

## Supplementary Tables

**Supplementary Table 1:** List of genes that are profiled by the seqFISH experiment.

4931431F19Rik	Ctla4	Hnf1a	Obsl1	Cpne5
4932429P05Rik	Cyp2c70	Hoxb3	Olr1	Nes
Abca15	Cyp2j5	Hoxb8	Osr2	Acta2
Abca9	Dbx1	Hyal5	Plid1	Gja1
Adcy4	Dcstamp	Kif16b	Plid5	Omg
Aldh3b2	Ddb2	Laptm5	Poln	Nov
Ankle1	Egln3	Lefty2	Ppp1r3b	Col5a1
Ano7	Fam69c	Lhx3	Psmd5	Dcx
Anxa9	Fbll1	Lhx4	Rbm31y	Itpr2
Arhgef26	Foxa1	Lmod1	Rrm2	Rhob
B3gat2	Foxa2	Mertk	Scml2	Sox2
Barhl1	Foxd1	Mgam	Senp1	Cldn5
Bcl2l14	Foxd4	Mmgt1	Serpinb11	Mrc1
Blzf1	Galnt3	Mmp8	Sis	Tbr1
Bmpr1b	Gata6	Mrgprb1	Slc4a8	Pax6
Capn13	Gdf2	Murc	Slc6a16	Calb1
Cdc5l	Gdf5	Nell1	Spag6	Gda
Cdc6	Gm15688	Neurod4	Sumf2	Slc5a7
Cdh1	Gm6377	Neurog1	Tnfrsf1b	Sema3e
Cecr2	Gm805	Nfkb2	Vmn1r65	Mfge8
Cilp	Gpc4	Nfkbiz	Vps13c	Lyve1
Clec5a	Gpr114	Nhlh1	Wrn	Loxl1
Creb1	Gykl1	Nkd2	Zfp182	Slco1c1
Creb3l1	Hdx	Nlrp12	Zfp715	Amigo2

Csf2rb2	Hn1l	Npy2r	Zfp90	Kcnip2
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**Supplementary Table 2:** List of 43 genes used for cell type mapping.

Fbll1	Itpr2	Vps13c	Tnfrsf1b	Sox2
Hdx	Wrn	Sumf2	Vmn1r65	Rhob
Mrgprb1	Calb1	Pld1	Laptm5	Tbr1
Slc5a7	Abca9	Ankle1	Olr1	
Cecr2	Cpne5	Blzf1	Mertk	
Nell1	Npy2r	Cdc5l	Slco1c1	
Pax6	Cldn5	Cyp2j5	Mfge8	
Col5a1	Bmpr1b	Rrm2	Gja1	
Dcx	Spag6	Csf2rb2	Gda	
Arhgef26	Slc4a8	Gm805	Omg	

**Supplementary Table 3:** Astrocyte prediction accuracy, evaluated using fluorescent staining images. We examined and contrasted DAPI, Nissl staining on astrocyte cells. Percentage of cells with no Nissl, and with DAPI staining are recorded (these are accurate instances)

	% predicted astrocytes with weak or no Nissl stain	% predicted astrocytes with present Nissl stain	Total predicted astrocytes
Cortex Column 1	100%	0%	11
Cortex Column 2	88%	12%	25
Cortex Column 3	87%	13%	24
Cortex Column 4	87%	13%	24

**Supplementary Table 4:** List of 69 genes used for HMRF.

Calb1	Gdf5	Rbm31y	Zfp182	Pld5
Kcnip2	Nkd2	Creb3l1	Gpc4	Gm805
Tbr1	Fam69c	Nfkbiz	Obsl1	Clec5a
Nes	Sema3e	Hoxb8	Dcstamp	Serpnb11
Gda	Dcx	Adcy4	Poln	Zfp715

Col5a1	Lhx3	Mmgt1	Cdh1	Blzf1
Loxl1	Omg	Lhx4	Ppp1r3b	Bm6377
Sox2	Wrn	Lefty2	Mgam	Zfp90
Slc5a7	Aldh3b2	Gm15688	Hn1l	
Nov	Foxd1	Kif16b	Hdx	
Cpne5	Cyp2c70	Vmn1r65	Psm5	
Mrc1	Hnf1a	Foxa2	Bcl2l14	
Acta2	Slc4a8	Gpr114	Osr2	
Cyp2j5	Barhl1	Gata6	4931431F19Rik	
Lyve1	Egln3	Nhlh1	Lmod1	

**Supplementary Table 5:** Expanded domain specific signatures used for Tasic et al reanalysis

O1	gata6 aldh3b2 kcnips gm805 b3gat2 amigo2 cdc6
O2	serpinb11 fam69c capn13 ankle1 mmp8 cecr2 foxd4 barhl1
O3	lmod1 mmgt1 lefty2 hn1l foxd1 pld1 olr1
O4	lhx3 omg arhgef26
IS	adcy4 nkd2 cyp2j5 dbx1 zfp715 mgam senp1 hnf1a ddb2 nfkb2 blzf1
I2	hn1l cdc5l murc nhlh1 creb1
I3	gata6 vmn1r65 sema3e foxa1 obsl1
I1a	loxl1 clec5a cpne5 creb3l1 gpc4 calb1 sox2 nes vps13c
I1b	mrc1 nkd2 sema3e col5a1 dcx slc5a7 nov rhob pax6

## Supplementary Figures

**Supplementary Fig 1:** Quantile-quantile plot per gene for each of 113 genes shared between seqFISH and scRNAseq dataset. Q-Q plot shows the comparison of quantiles between scRNAseq (y-axis) and seqFISH (x-axis). Quantiles refer to expression z-score quantiles after each scRNAseq and seqFISH dataset has been transformed by row- and column-wise z-scoring.

**Supplementary Fig 2:** Robustness analysis of domain identifications by HMRF model with respect to cell-type marker filtering. (a) different scenarios. “ct” denotes “cell-type”. “Plus.11.ct.genes” denotes unfiltered scenario which added all 11 ct genes. (b, c) Agreement between domain assignment using different cell-type filtering settings quantified by (b) overall clustering consistency and (c) contingency table. (d) spatial patterns found by HMRF in each scenario, in comparison with 69-gene HMRF.

**Supplementary Fig 3:** Comparison between the (a) spatial domain annotation and (b) major cell type annotation. tSNE constructed from the 69 genes used in HMRF and shows the seqFISH dataset.

**Supplementary Fig 4:** Enrichment of cell types in spatial domains. Enrichment is calculated as  $(\text{num. cells}) / \sqrt{(\text{colsum} \times \text{rowsum})}$ , where number of cells refers to cells that overlap between a domain and a cell type. Col- and row-sums refer to the overlap table.

**Supplementary Fig 5:** Spatial expression of domain marker genes. Representative genes of the 9 domains include Barhl1 (O2), Nfkb2 (IS), Col5a1 (I1a), Aldh3b2 (O1), Calb1 (I1b), Omg (O4), Nhlh1 (I2), Gata6 (I3), and Plid1 (O3). Black outlines around some cells highlight the domain annotations.

**Supplementary Fig 6:** General domain signatures transcend cell types. For cells annotated to each cell type : spatial domain pair; only those containing at least 4 cells are represented. Top row: domain type; 2nd row: cell type. The heatmap below shows the average level of domain associated genes.

**Supplementary Fig 7:** Distribution of expression levels representative of domain- and cell-type specific marker genes. (a) Representative domain-specific marker genes. The corresponding domains are indicated in parentheses in title. (b) Representative cell-type specific marker genes. The corresponding cell types are indicated in parentheses in title. Each box represents the distribution associated with the intersection of a specific cell type and spatial domain pair. Only pairs which contain >5 cells are analyzed. Groups ordered by domain.

**Supplementary Fig 8:** Comparison of domain specific genes with Allen Brain Atlas. Genes compared are: Calb1, Sema3e, Gda, Nell1, Tbr1, Cpne5, Gdf5, Nov, Aldh3b2, Nkd2, Serpinb11. For each gene, the top right image shows the Allen Brain Atlas ISH staining. Bottom

right shows the z-scored expression in microdissection cell clusters from Zeisel et al and Tasic et al scRNAseq datasets. SeqFISH profiles agree well with existing resources.

**Supplementary Fig 9:** Metagene expression levels. (a) 9 metagenes each marking a different spatial domain. (b) the spatial domain annotations.

**Supplementary Fig 10:** Applications of domain metagene signatures on mapping the domain patterns of glutamatergic cells. Shown are glutamatergic cells only. Red indicates metagene expression.

**Supplementary Fig 11:** A zoomed-in view of comparison between spatial domain annotations (left) and metagene expression levels (right) at domain boundaries indicated in Fig 3b.

**Supplementary Fig 12:** Comparison of morphological features across different spatial domains. 6 of the 15 morphological features extracted from Nissl staining images are significantly different across domains. Significance is judged by both of the following criteria, whereby 1) each domain is compared to an individual domain and is  $P < 0.05$  in at least 7 of 8 one-vs-one K-S tests, and 2) each domain is compared to all cells in remaining domains ( $P < 0.00001$ , one-vs-rest test). (a) The distribution of the 6 significant features across domains. (b) The P-values obtained from the one-vs-rest tests.

**Supplementary Fig 13:** ISH validation of additional spatial domain markers identified from integrative analysis. Source: Allen Brain Atlas.

**Supplementary Fig 14:** Overlap between spatial domain and glutamatergic subtype annotations for the the Tasic et al dataset. (a) Overlap between domain- and cell subtype-specific genes focused within the 125-gene fraction. (b) Overlap between cells annotated as a specific domain vs subtype.

**Supplementary Fig 15:** Complete cell subtype annotations overlaid on tSNE of Tasic et al glutamatergic cells based on metagene expression.

**Supplementary Fig 16:** Comparison of metagene-recovered spatial populations with cell subtypes in Tasic et al dataset. (a) Overlay of expression patterns of representative cell subtype markers (*col5a1*, *cpne5*, *sema3e*, *serpinb11*) on t-SNE plot that was generated in the same way as Fig 4a (obtained from metagene signatures). Red demarcates cells expressing the gene. It can be seen that these genes served as markers of both cell subtypes and domains. (b) Some distinct populations recovered by metagenes do not correspond to any specific cell subtypes identified by Tasic et al. Shown are three examples (O1, I2, and O4). The second row shows the subtype annotations.

**Supplementary Fig 17:** Expression of astrocyte-associated domain genes in an external astrocyte expression database (Zhang et al 2016). Low-level expression is defined as  $< 10$  FPKM. High level is between 10 and 160 FPKM.

**Supplementary Fig 18:** Spatial organization of the mouse olfactory bulb as revealed by the HMRF model. (a) This spatial transcriptome dataset was generated by Stahl et al 2016. and obtained by using tissue microarray to barcode spatial locations at a 100um resolution followed by RNA sequencing. (b) Spatial domains identified by using a 5-state HMRF model. (c) Expression patterns of representative marker genes. (d) The anatomic structure identified by hematoxylin and eosin staining.

**Supplementary Fig 19:** Spatial organization of the mouse dentate gyrus as revealed by the HMRF model. This is a 249-gene seqFISH dataset (Shah et al 2016) with single-cell spatial and transcriptomic information. (a) Spatial domains identified by the 5-state HMRF model. (b) Schematic of the anatomic structure at dentate gyrus. Rectangular boxes indicate the imaging fields shown in (a). (c) The expression pattern of a number of representative marker genes.

Methods:

**Supplementary Fig 20:** Estimates of imaging bias in the seqFISH data. Cortex is divided into 20 adjacent fields of view (shortened as fields). We divide each field into a 50 bin-by-50 bin grid. Then for each bin, we compute the average expression level at that bin over all 20 fields. Together this forms an overall bias map. Principal component analysis was applied to the bias map to model the most significant bias patterns among genes. The top PCs are shown below representing the major bias patterns.

**Supplementary Fig 21:** Dependency of cell-type mapping accuracy on the number of genes used. (a) Relationship between the 8 major, 22 finer, and 49 minor cell types determined by Tasic et al. (b,c,d) Cross-validation estimated mapping accuracy associated with (b) 8 major, (c) 22 finer, and (d) 49 minor classes.

**Supplementary Fig 22:** Cross-validation estimated mapping accuracy for individual cell types. (a) Receiver operating curves (ROC) for each of the eight major cell types. (b) Cross validation accuracies of individual cell types.

**Supplementary Fig 23:** Robustness analysis of our HMRF model. Agreement between domain assignment using different numbers of top spatially coherent genes. Agreement is quantified by (a) contingency table and (b) adjusted mutual information (left) and the proportion of cells clustered consistently (i.e. the diagonal of matrix in (a)) (right).

**Supplementary Fig 24:** Robustness analysis of beta in our HMRF model. Agreement between domain assignment using different betas. Agreement is quantified in (a) by the adjusted mutual information (left) and the proportion of cells clustered consistently (right) (i.e. the diagonal of matrix in (b)). (b) Overlap matrix in each case. (c) Spatial pattern comparison.

**Supplementary Fig 25:** Robustness analysis of the HMRF model against disruption of spatial patterns. A subset of cells at various fractions ( $p=0.1, 0.2, 0.4, \text{ and } 0.99$ ) were randomly selected and switched spatial locations. 100 different random samples were selected for each

parameter setting. For each perturbed dataset, the HMRF model was applied to identify spatial domains. Goodness-of-fit was quantified by using the log-likelihood. Blue vertical line indicates the log-likelihood for the original data set.

