

**Patterns, Volume 5**

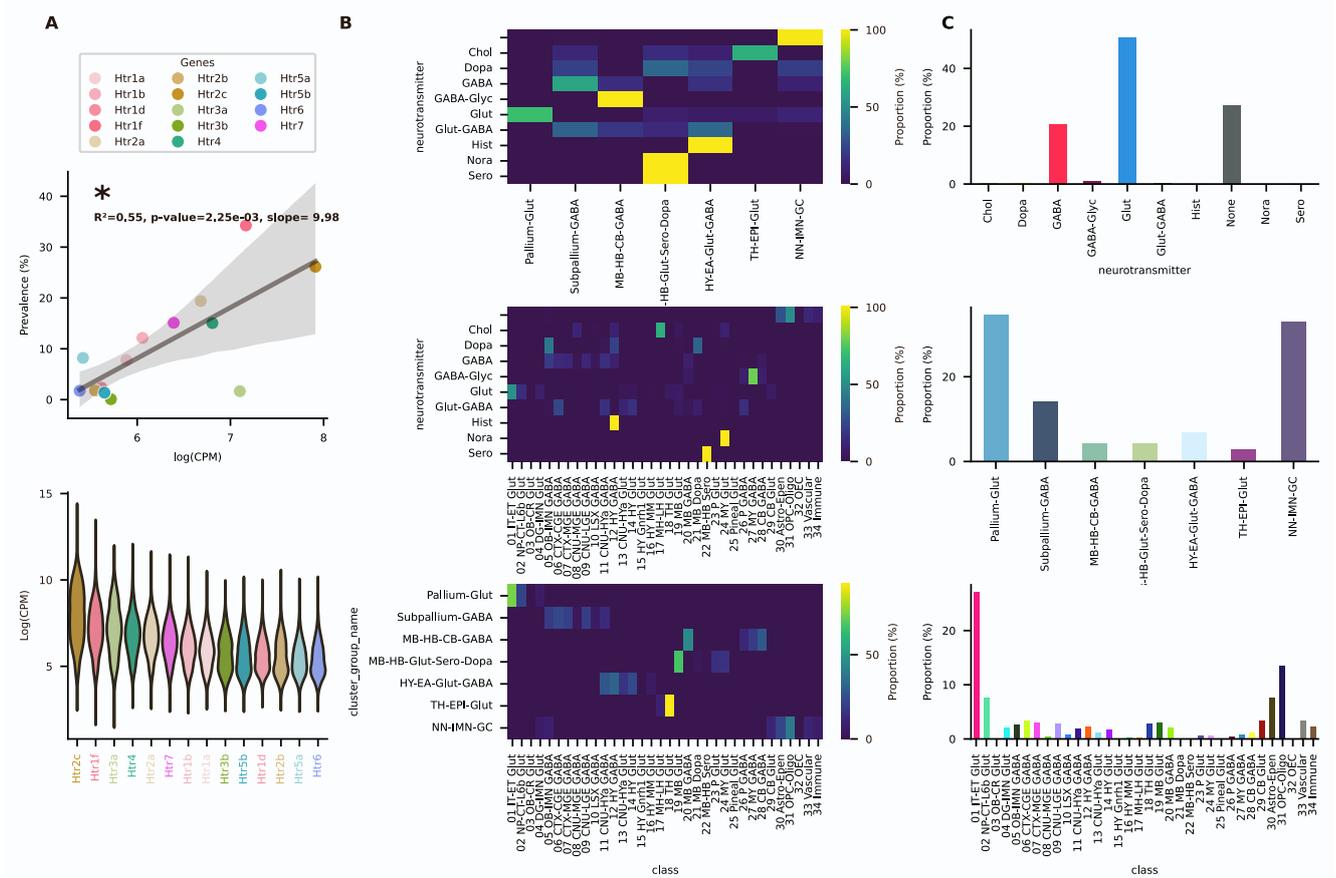
**Supplemental information**

**Transcriptomic mapping  
of the 5-HT receptor landscape**

**Roberto De Filippo and Dietmar Schmitz**



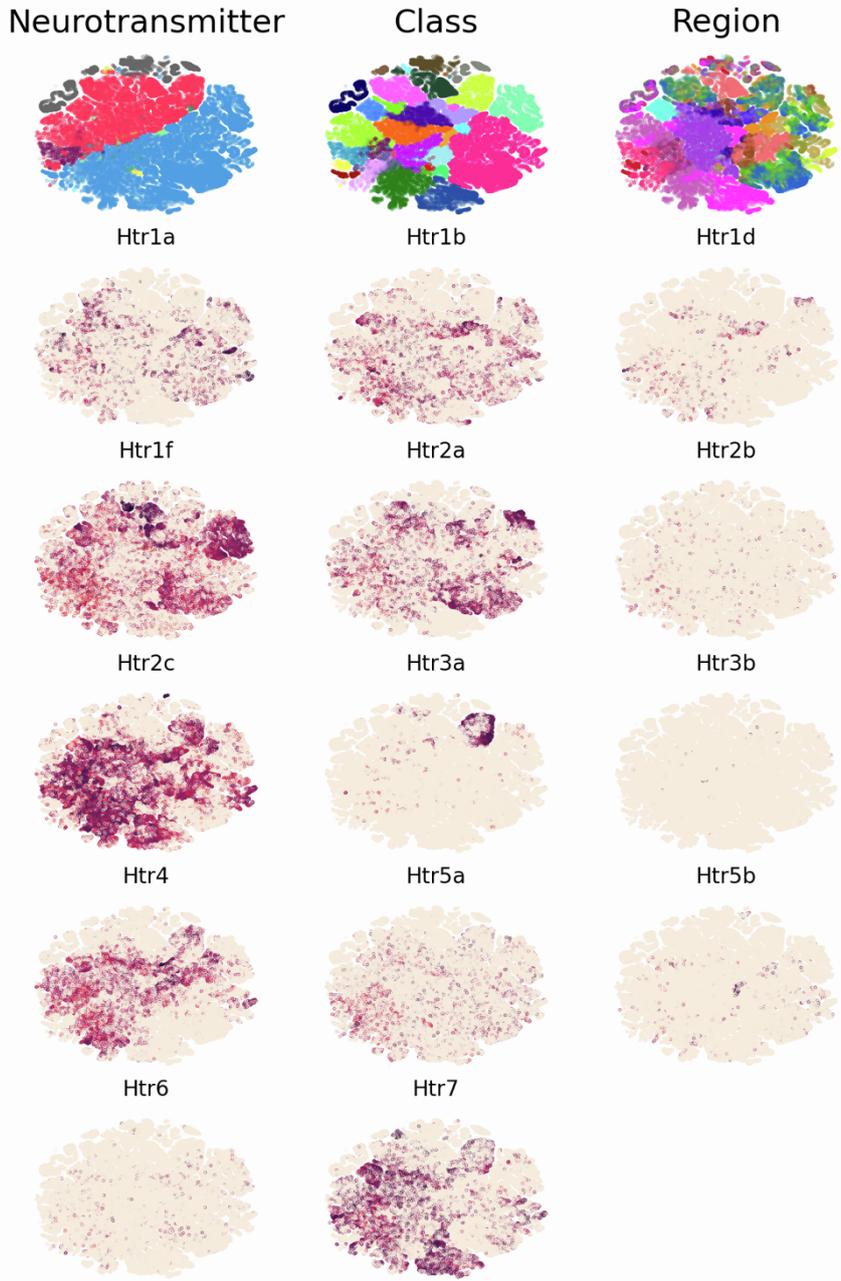
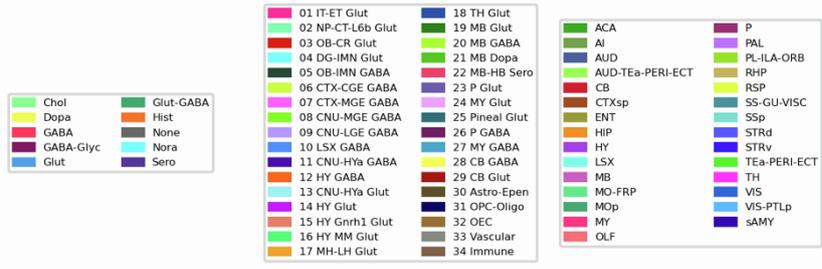
18 **Supplementary Figures**



