]. The two-dimensional full width at half maximum (FWHM) of the ml-KDE was plotted on top of the respective spatial plot.

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