**Supplementary Fig 26:** SeqFISH expression z-scores approximately follow a normal distribution.

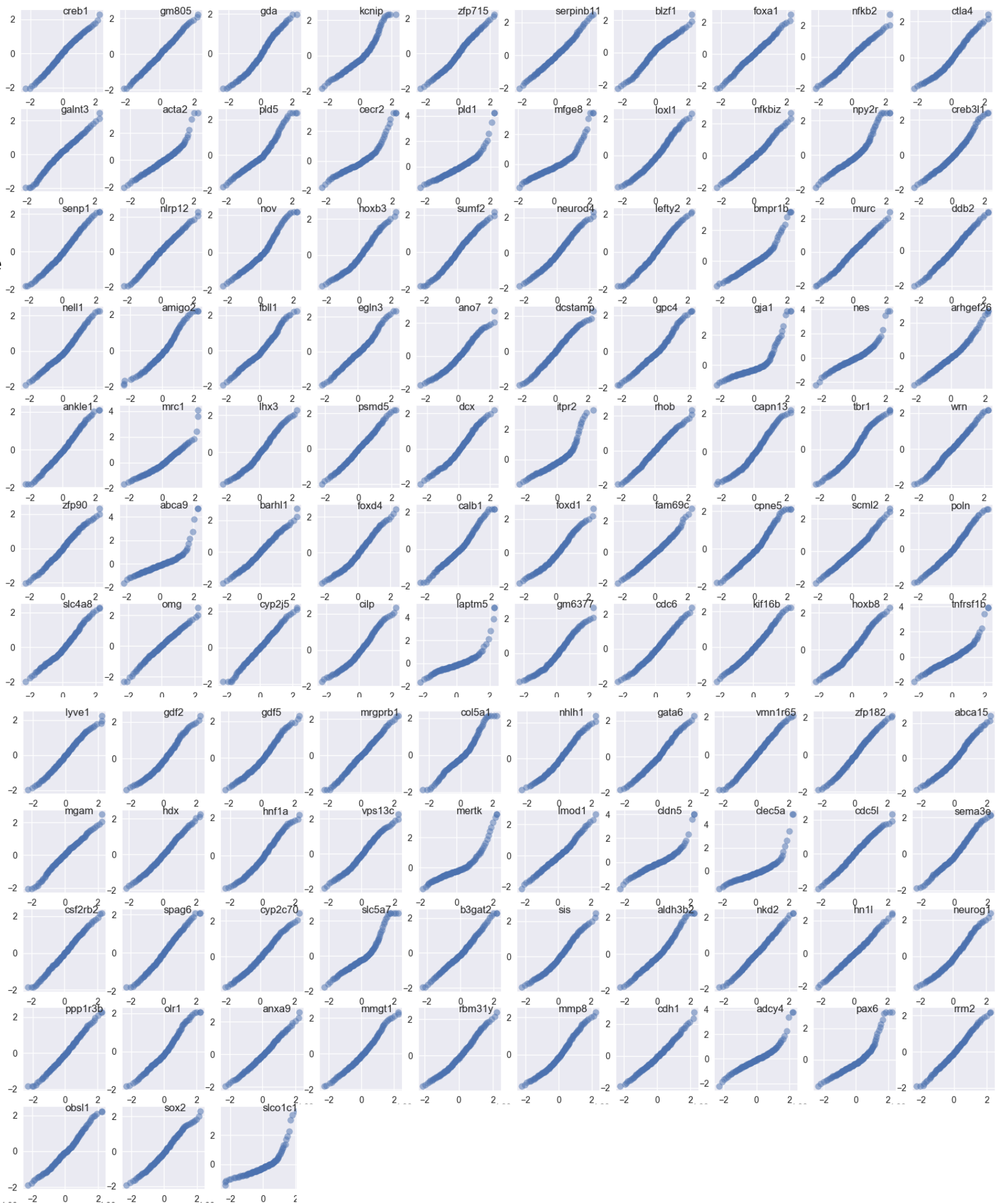
**Supplementary Fig 27:** Domain signatures obtained by non-parametric Mann-Whitney U test. (a) general domain signature, complementary to Fig 2d. (b) glutamatergic restricted signature, complementary to Fig 3b, middle panel.





# SFig 1

Expr. z-score  
 ↑  
 seqFISH  
 ↑  
 Expr. z-score



# SFig 2

a

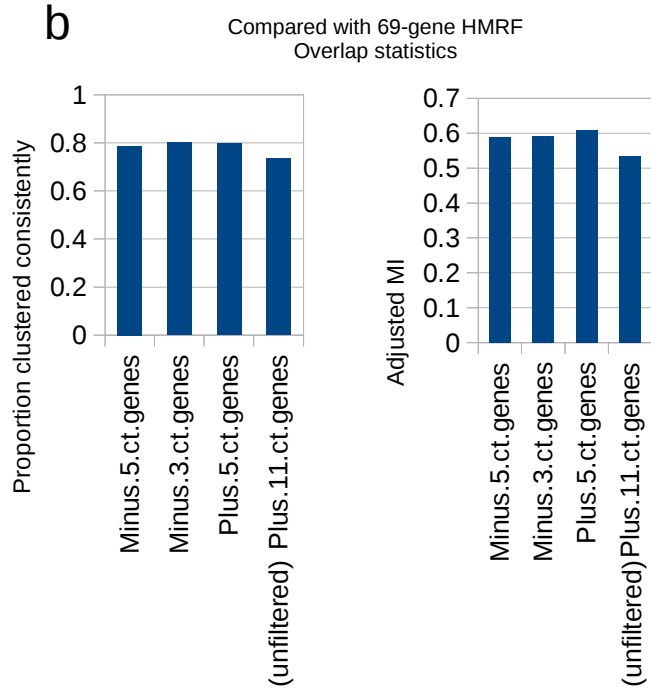
**Baseline:**  
69-gene HMRF (already removed 11 cell type (ct) genes)

**Minus.5.ct.genes:**  
remove 5 additional ct genes (64-gene HMRF)

**Minus.3.ct.genes:**  
remove 3 additional ct genes (66-gene HMRF)

**Plus.5.ct.genes:**  
add back 5 ct genes (74-gene HMRF)

**Plus.11.ct.genes (unfiltered):**  
add back all 11 ct genes (80-gene HMRF)

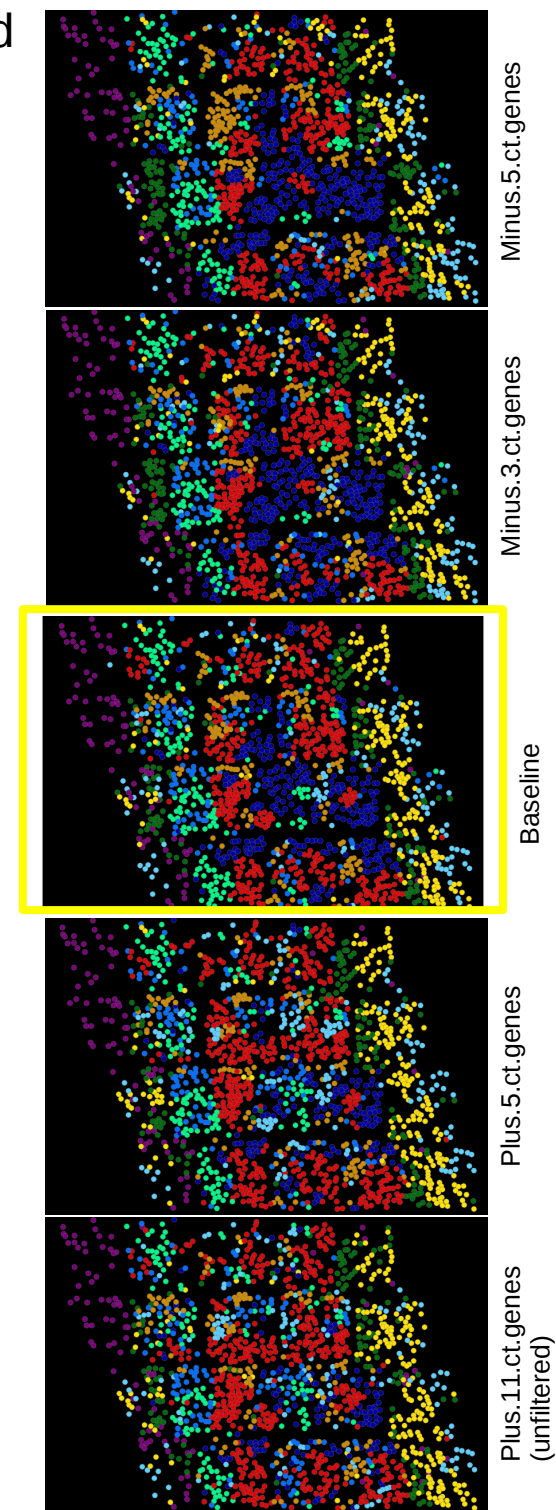


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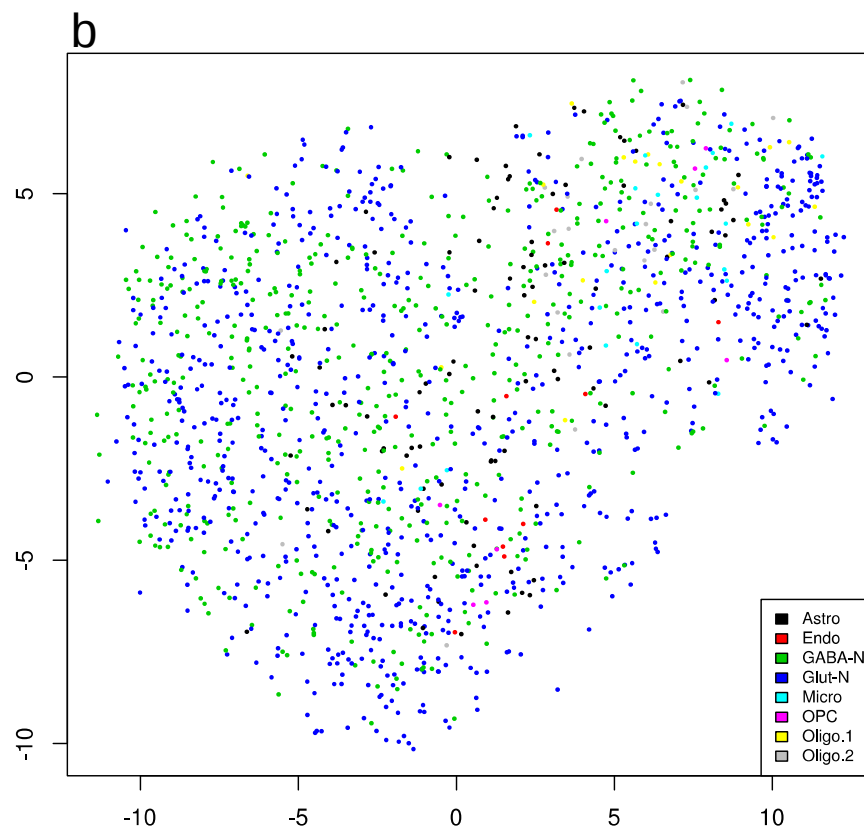
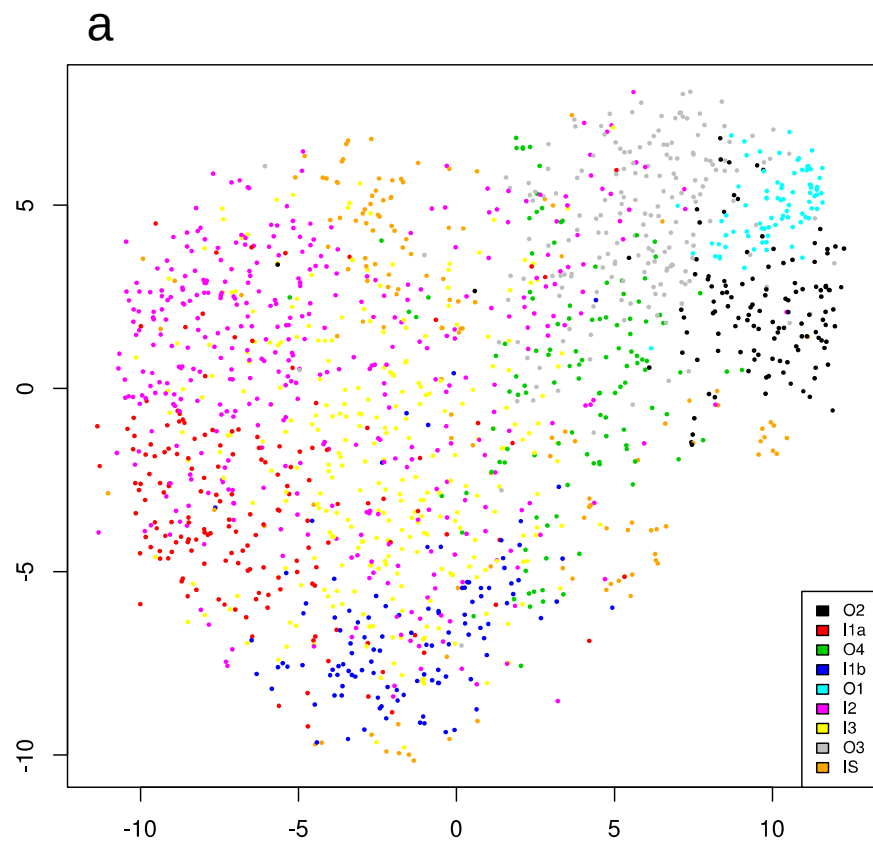
Compared with 69-gene HMRF  
Overlap matrices