19

20 **Figure S1. Htrs transcription and hierarchical clustering visualization.**

21 (A) Top: Linear regression model fit between prevalence (y axis) and amount of intracellular  
 22 expression (x axis) for each Htrs. Bottom: violin plots showing distribution of intracellular  
 23 amount of expression for each Htrs. (B) Heatmaps showing relationship between  
 24 neurotransmitter, class and neighborhoods. (C) Bar plots representing the size of each group  
 25 when cells are categorized by neurotransmitter (top), neighborhood (middle) and  
 26 (bottom).

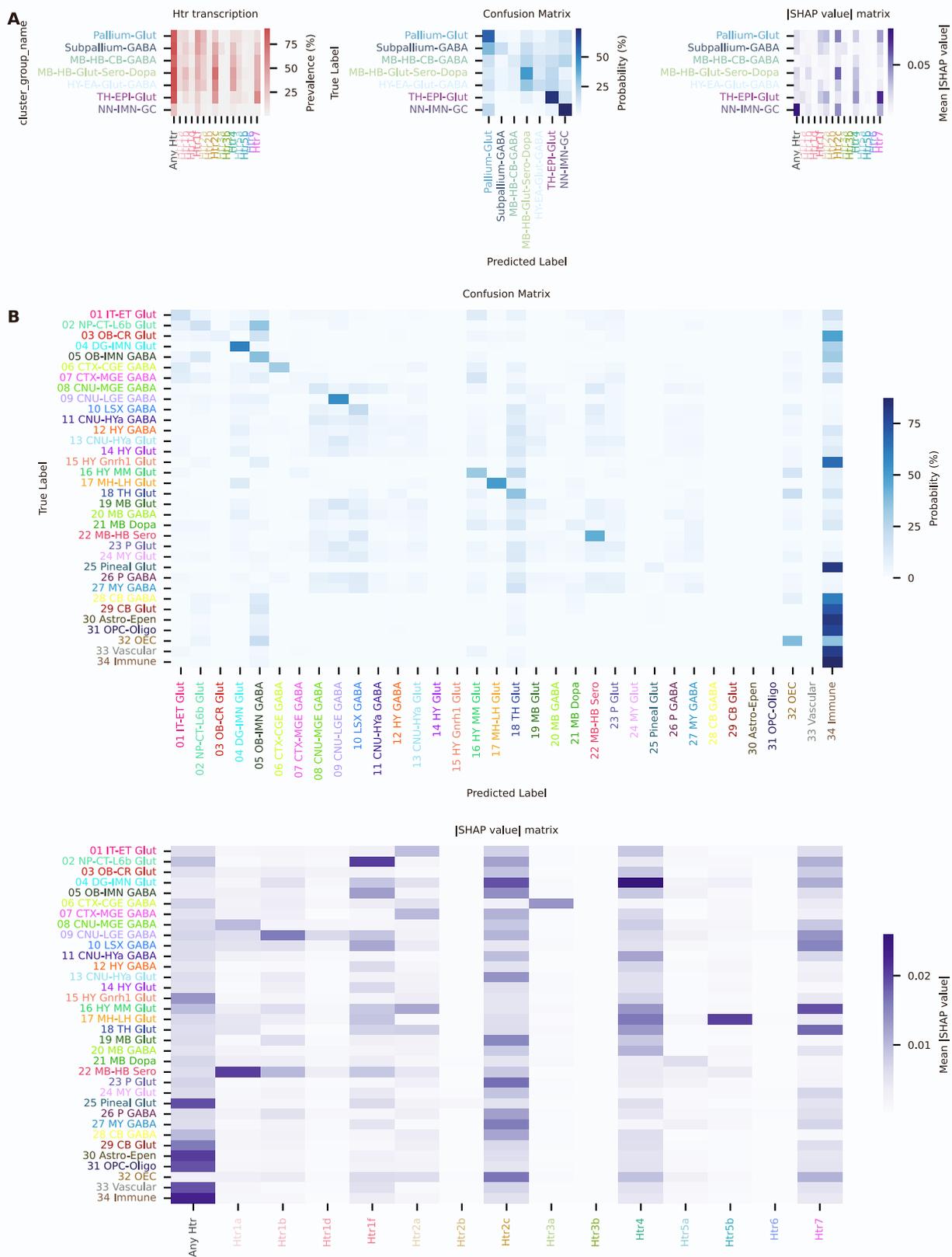


27

28 **Figure S2. UMAP distribution of each Htr.**

29 UMAP-associated neurotransmitter, class and dissection region metadata (first row) and

30 UMAP distribution of each Htr.

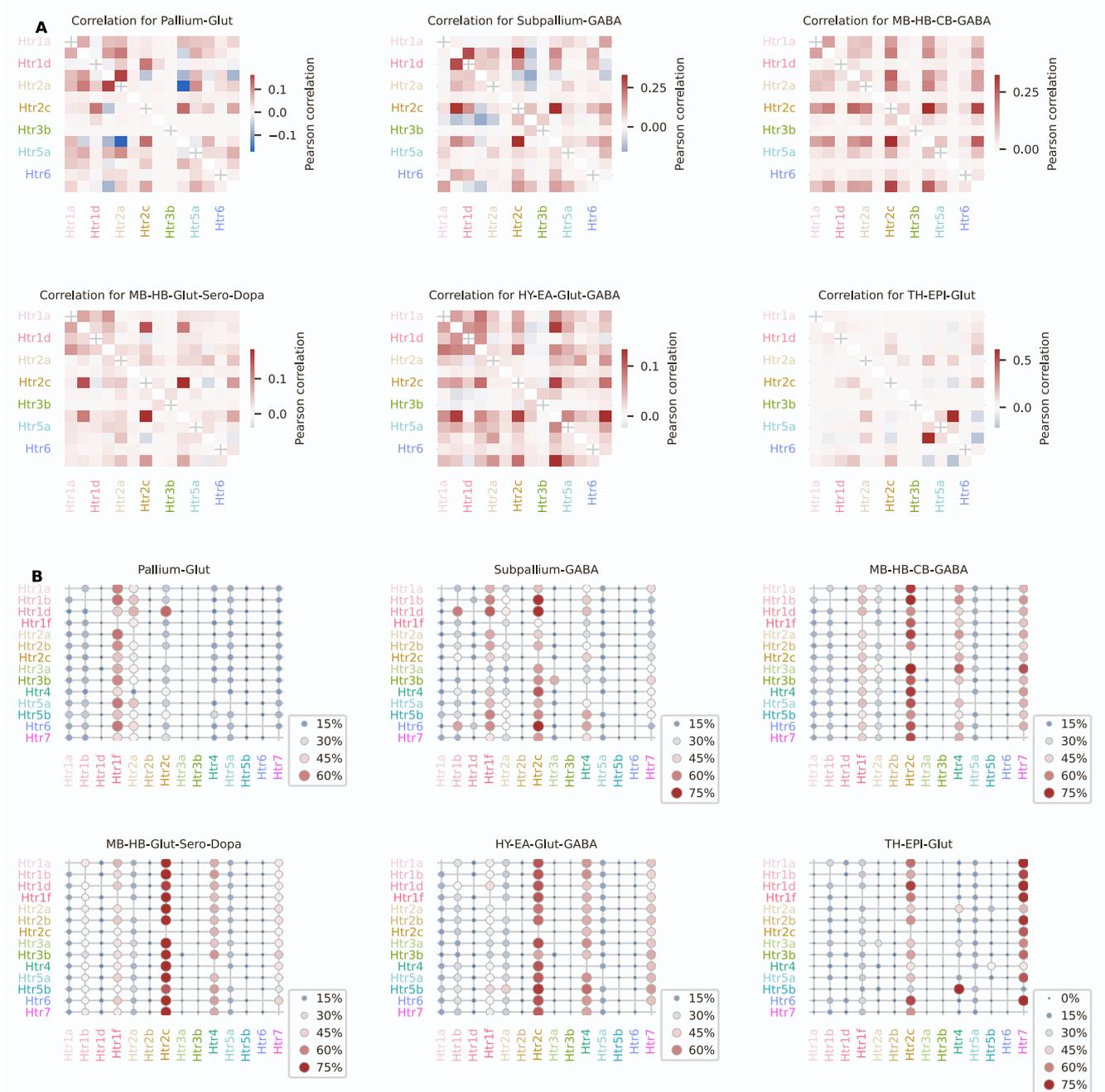


31

32 **Figure S3. Htrs features across neighborhoods and classes.**

33 (A) Htrs prevalence across neighborhoods (left). Confusion matrix related to the decoding of  
 34 neighborhoods classification from Htrs transcription (middle). SHAP values matrix associated  
 35 to the neighborhood decoding (right). (B) Confusion matrix related to the decoding of classes

36 classification from Htrs transcription (left). SHAP values matrix associated to the class  
37 decoding (right).