		Minus.5.ct.genes HMRF									
69-gene HMRF	69-gene HMRF	271	5	3	0	0	0	0	20	0	20
	Minus.5.ct.genes HMRF	8	83	1	0	0	0	0	9	0	7
	Minus.3.ct.genes HMRF	5	0	8	113	23	9	0	1	0	0
	Plus.5.ct.genes HMRF	13	1	13	3	130	6	0	0	0	0
	Plus.11.ct.genes HMRF (unfiltered)	0	0	3	1	5	67	0	0	0	0
	Baseline	23	7	0	0	0	0	0	124	1	2
	Minus.5.ct.genes	23	6	6	4	2	0	0	119	12	0
	Minus.3.ct.genes	41	6	12	0	1	0	12	14	233	0
	Plus.5.ct.genes	81	5	11	2	17	0	0	2	3	0
	Plus.11.ct.genes (unfiltered)	3	233	45	7	1	1	0	15	5	0
69-gene HMRF	69-gene HMRF	2	23	24	15	3	0	1	23	8	
	Minus.5.ct.genes HMRF	8	8	6	104	1	0	0	0	2	
	Minus.3.ct.genes HMRF	15	1	11	2	142	4	3	2	1	
	Plus.5.ct.genes HMRF	2	0	1	0	5	72	2	0	0	
	Plus.11.ct.genes HMRF (unfiltered)	9	0	6	1	18	5	115	0	0	
	Baseline	0	1	17	3	0	0	0	114	3	
	Minus.5.ct.genes	0	7	10	1	0	0	0	9	89	0
	Minus.3.ct.genes	86	28	3	3	0	11	0	1	0	0
	Plus.5.ct.genes	5	144	5	5	0	4	0	0	1	0
	Plus.11.ct.genes (unfiltered)	0	10	99	2	0	2	0	0	1	0
69-gene HMRF	69-gene HMRF	7	62	17	2	0	0	10	1	3	2
	Minus.5.ct.genes HMRF	0	0	0	0	73	0	1	5	1	0
	Minus.3.ct.genes HMRF	3	13	1	3	0	130	1	0	0	0
	Plus.5.ct.genes HMRF	0	1	0	3	7	1	171	12	26	0
	Plus.11.ct.genes HMRF (unfiltered)	0	3	1	7	2	0	4	100	3	0
	Baseline	10	17	9	28	0	7	9	0	86	0
	Minus.5.ct.genes	74	5	8	0	0	1	1	0	0	0
	Minus.3.ct.genes	3	99	16	0	1	3	4	0	3	0
	Plus.5.ct.genes	5	12	154	2	1	38	1	1	1	0
	Plus.11.ct.genes (unfiltered)	0	0	0	113	15	0	5	5	1	0
69-gene HMRF	69-gene HMRF	0	0	1	5	110	4	14	3	2	0
	Minus.5.ct.genes HMRF	0	2	6	9	25	68	18	7	11	0
	Minus.3.ct.genes HMRF	0	2	2	22	85	2	14	8	17	0
	Plus.5.ct.genes HMRF	0	0	0	12	31	0	7	84	4	0
	Plus.11.ct.genes HMRF (unfiltered)	0	1	0	2	10	4	7	3	96	0
	Baseline	0	0	0	0	0	0	0	0	0	0
	Minus.5.ct.genes	0	0	0	0	0	0	0	0	0	0
	Minus.3.ct.genes	0	0	0	0	0	0	0	0	0	0
	Plus.5.ct.genes	0	0	0	0	0	0	0	0	0	0
	Plus.11.ct.genes (unfiltered)	0	0	0	0	0	0	0	0	0	0

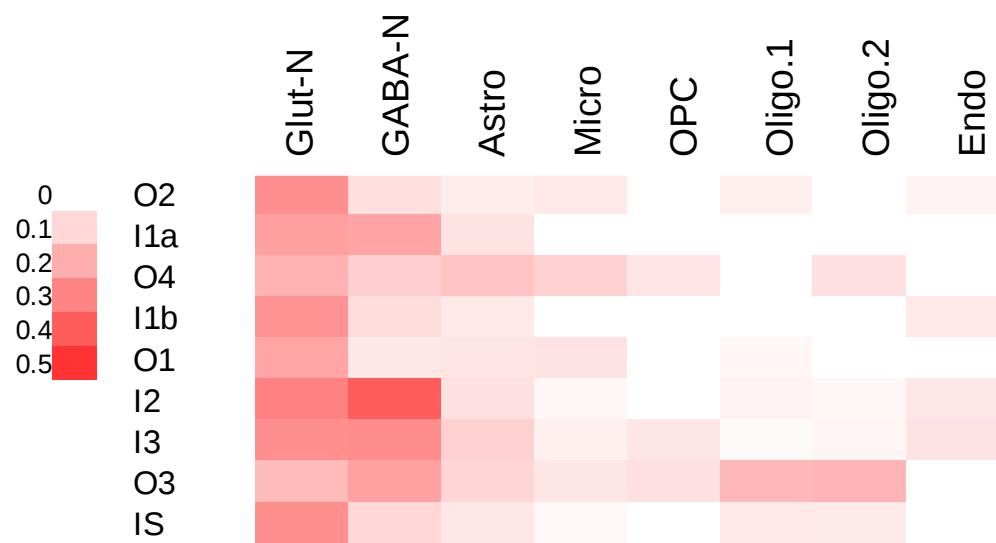
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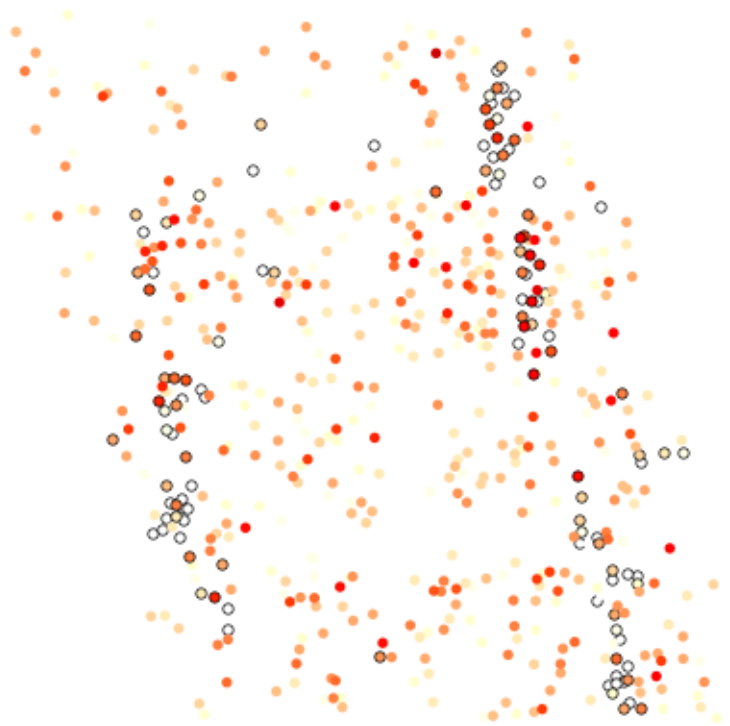
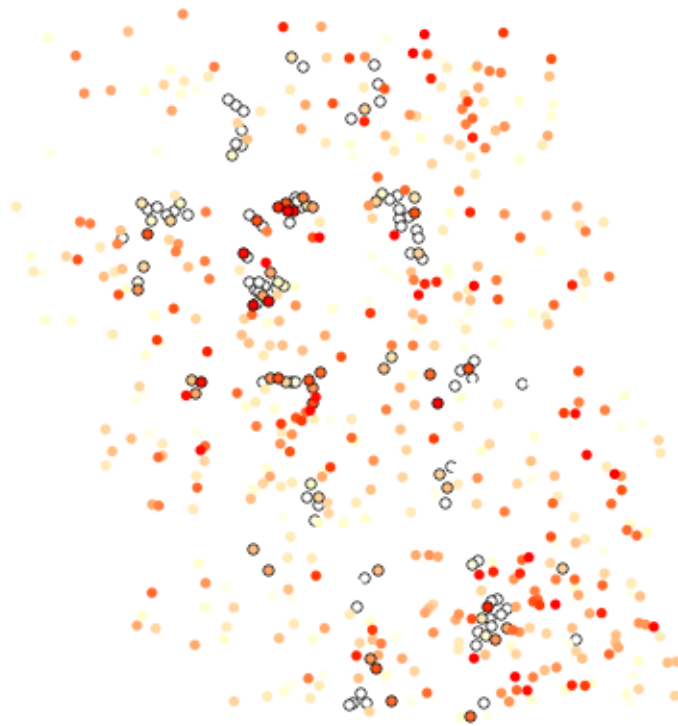
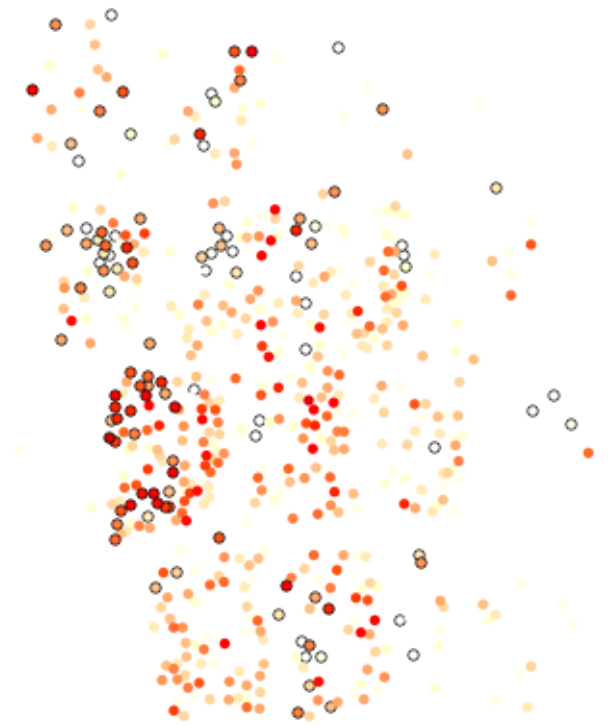
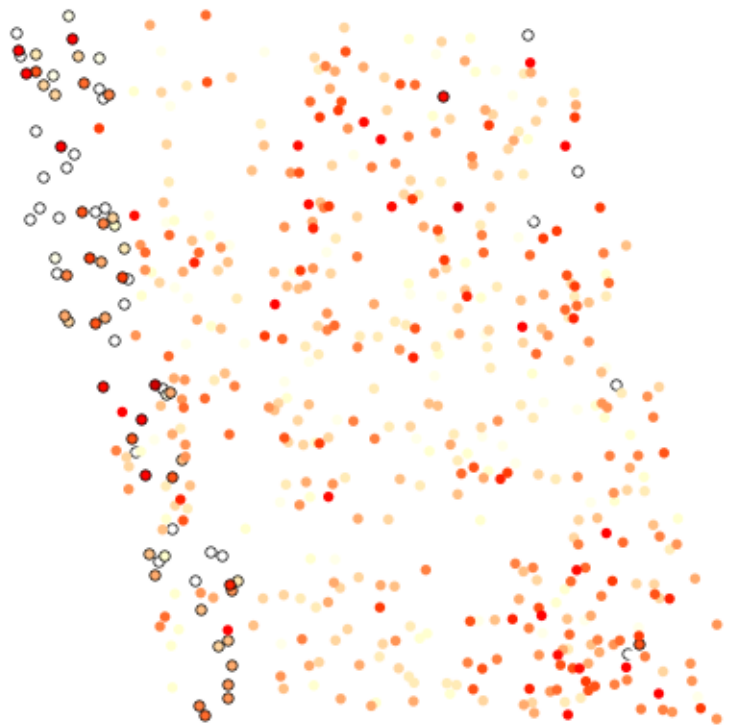
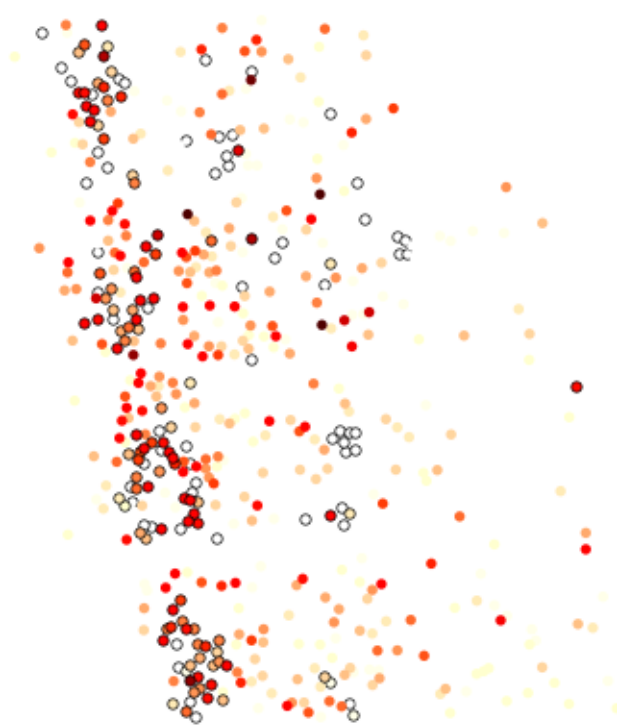
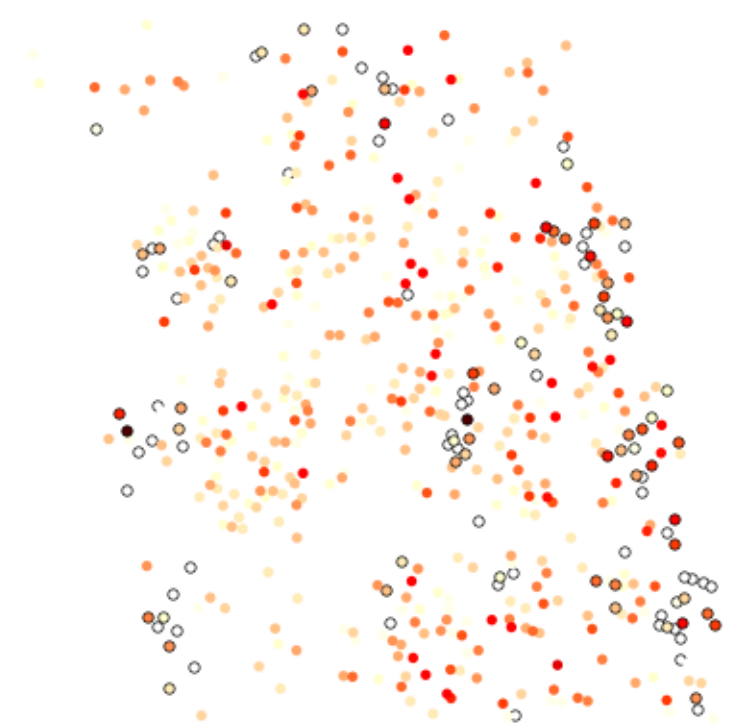
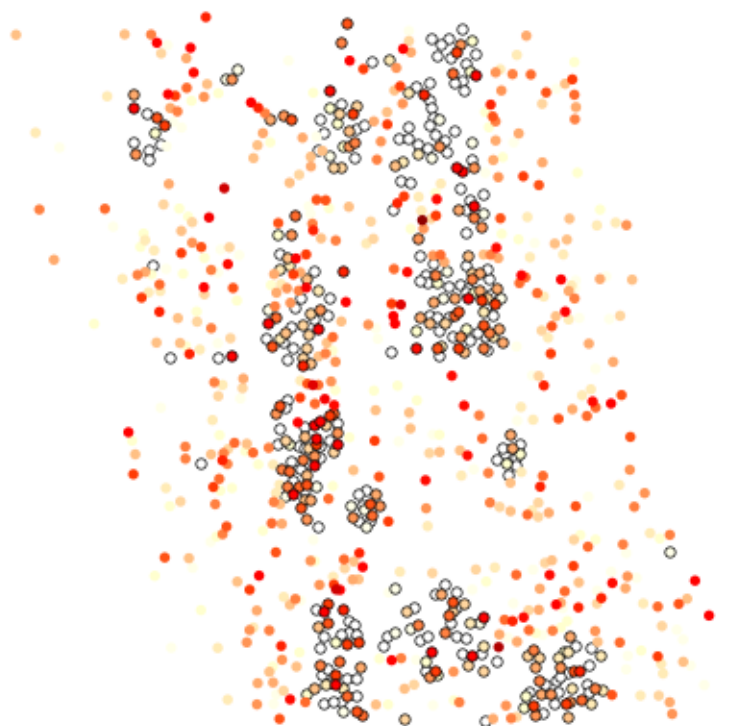
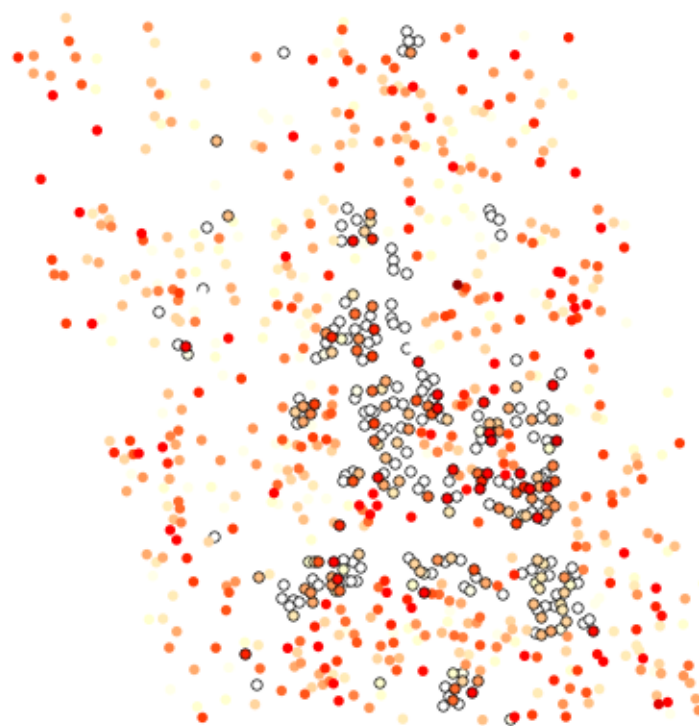
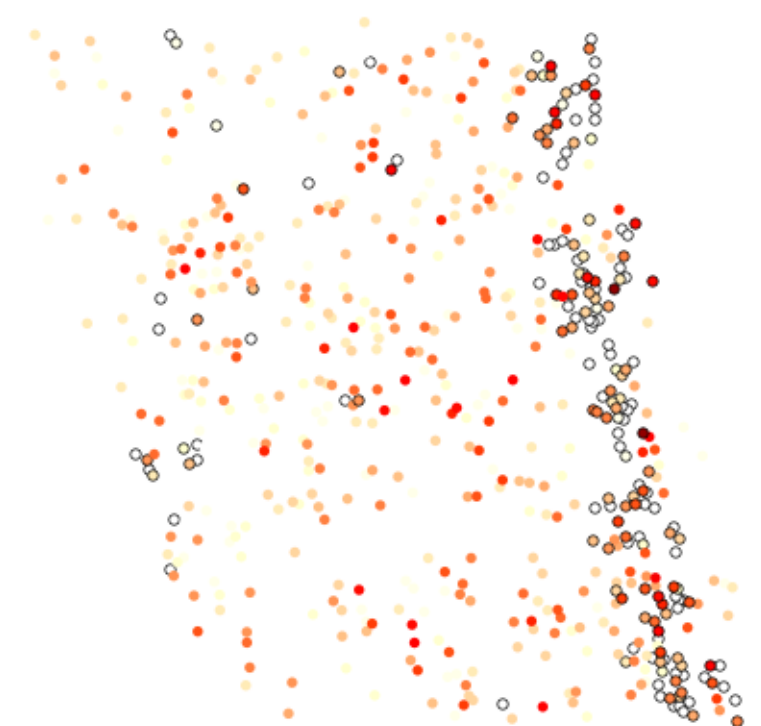


SFig 3

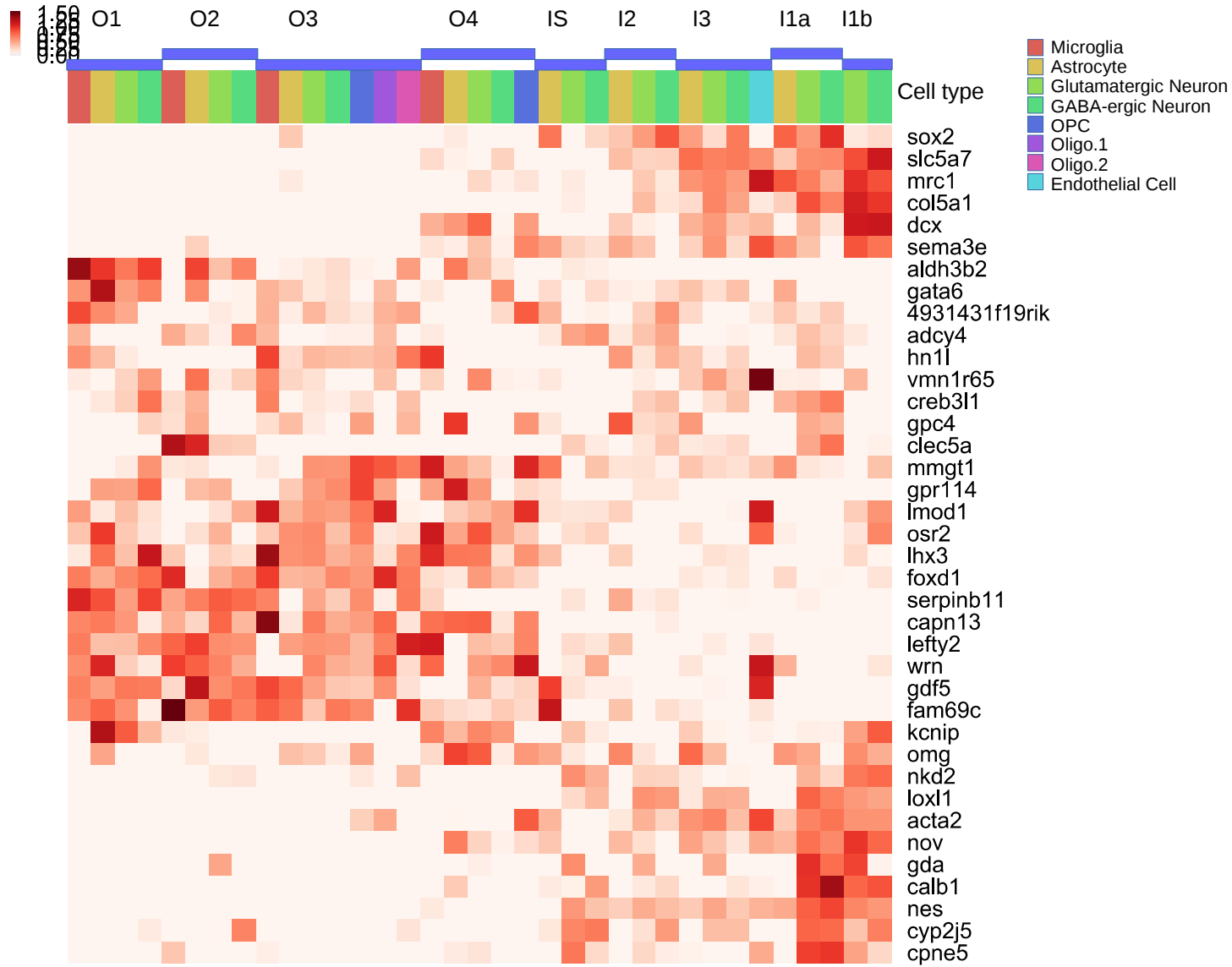


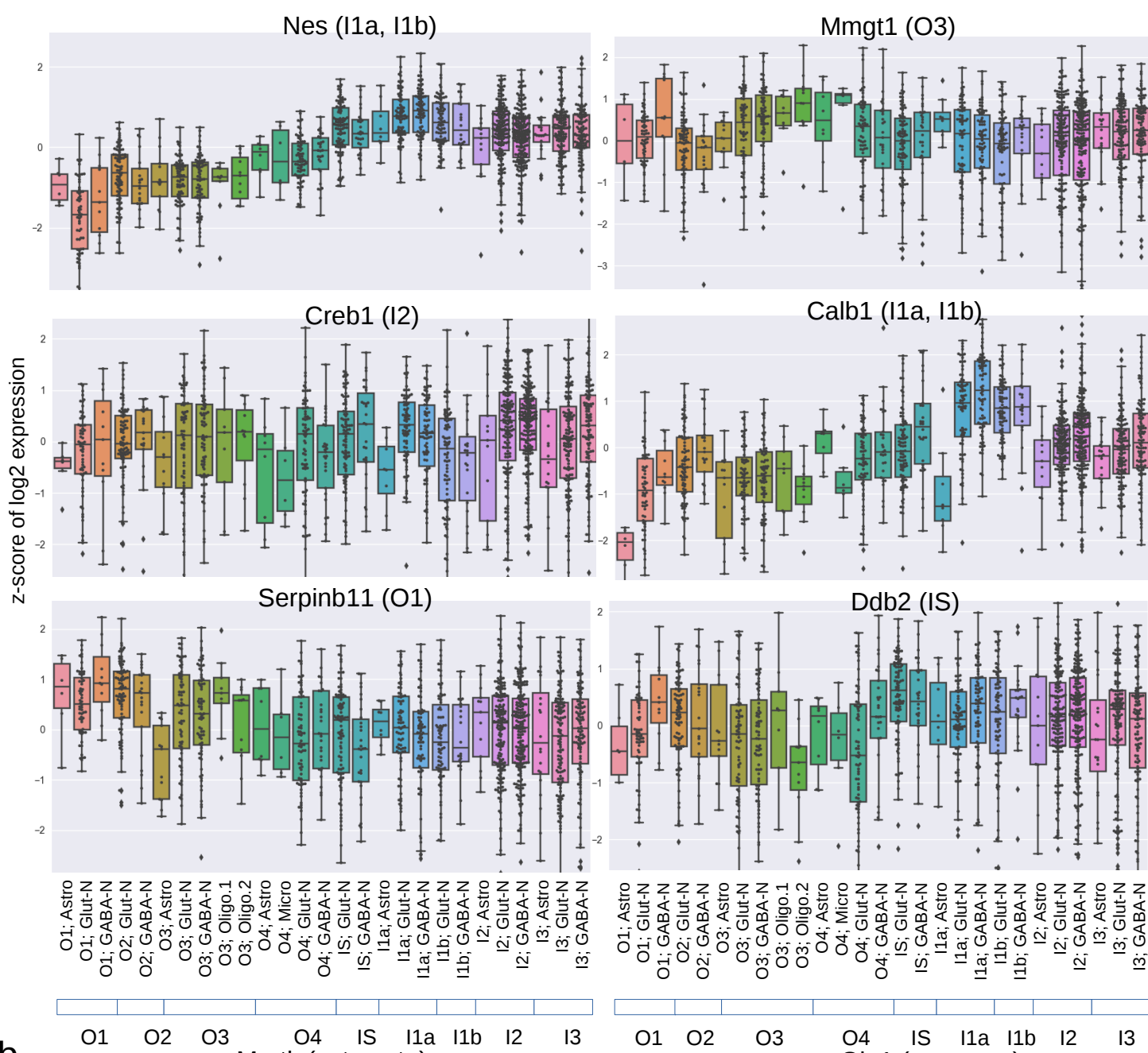
SFig 4



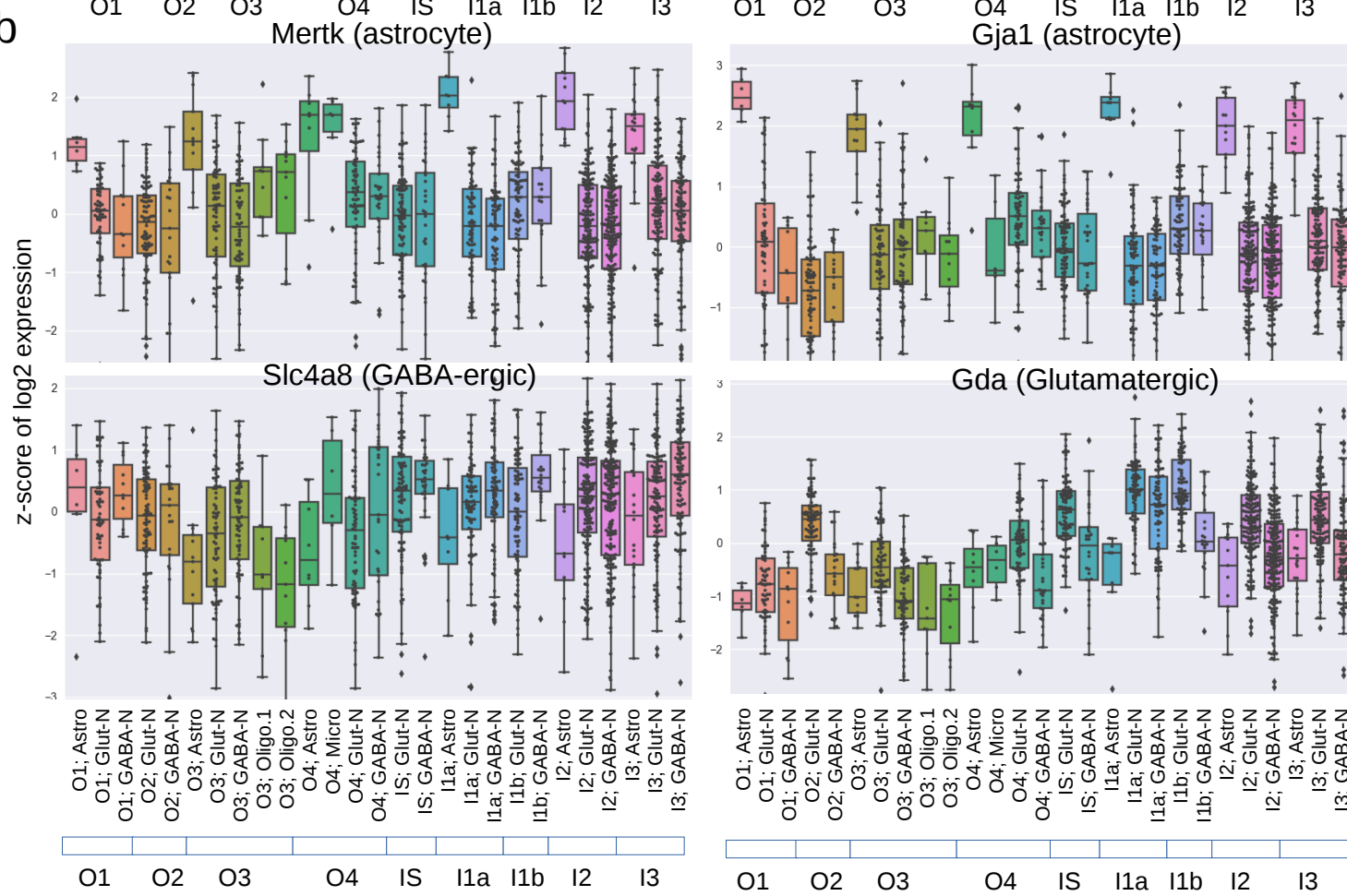
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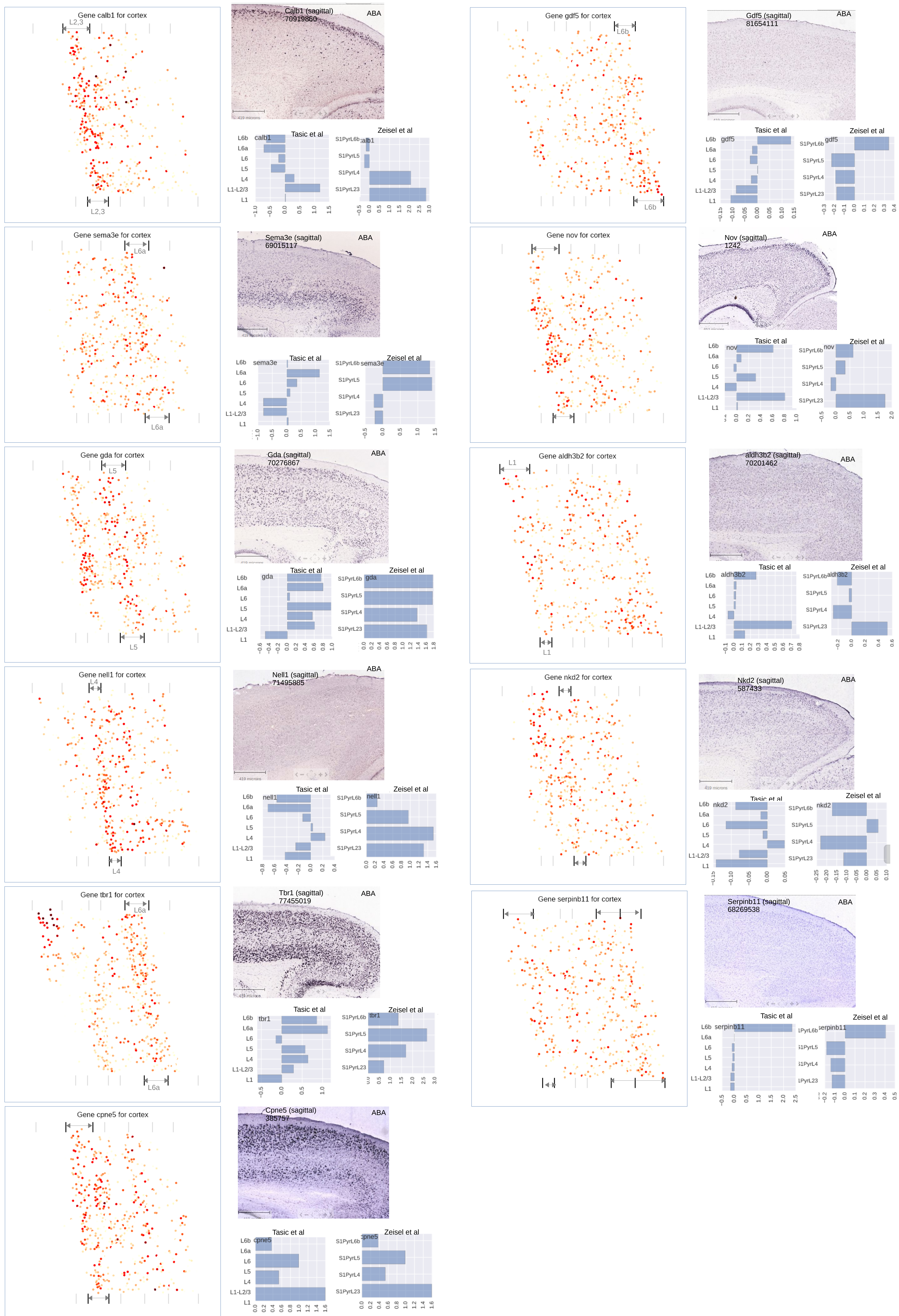
SFig 6