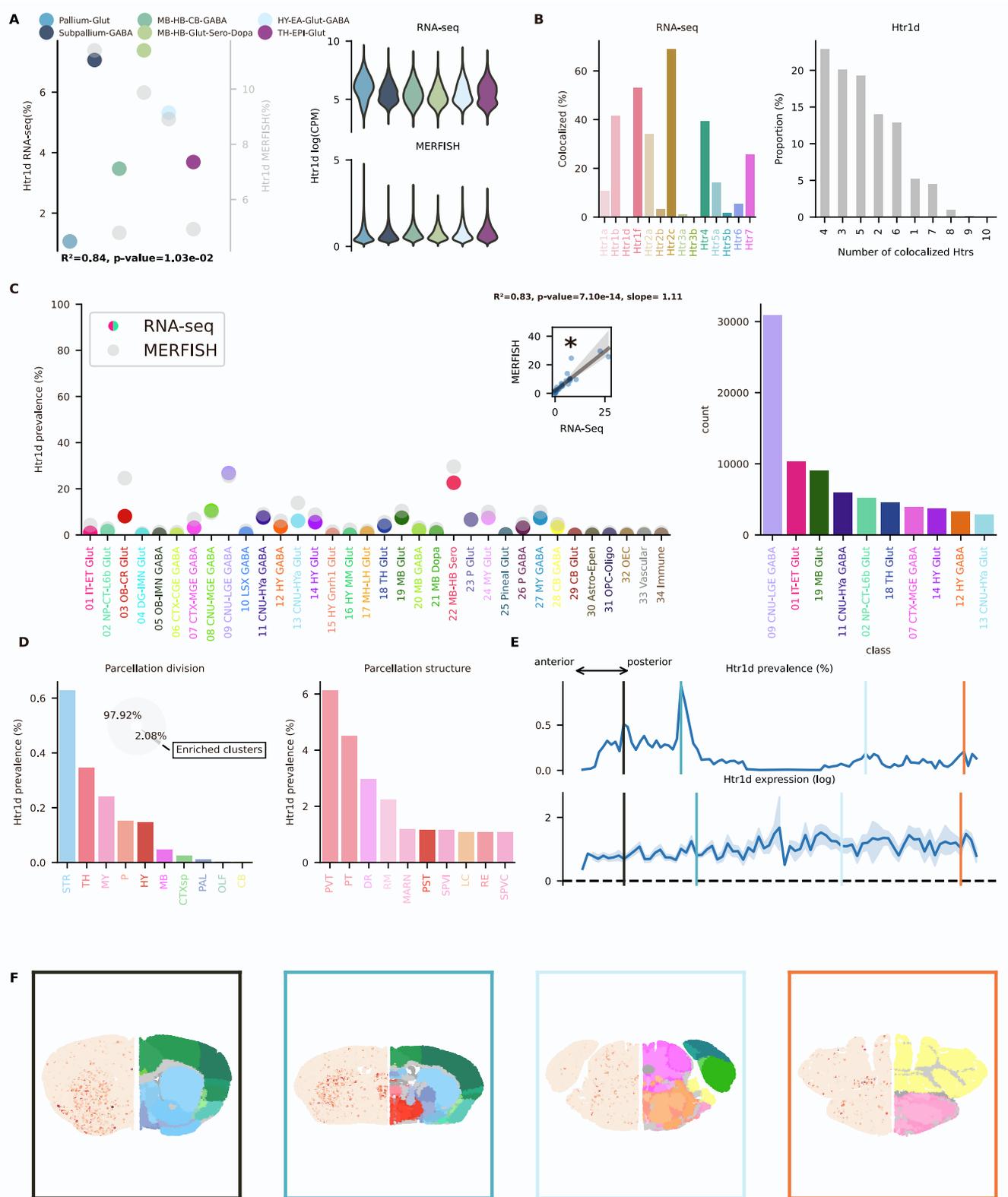


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39 **Figure S4. Correlation and co-localization patterns across neighborhoods.**

40 (A) Correlation matrices between pairs of Htrs in each neighborhood. (B) co-localization

41 matrices of Htrs transcription in each neighborhood.

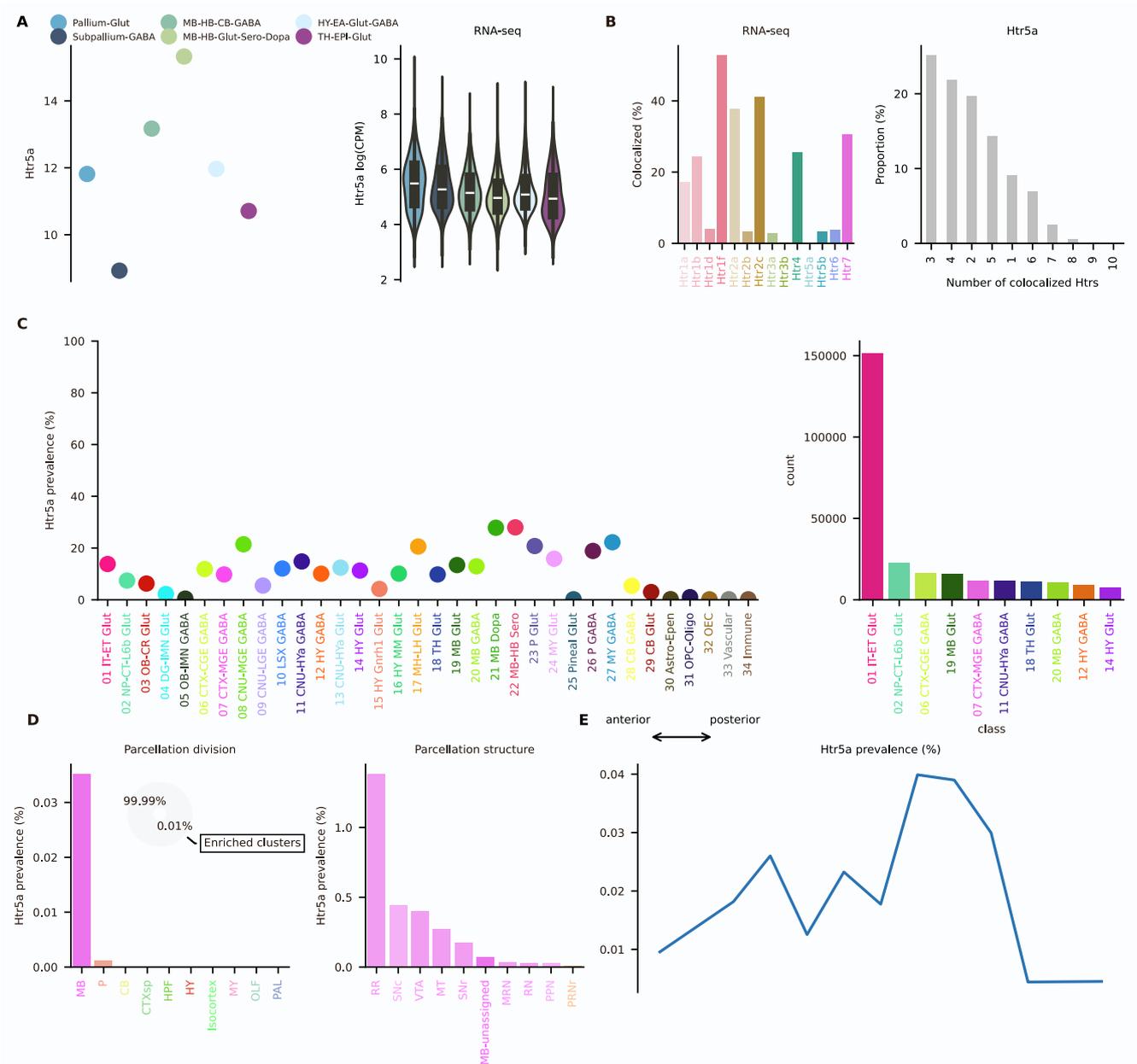


42

43 **Figure S5. Htr1d transcription.**

44 (A) On the left, Htr1d prevalence across neighborhoods with squared Pearson correlation  
 45 coefficient ( $R^2$ ) between scRNA-seq and MERFISH dataset. On the right, amount of Htr1d  
 46 RNA detected using scRNA-seq (top) and MERFISH (bottom). (B) Amount of co-localization  
 47 with each Htrs by cells expressing Htr1d RNA (left). Number of Htrs RNA detected in cells  
 48 expressing Htr1d RNA (right). (C) Prevalence of Htr1d RNA across all classes of cells in

49 scRNA-seq and MERFISH dataset. Inset represents the linear regression between the two  
50 datasets. On the right, absolute number of cells expressing Htr1d RNA by class ranked in  
51 descending order (top ten). (D) Prevalence of Htr1d RNA across divisions (left) and structures  
52 (right). Inset represents the proportion of cells expressing Htr1d RNA that belongs to enriched  
53 clusters. (E) Top: Prevalence of cells from enriched clusters across the antero-posterior axis,  
54 identified in the scscRNA-seq dataset and cross-referenced in the MERFISH dataset. Bottom:  
55 average amount of RNA expression found in enriched clusters cross-referenced in the  