**b**

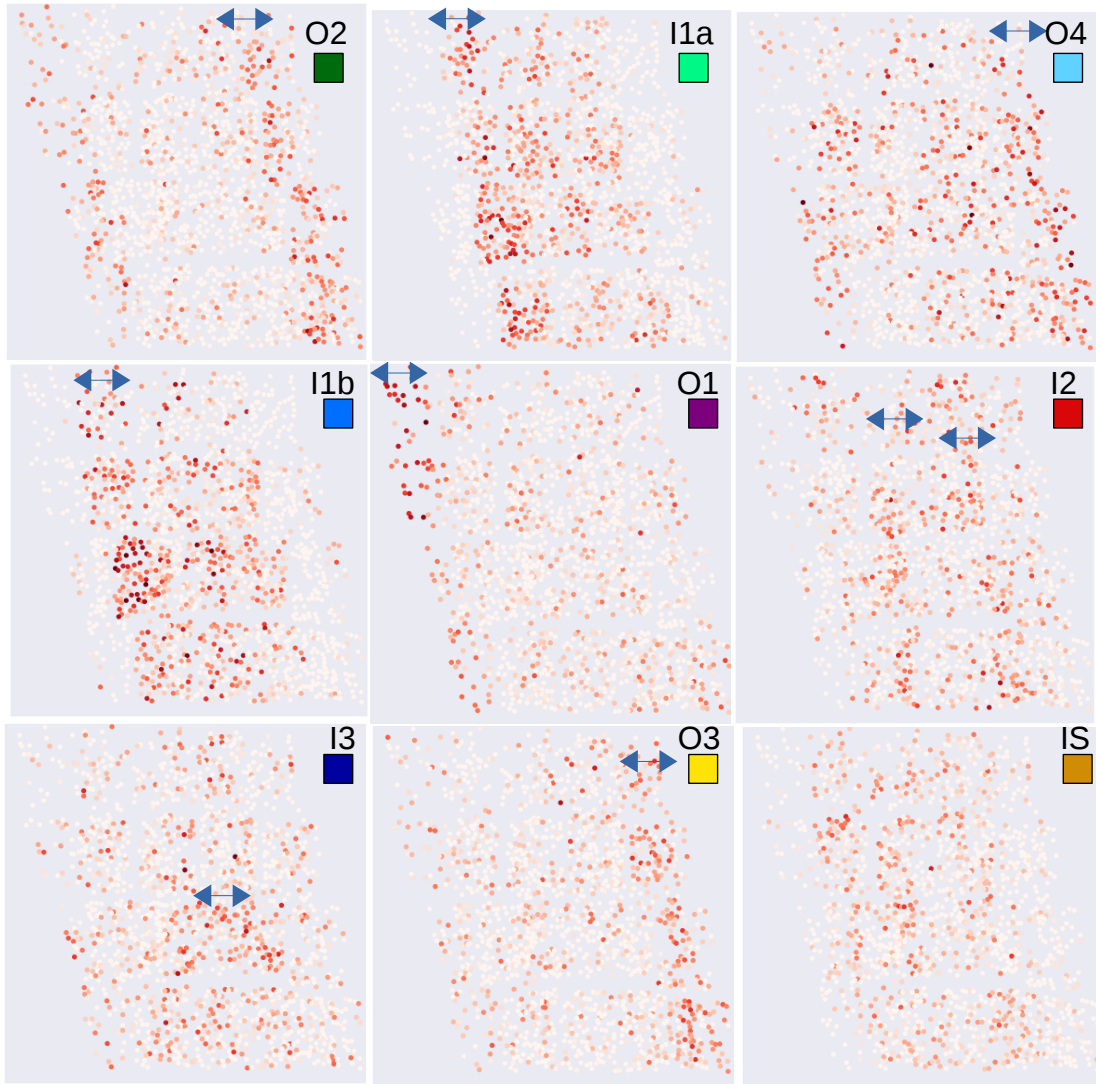




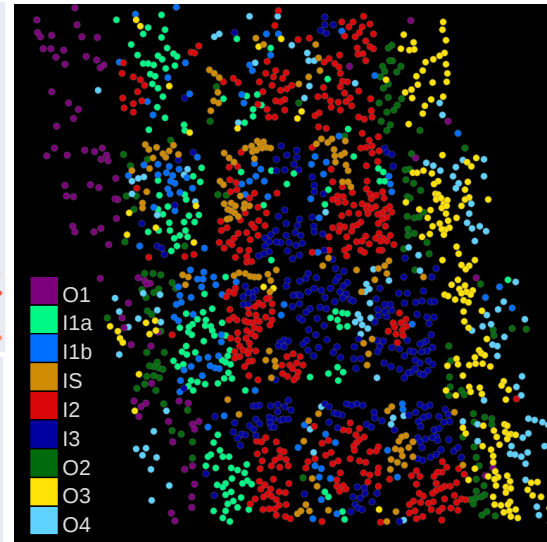


SFig 9

a

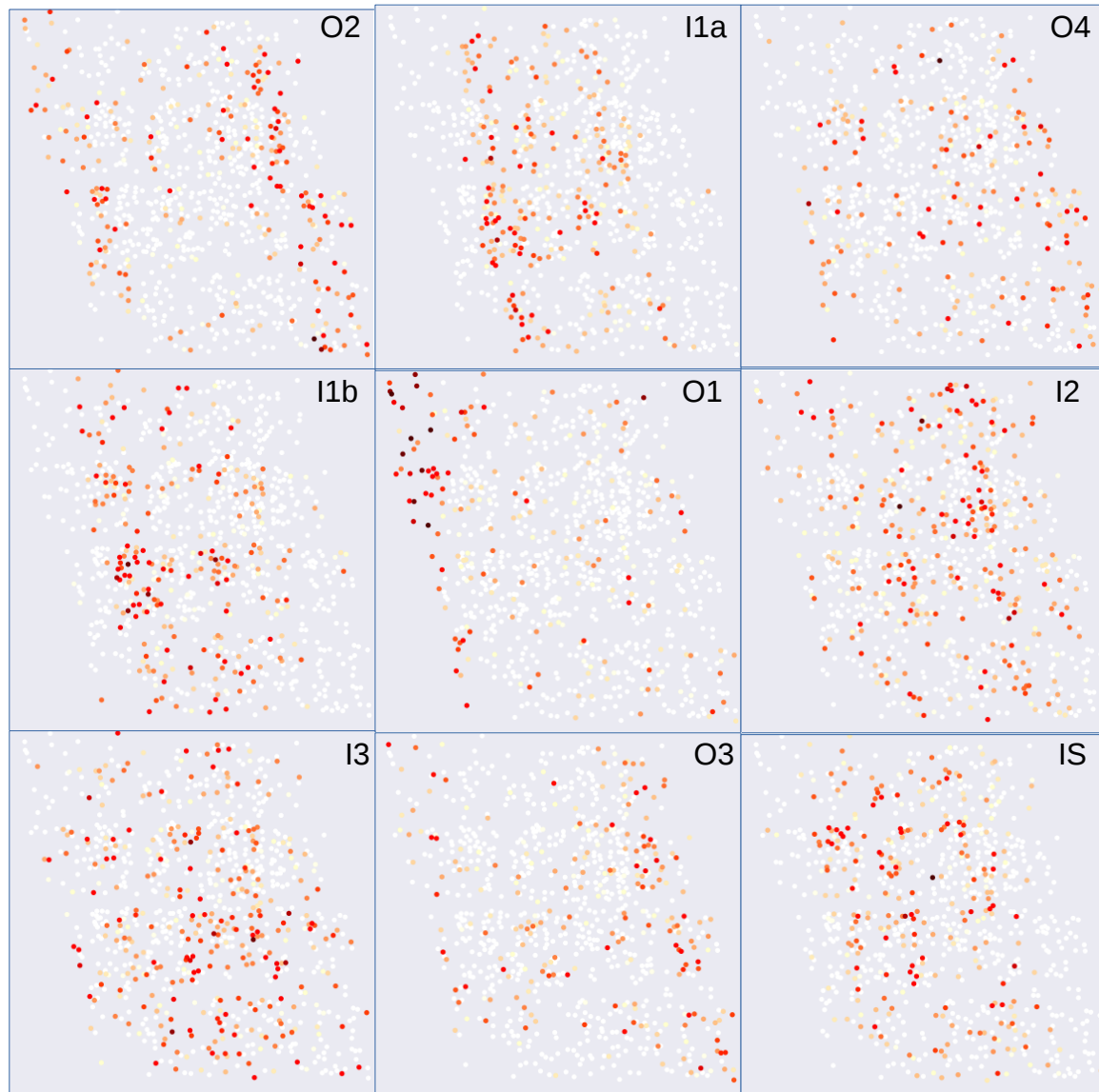


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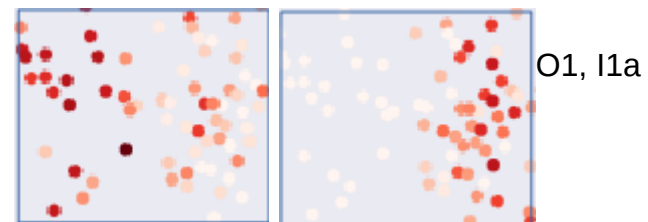
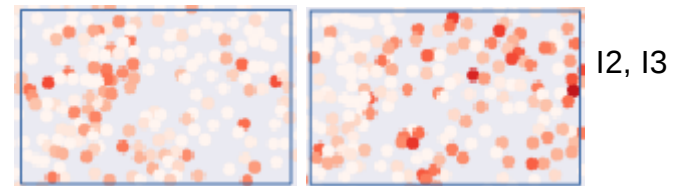
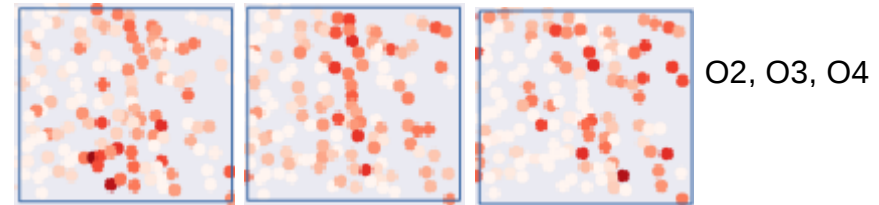
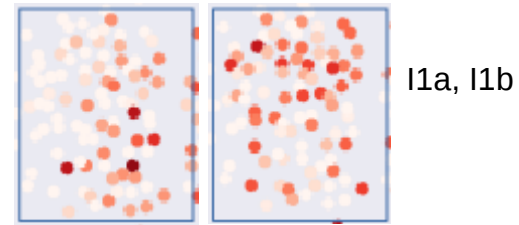
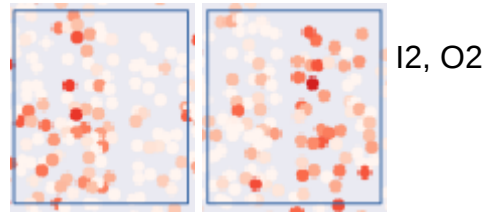
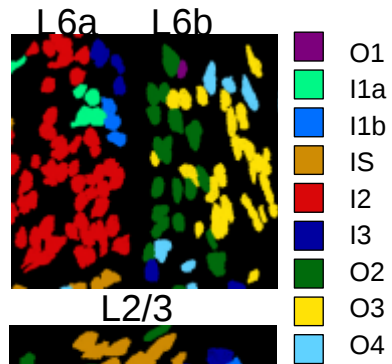
SFig 10

Glutamatergic cells



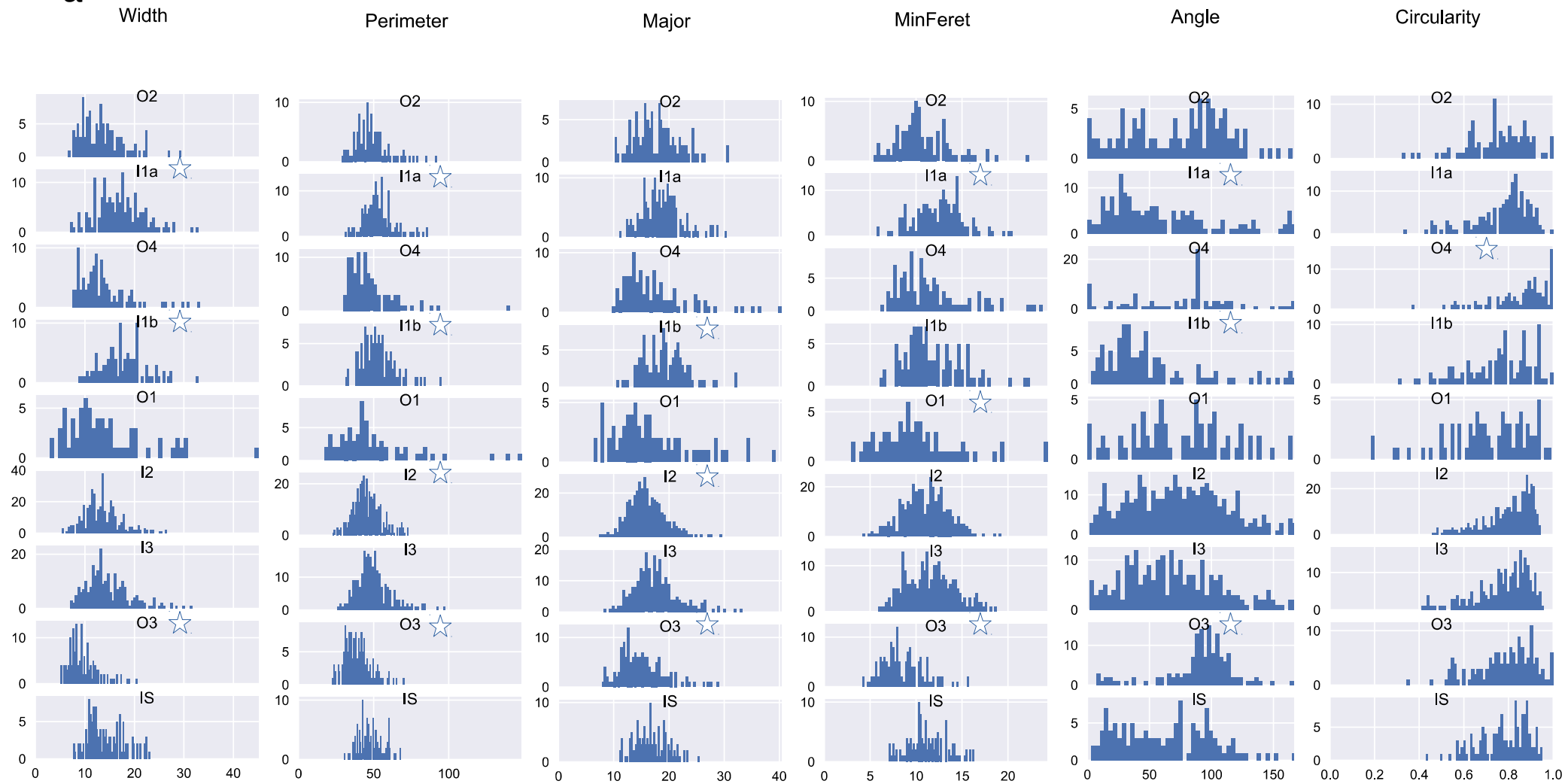
SFig 11

Spatial domain



# SFig 12

a



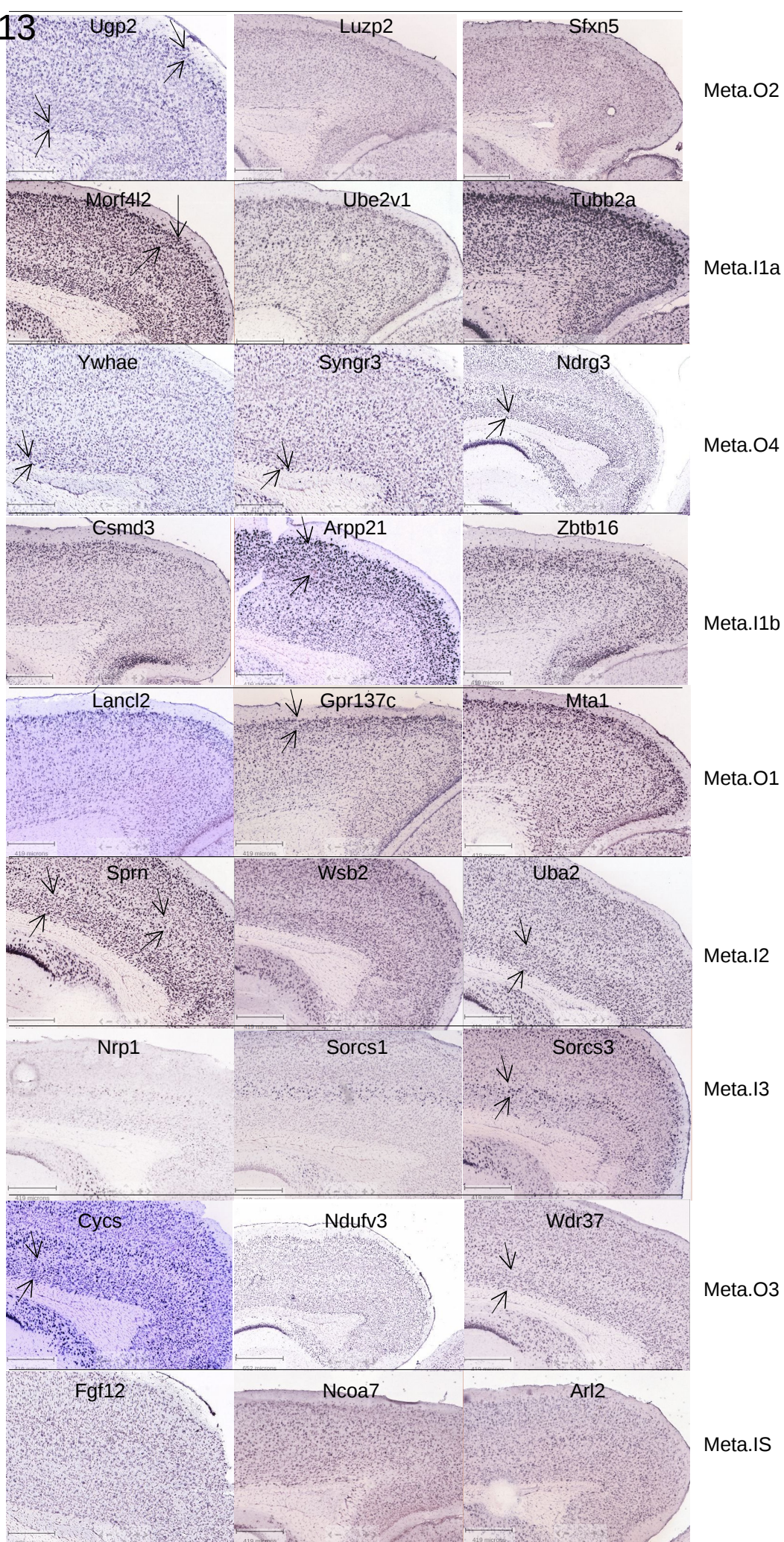
b

## Glutamatergic Cells

	Perimeter	Width	Angle	MinFeret	Circularity	Major
O2	-	-	-	-	-	-
I1a	1.78E-05	3.60E-08	8.17E-06	-	-	-
O4	-	-	-	-	7.00E-12	-
I1b	-	1.75E-10	7.90E-08	-	-	-
O1	-	-	-	0.00288	4.46E-05	-
I2	-	-	-	-	-	3.89E-05
I3	-	0.0158	-	-	-	-
O3	4.46E-10	1.26E-19	2.53E-10	8.67E-14	-	-
IS	-	-	-	-	-	-

## All cells

	Perimeter	Width	Angle	MinFeret	Circularity	Major
O2	-	-	-	-	-	-
I1a	1.07E-14	4.34E-17	-	3.02E-11	-	-
O4	-	-	-	-	6.18E-12	-
I1b	1.24E-05	1.60E-14	6.28E-11	-	-	2.74E-06
O1	-	-	-	0.002773	-	-
I2	-	-	-	-	-	1.30E-08
I3	-	-	-	-	-	-
O3	2.32E-20	6.80E-37	6.70E-18	5.27E-26	-	1.50E-10
IS	-	-	-	-	-	-