56 MERFISH dataset. (F) Expression of Htr1d RNA detected by MERFISH in 4 representative  
57 slices. Border color represents the position on the antero-posterior axis.

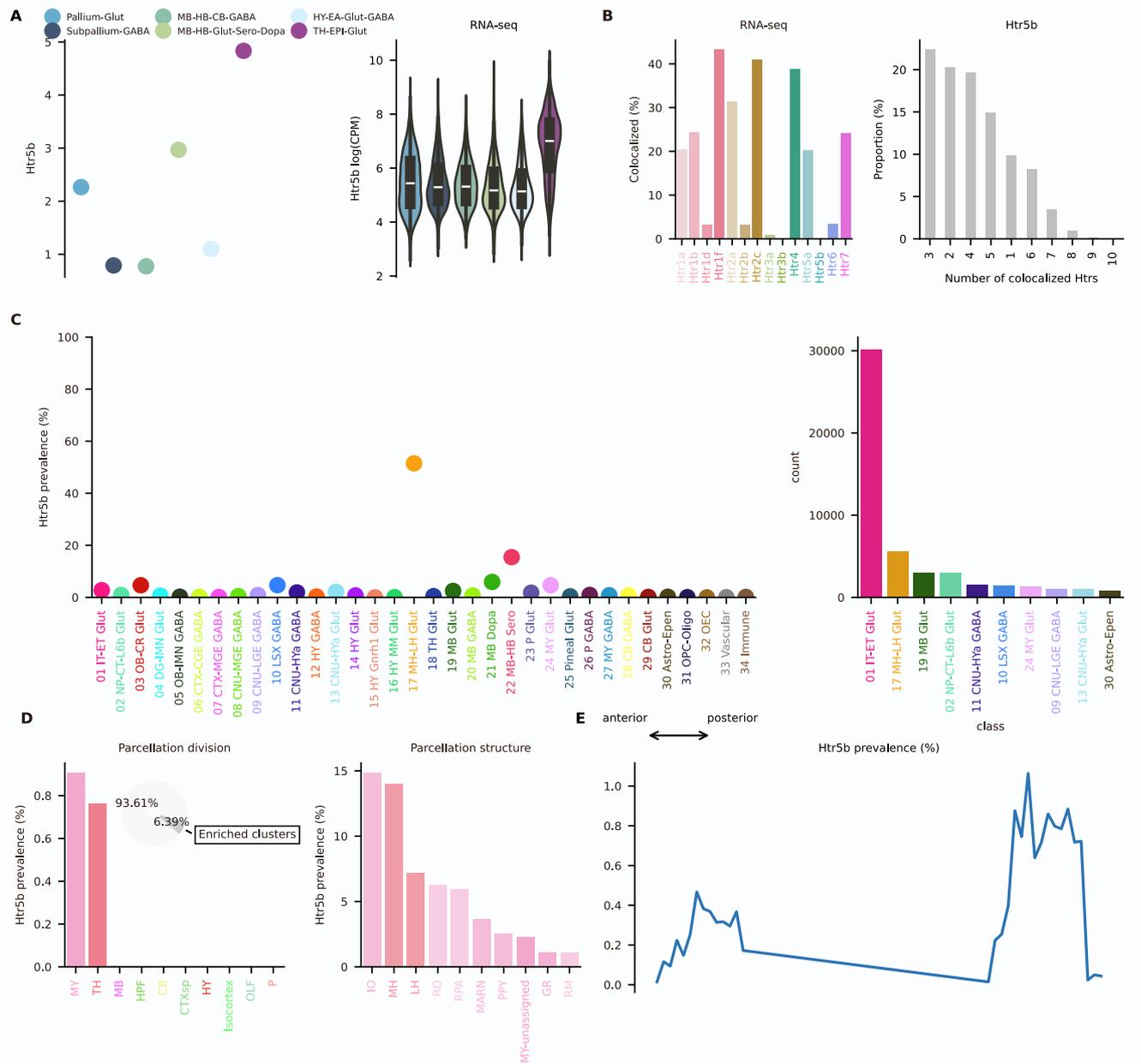


58

59 **Supplementary Figure S6. Htr5a transcription.**

60 (A) On the left, Htr5a prevalence across neighborhoods with squared Pearson correlation  
 61 coefficient ( $R^2$ ) between scRNA-seq and MERFISH dataset. On the right, amount of Htr5a  
 62 RNA detected using scRNA-seq (top) and MERFISH (bottom). (B) Amount of co-localization  
 63 with each Htr5s by cells expressing Htr5a RNA (left). Number of Htr5s RNA detected in cells  
 64 expressing Htr5a RNA (right). (C) Prevalence of Htr5a RNA across all classes of cells in scRNA-  
 65 seq and MERFISH dataset. Inset represents the linear regression between the two datasets.  
 66 On the right, absolute number of cells expressing Htr5a RNA by class ranked in descending  
 67 order (top ten). (D) Prevalence of Htr5a RNA across divisions (left) and structures (right). Inset  
 68 represents the proportion of cells expressing Htr5a RNA that belongs to enriched clusters. (E)

- 69 Prevalence of cells from enriched clusters across the antero-posterior axis, identified in the  
70 scscRNA-seq dataset and cross-referenced in the MERFISH dataset.

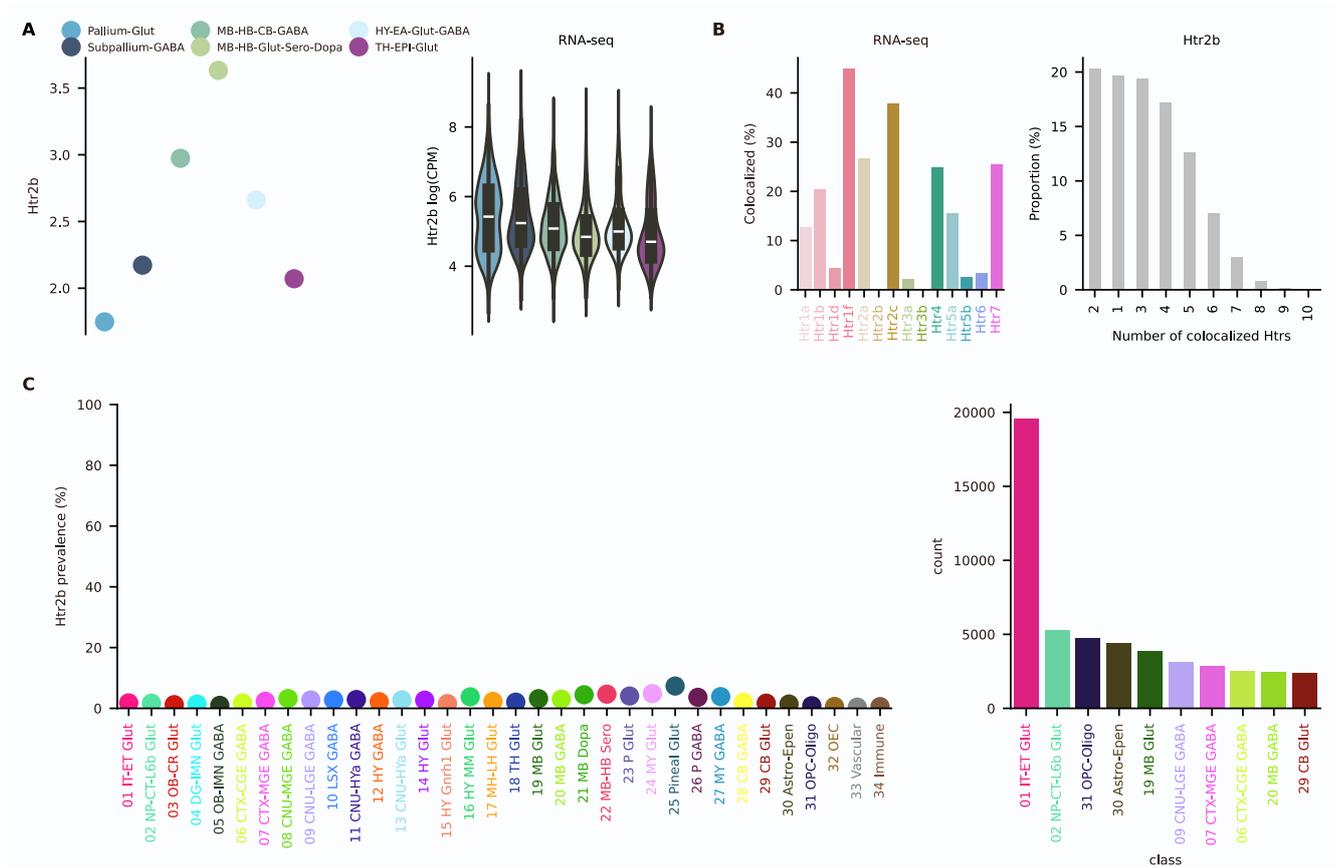


71

72 **Figure S7. Htr5b transcription.**

73 (A) On the left, Htr5b prevalence across neighborhoods with squared Pearson correlation  
 74 coefficient ( $R^2$ ) between scRNA-seq and MERFISH dataset. On the right, amount of Htr5b  
 75 RNA detected using scRNA-seq (top) and MERFISH (bottom). (B) Amount of co-localization  
 76 with each Htrs by cells expressing Htr5b RNA (left). Number of Htrs RNA detected in cells  
 77 expressing Htr5b RNA (right). (C) Prevalence of Htr5b RNA across all classes of cells in  
 78 scRNA-seq and MERFISH dataset. Inset represents the linear regression between the two  
 79 datasets. On the right, absolute number of cells expressing Htr5b RNA by class ranked in  
 80 descending order (top ten). (D) Prevalence of Htr5b RNA across divisions (left) and structures  
 81 (right). Inset represents the proportion of cells expressing Htr5b RNA that belongs to enriched