**SFig 13**

# SFig 14

## Gene overlap (within 125 genes)

## Cell overlap

$-\log_{10}(P)$

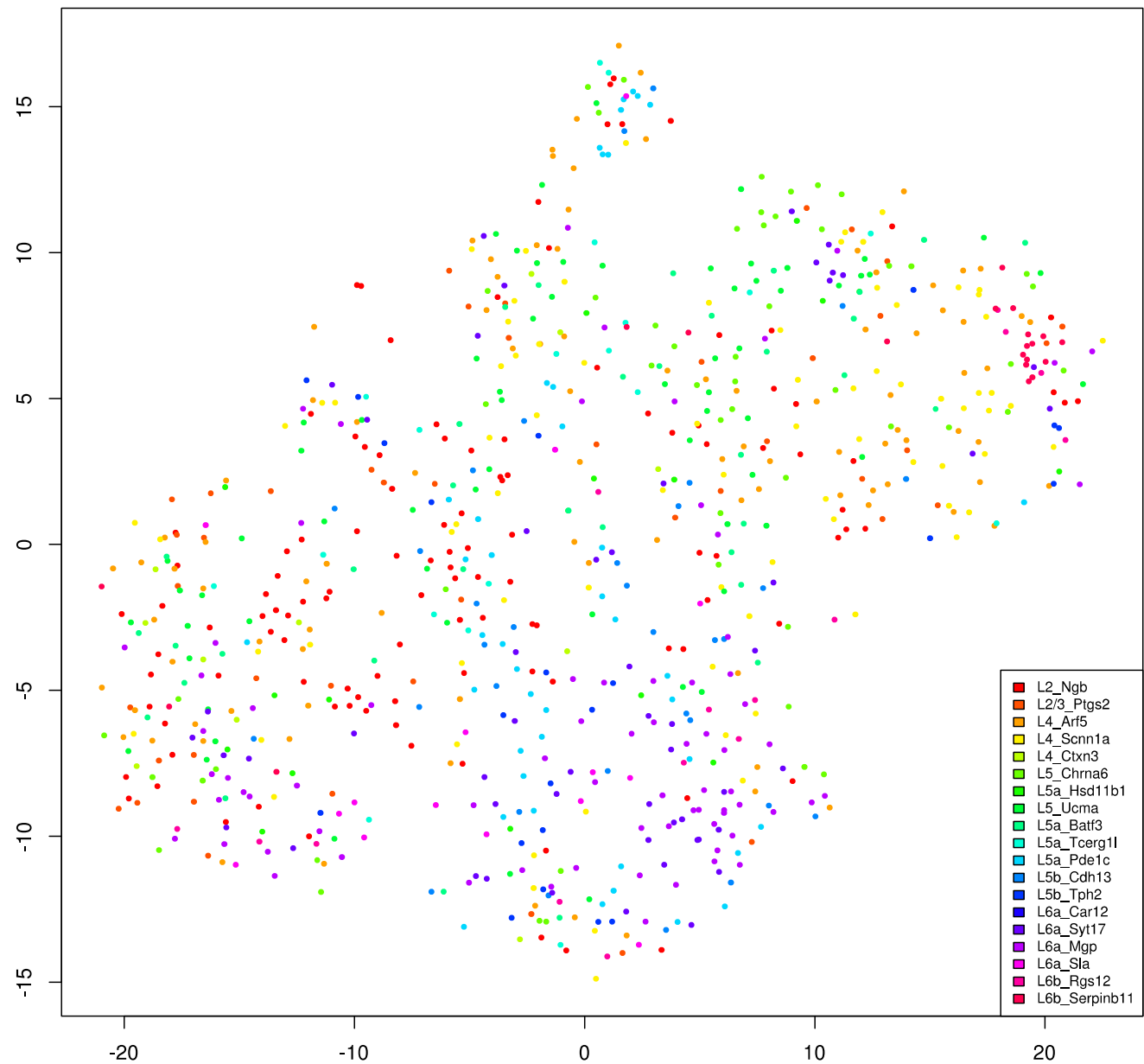
0  
2  
4  
6  
8  
10

	I1a	I1b	I2	I3	IS	O1	O2	O3	O4
L2/3_Ptgs2	10.2	2.3	0.5	1.1	3.7	5.7	2.5	0.8	3.7
L2_Ngb	9.4	2.8	0.7	1.4	2.7	2.8	1.3	1.0	4.2
L4_Arf5	3.9	2.3	1.2	2.7	2.2	3.9	2.5	1.9	1.5
L4_Ctxn3	1.9	0.8	10.0	1.0	0.7	0.8	3.8	7.4	1.4
L4_Scnn1a	1.5	1.5	10.0	0.8	0.5	4.0	1.7	7.5	1.1
L5_Chma6	1.5	1.5	1.0	1.7	1.5	6.2	3.9	3.2	2.1
L5_Ucma	1.4	5.6	2.2	6.3	1.4	1.4	1.5	1.2	2.0
L5a_Batf3	2.8	2.8	2.9	1.4	2.7	2.8	1.3	1.0	1.8
L5a_Hsd11b1	1.3	3.1	2.0	1.5	5.0	1.3	1.4	2.7	1.9
L5a_Pde1c	1.5	3.6	2.5	4.0	1.5	1.5	1.7	1.4	2.1
L5a_Tcerg1l	1.0	2.0	1.5	2.2	2.0	2.0	2.1	1.8	2.6
L5b_Cdh13	4.5	6.6	1.5	5.2	4.3	1.1	1.2	0.9	1.0
L5b_Tph2	6.1	10.8	0.5	4.9	2.3	1.0	1.1	2.1	3.9
L6a_Car12	3.6	3.6	1.0	4.0	1.5	1.5	1.7	1.4	2.1
L6a_Mgp	0.8	8.9	10.0	4.0	0.7	0.8	2.2	2.7	1.4
L6a_Sla	1.1	9.0	1.5	3.1	1.1	2.6	2.9	2.3	1.7
L6a_Syt17	5.6	5.6	0.9	6.3	1.4	1.4	1.5	1.2	2.0
L6b_Rgs12	1.7	1.0	1.2	4.5	1.7	1.7	1.8	1.5	2.3
L6b_Serpinb11	1.3	1.3	2.0	1.5	3.0	3.1	8.4	4.6	1.9

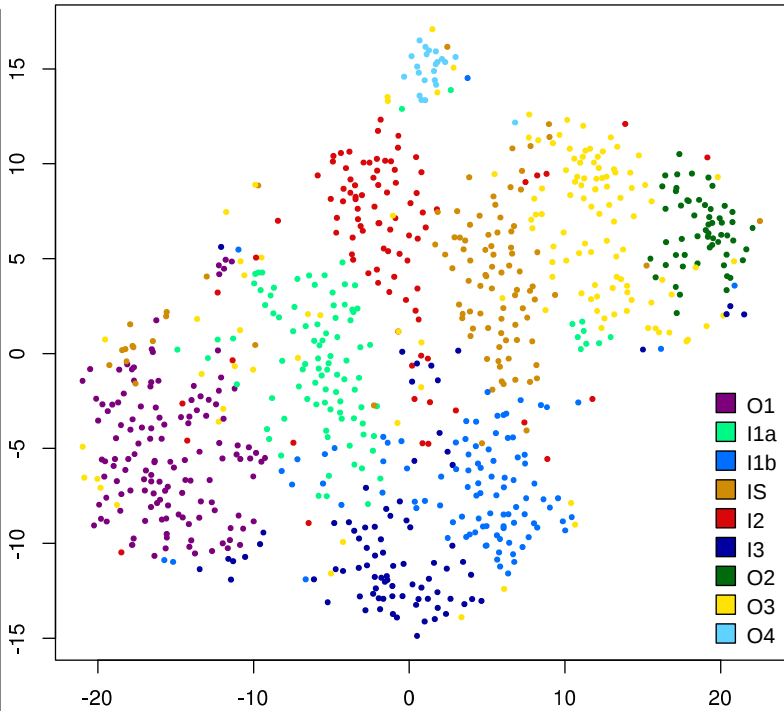
	I1a	I1b	I2	I3	IS	O1	O2	O3	O4
L2/3_Ptgs2	10.1	0.0	0.0	0.0	0.8	3.3	0.0	0.0	0.1
L2_Ngb	1.5	1.0	0.1	0.0	0.1	1.0	0.1	0.2	2.7
L4_Arf5	0.2	0.0	0.9	0.1	0.6	1.8	0.2	1.1	0.1
L4_Ctxn3	0.2	0.1	0.8	0.1	0.3	0.0	2.8	2.1	0.0
L4_Scnn1a	0.0	0.0	0.9	0.0	0.3	0.4	0.9	4.4	0.1
L5_Chma6	0.1	0.1	0.4	0.5	0.4	3.3	0.3	0.6	0.6
L5_Ucma	0.1	0.2	0.6	1.1	0.5	1.5	0.2	0.6	0.4
L5a_Batf3	0.4	0.0	3.8	0.0	2.1	0.3	0.1	0.2	0.6
L5a_Hsd11b1	0.0	0.0	0.1	0.3	2.7	0.0	0.8	2.7	1.3
L5a_Pde1c	1.2	0.0	1.8	0.5	0.4	0.1	0.1	0.4	1.9
L5a_Tcerg1l	0.2	0.0	0.4	0.1	3.5	0.5	0.0	1.4	0.2
L5b_Cdh13	2.1	0.9	0.5	1.6	0.0	0.0	0.0	0.1	5.3
L5b_Tph2	0.7	3.1	0.1	1.0	0.3	0.0	0.0	0.2	1.3
L6a_Car12	0.6	0.1	0.6	6.7	0.0	0.0	0.7	0.0	0.3
L6a_Mgp	0.1	2.5	0.2	3.3	0.0	0.2	0.1	0.1	0.1
L6a_Sla	0.0	12.9	0.0	0.9	0.0	1.4	0.0	0.0	0.1
L6a_Syt17	0.3	1.6	0.6	1.2	0.3	0.3	0.2	0.1	1.2
L6b_Rgs12	0.1	3.0	0.3	0.7	0.1	0.7	1.8	0.0	0.5
L6b_Serpinb11	0.0	0.0	0.0	0.1	0.4	0.4	14.2	0.1	0.4