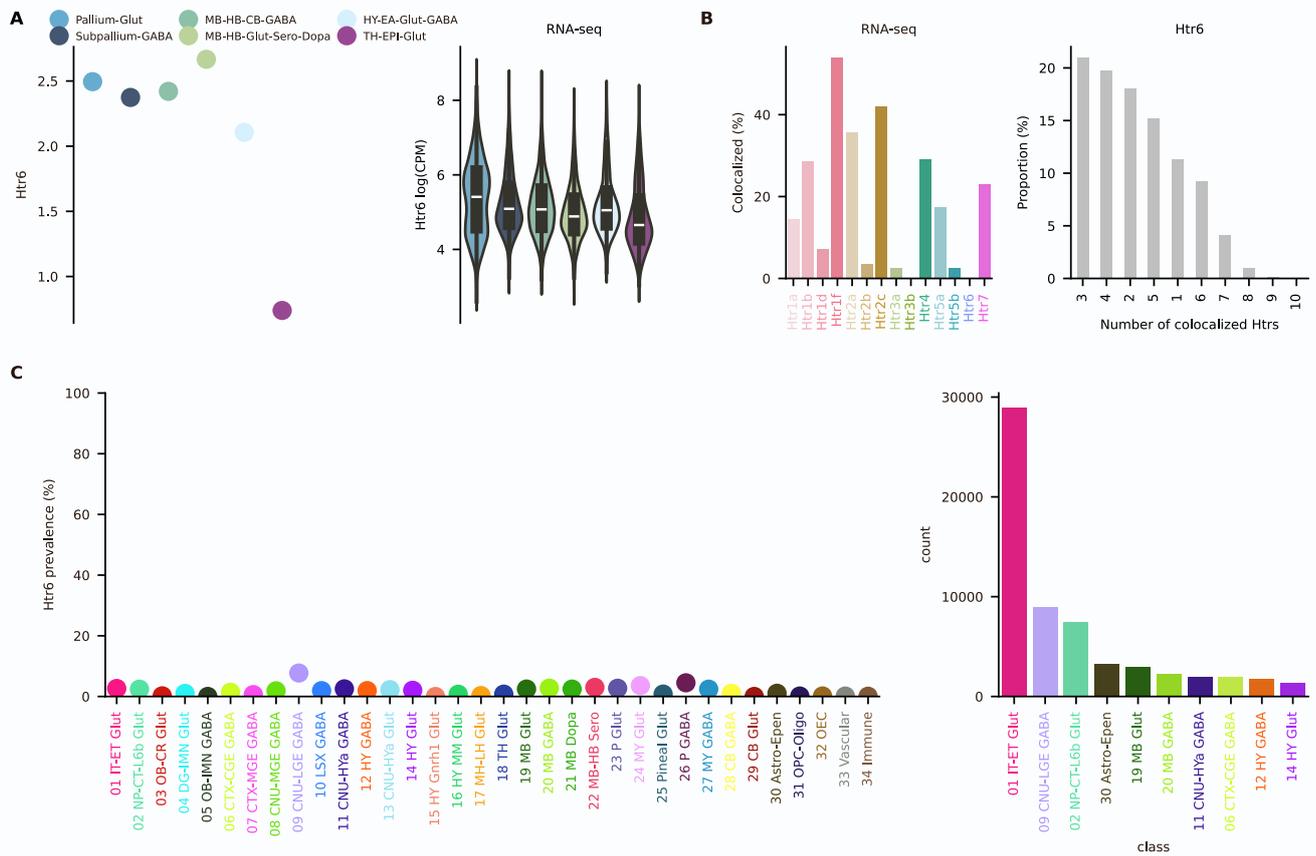
82 clusters. (E) Prevalence of cells from enriched clusters across the antero-posterior axis,  
83 identified in the scscRNA-seq dataset and cross-referenced in the MERFISH dataset.



84

85 **Supplementary Figure S8. Htr2b transcription.**

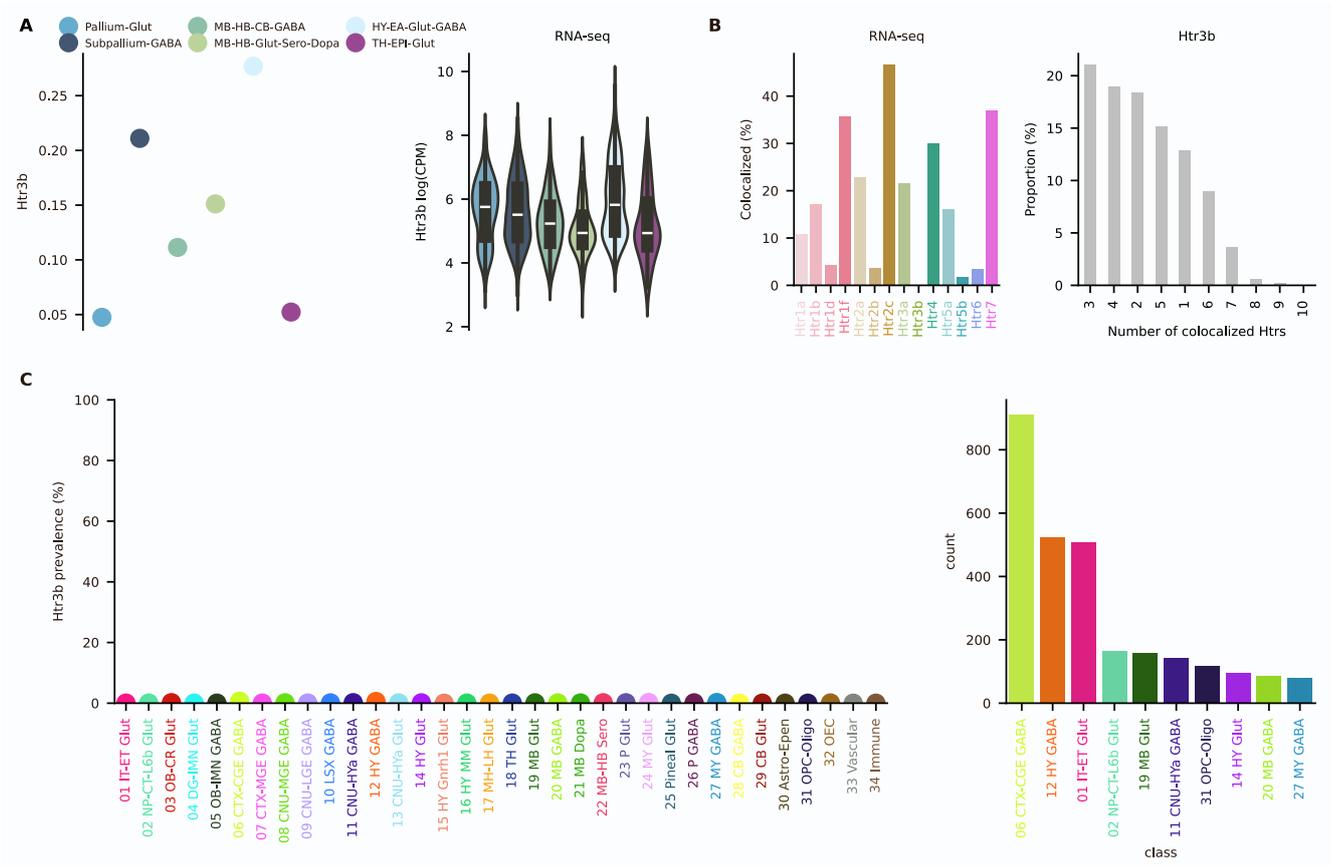
86 (A) On the left, Htr2b prevalence across neighborhoods with squared Pearson correlation  
 87 coefficient ( $R^2$ ) between scRNA-seq and MERFISH dataset. On the right, amount of Htr2b  
 88 RNA detected using scRNA-seq (top) and MERFISH (bottom). (B) Amount of co-localization  
 89 with each Htrs by cells expressing Htr2b RNA (left). Number of Htrs RNA detected in cells  
 90 expressing Htr2b RNA (right). (C) Prevalence of Htr2b RNA across all classes of cells in  
 91 scRNA-seq and MERFISH dataset. Inset represents the linear regression between the two  
 92 datasets. On the right, absolute number of cells expressing Htr2b RNA by class ranked in  
 93 descending order (top ten).



94

95 **Figure S9. Htr6 transcription.**

96 (A) On the left, Htr6 prevalence across neighborhoods with squared Pearson correlation  
 97 coefficient ( $R^2$ ) between scRNA-seq and MERFISH dataset. On the right, amount of Htr6 RNA  
 98 detected using scRNA-seq (top) and MERFISH (bottom). (B) Amount of co-localization with  
 99 each Htrs by cells expressing Htr6 RNA (left). Number of Htrs RNA detected in cells expressing  
 100 Htr6 RNA (right). (C) Prevalence of Htr6 RNA across all classes of cells in scRNA-seq and  
 101 MERFISH dataset. Inset represents the linear regression between the two datasets. On the  
 102 right, absolute number of cells expressing Htr6 RNA by class ranked in descending order (top  
 103 ten).



104

105 **Figure S10. Htr3b transcription.**

106 (A) On the left, Htr3b prevalence across neighborhoods with squared Pearson correlation  
 107 coefficient ( $R^2$ ) between scRNA-seq and MERFISH dataset. On the right, amount of Htr3b  
 108 RNA detected using scRNA-seq (top) and MERFISH (bottom). (B) Amount of co-localization  
 109 with each Htrs by cells expressing Htr3b RNA (left). Number of Htrs RNA detected in cells  
 110 expressing Htr3b RNA (right). (C) Prevalence of Htr3b RNA across all classes of cells in  
 111 scRNA-seq and MERFISH dataset. Inset represents the linear regression between the two  
 112 datasets. On the right, absolute number of cells expressing Htr3b RNA by class ranked in  
 113 descending order (top ten).

<b>name</b>	<b>description</b>
<b>HY-EA-Glut-GABA</b>	Glutamatergic and GABAergic neurons in hypothalamus and extended amygdala, also including all non-pallium glutamatergic neurons in cerebral nuclei (1404 clusters)
<b>MB-HB-CB-GABA</b>	GABAergic neurons in midbrain, hindbrain, and cerebellum (1040 clusters)
<b>MB-HB-Glut-Sero-Dopa</b>	Glutamatergic, serotonergic and dopaminergic neurons in midbrain and hindbrain (1431 clusters)
<b>NN-IMN-GC</b>	Non-neuronal cells, immature neurons, granule cells in dentate gyrus, olfactory bulb and cerebellum, and neurons in pineal gland (248 clusters)
<b>Pallium-Glut</b>	Glutamatergic neurons from cerebral cortex (derived from the developmental pallium), including isocortex, hippocampal formation, olfactory areas, and cortical subplate (517 clusters)
<b>Subpallium-GABA</b>	Telencephalic GABAergic neurons from cerebral cortex and cerebral nuclei, as well as some from the hypothalamic preoptic area, which are derived from the developmental subpallium (1051 clusters)
<b>TH-EPI-Glut</b>	Glutamatergic neurons from thalamus and epithalamus (i.e., medial and lateral habenula) (148 clusters)
<b>WholeBrain</b>	All cells in the whole mouse brain (5322 clusters)

114

115 **Table 1. Neighborhoods descriptions.**

116 Description of cells belonging to each neighborhood group.

117

118 **Table 2. Region acronyms.**

119 Allen Mouse Brain Common Coordinate Framework (CCF) acronyms.

Htr	Defining Feature
Htr1a	Expressed in an important fraction of Sero neurons of the raphe and some HPF excitatory neurons
Htr1b	Expressed in many inhibitory striatal neurons and Sero neurons
Htr1d	Expressed in the striatum, although at much lower levels
Htr1f	Widely expressed in telencephalic structures, especially the Isocortex, with a peak in frontal olfactory structures
Htr2a	Prevalent in glutamatergic cells of the cortical subplate (CLA and EPd) and the mammillary bodies (TMd, PMd), and hippocampal interneurons
Htr2b	Rarely transcribed and is present in some neurons of the pineal gland
Htr2c	Broadly transcribed, especially in the STR, excitatory neurons of the amygdala (LA, BLA and BMA) and RSPv, OLF neurons and structures in MB, P, MY and CB
Htr3a	Uniquely observed in cortical gabaergic neurons of the 06 CTX-CGE GABA class
Htr3b	Uniquely observed in cortical gabaergic neurons of the 06 CTX-CGE GABA class
Htr4	Transcribed at high levels in the OT, excitatory cells of the hippocampus proper and DG, and Chol neurons of the TH (17 MH-LH Glut)
Htr5a	Transcribed at low levels with only one enriched cluster in the MB
Htr5b	Transcribed only in few cells, specifically in Chol neurons of the TH
Htr6	Does not feature any enriched cluster, some cells in CA3 transcribed this Htr
Htr7	Widely transcribed in subcortical structures, especially in some TH nuclei (PF, PVT, IAD and PT), the mammillary complex (MM and PMd), the lateral septal nucleus (LSv) and the fasciola cinerea of the HPF

120 **Table 3. Htrs defining features.**

121 Table listing the defining feature of each Htr trascription pattern.