SFig 15

a

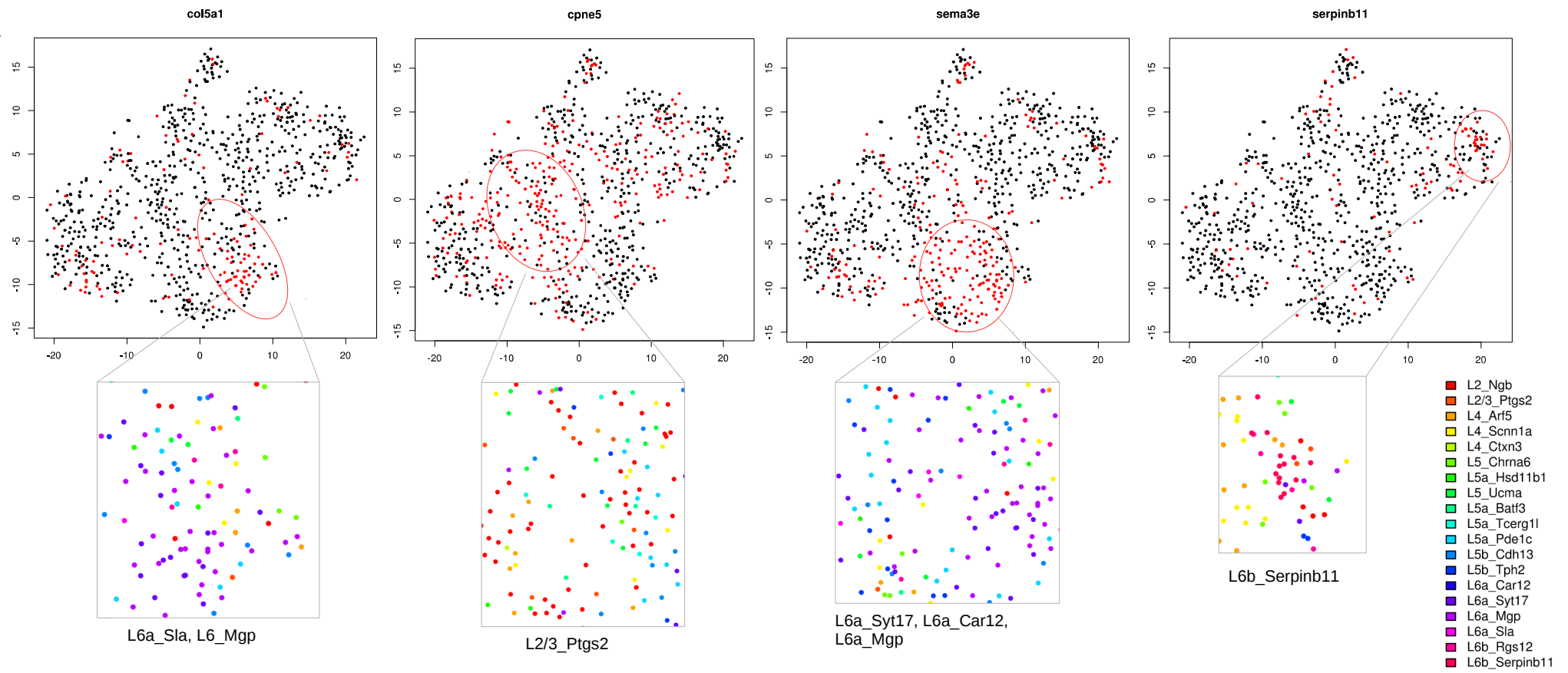


b

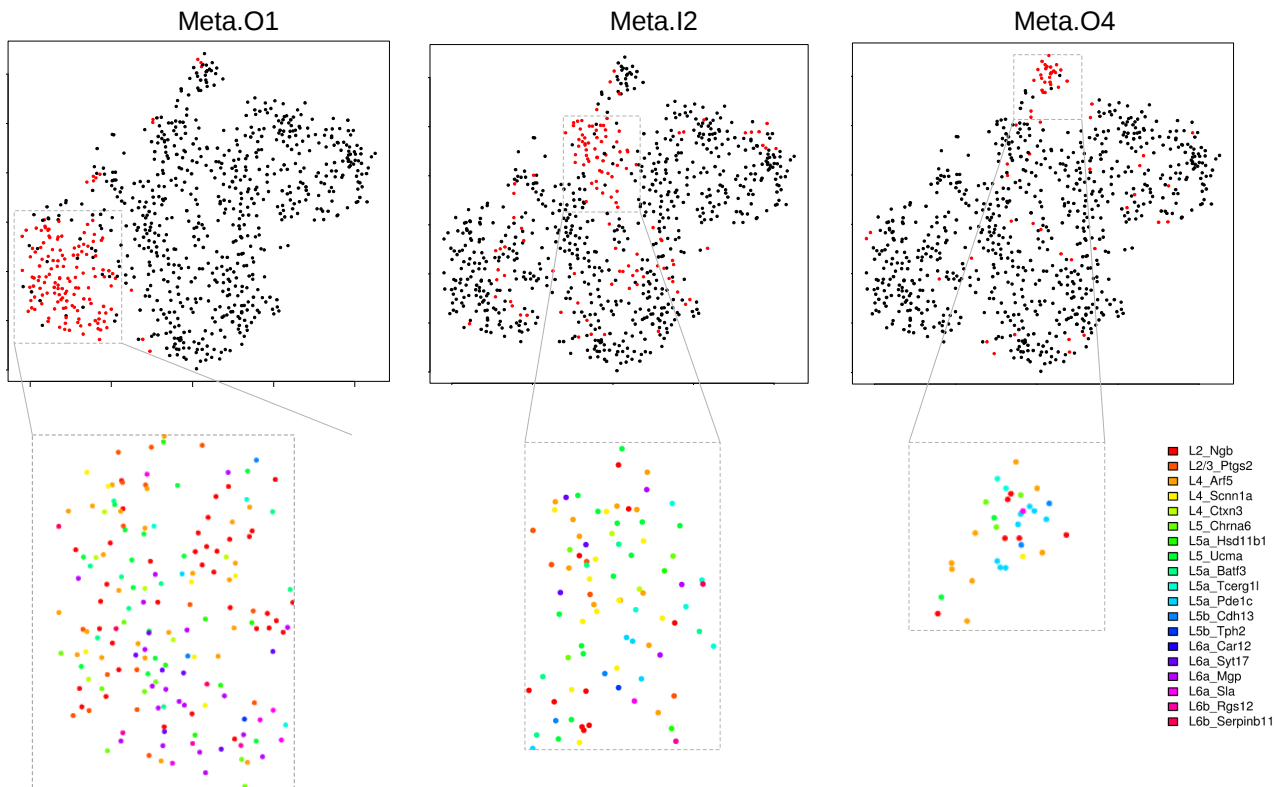


# SFig 16

a

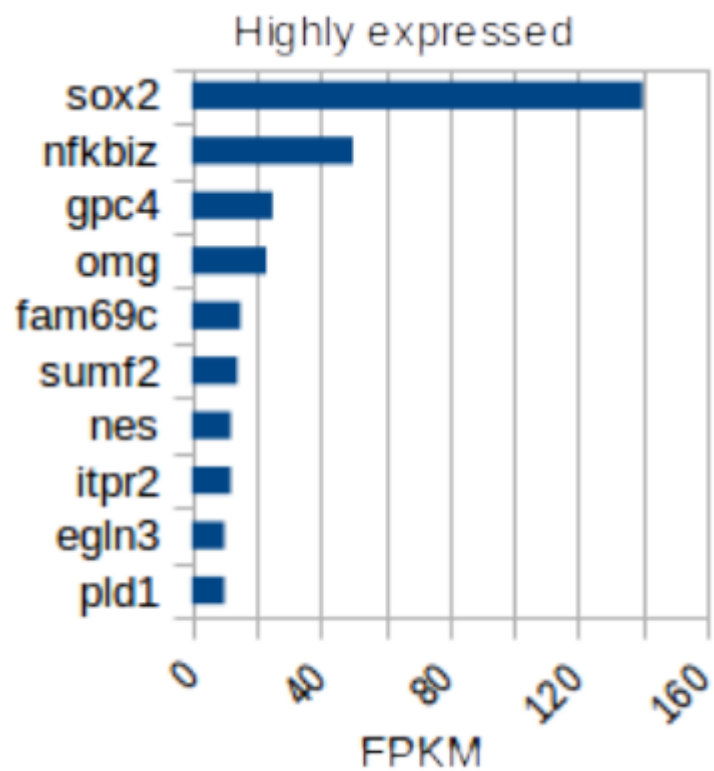
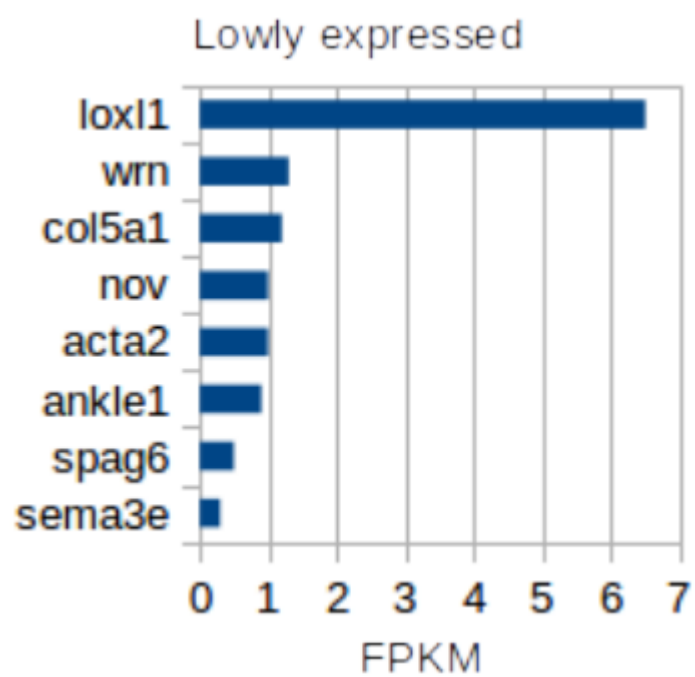


b



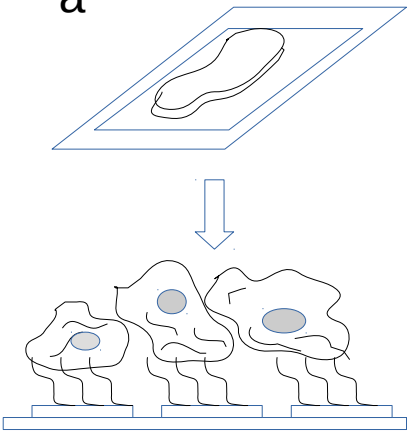


SFig 17



# SFig 18

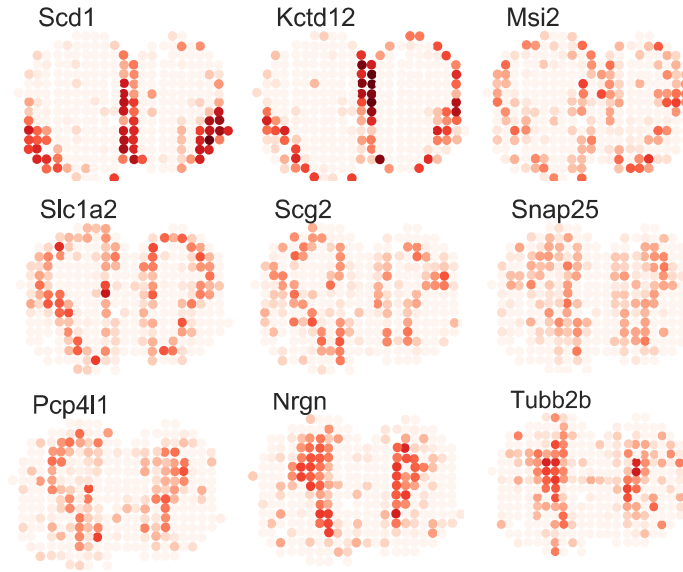
a



b



c

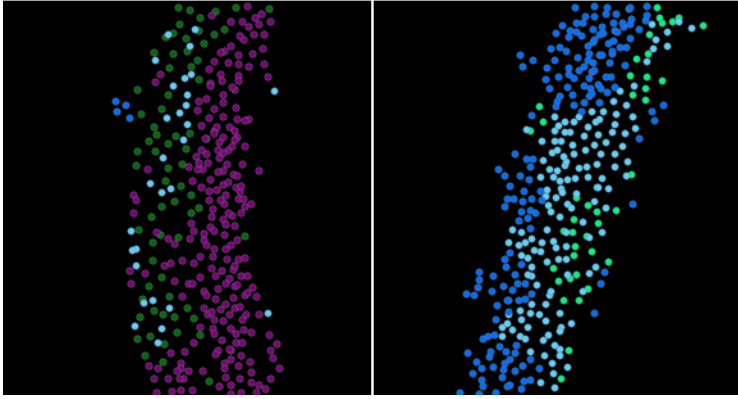


d

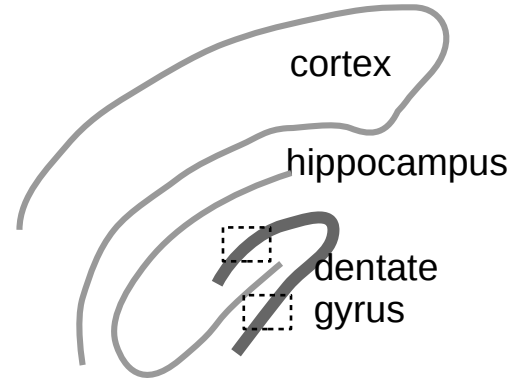


SFig 19

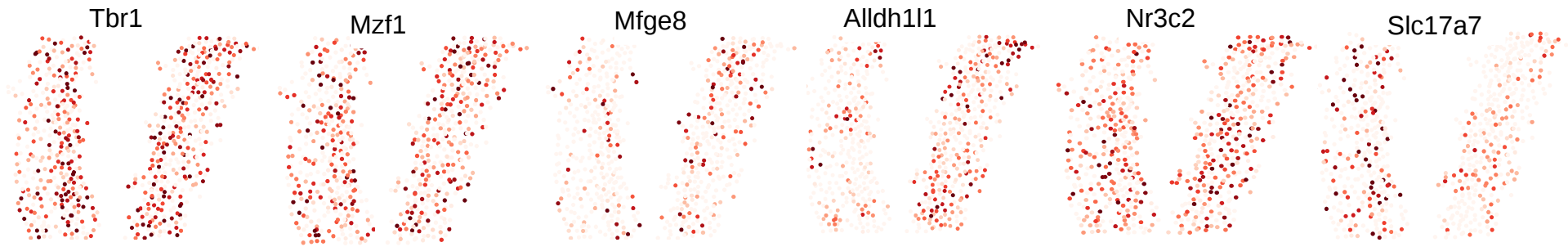
a



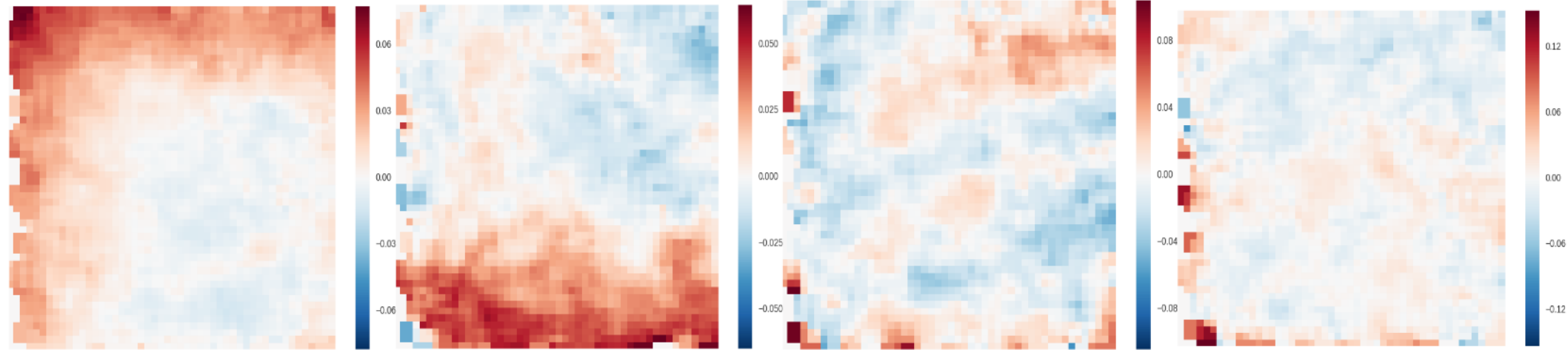
b



c



SFig 20



# SFig 21

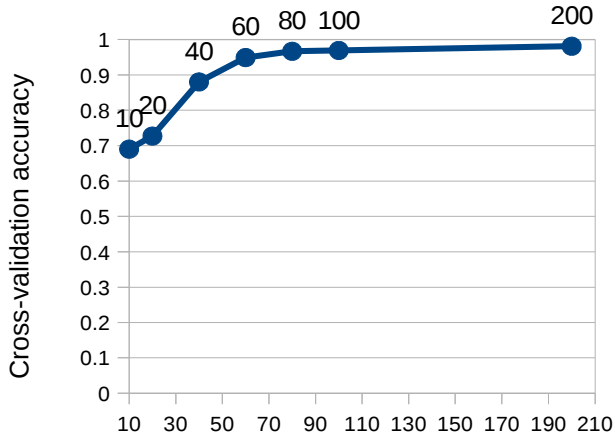
## a

8 major classes  
22 finer classes  
49 minor classes

8 major classes	Oligo.1	Oligo.2	OPC	Astro	Micro	Endo	Glut-N															GABA-N																											
22 finer classes	Oligo.1	Oligo.2	OPC	Astro	Micro	Endo	L2/3	L6a	L4_Arf5	L4_Ctxn3/	Scnn1a	L5_Ucma /	Chma6	L5a	L5b	L6a	L6b	Vip	Sncg	Ndnf	Igtp/Smad3	Sst	Pvalb_1	Pvalb_2																									
49 minor classes	Oligo_96_Rik	Oligo_Opalin	OPC_Pdgfra	Astro_Gja1	Micro_Ctss	Endo_Myl9	Endo_Tbc1d4	L2/3_Ptgs2	L2_Ngb	L6a_Car12	L6a_Syt17	L4_Arf5	L4_Ctxn3	L4_Scnn1a	L5_Ucma	L5_Chma6	L5a_Pde1c	L5a_Hsd11b1	L5a_Batf3	L5a_Tcerg1l	L5b_Cdh13	L5b_Tph2	L6a_Mgp	L6a_Sla	L6b_Rgs12	L6b_Serpinb11	Vip_Mybpc1	Vip_Parm1	Vip_Chat	Vip_Gpc3	Sncg	Vip_Sncg	Ndnf_Car4	Ndnf_Cxci14	Igtp	Smad3	Sst_Chodl	Sst_Tacstd2	Sst_Th	Sst_Cbln4	Sst_Cdk6	Sst_Myh8	Pvalb_Obox3	Pvalb_Rspo2	Pvalb_Tacr3	Pvalb_Wt1	Pvalb_Cpne5	Pvalb_Gpx3	Pvalb_Tpbg

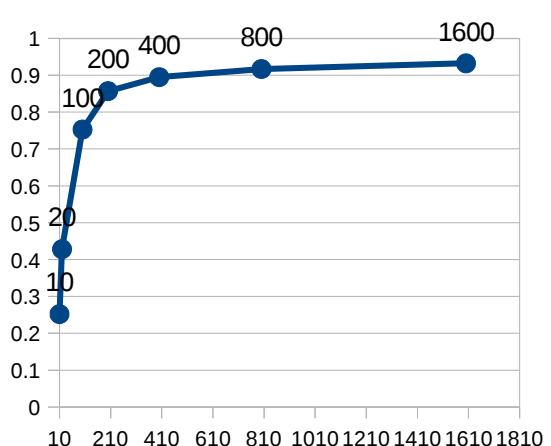
## b

### 8 major classes



## c

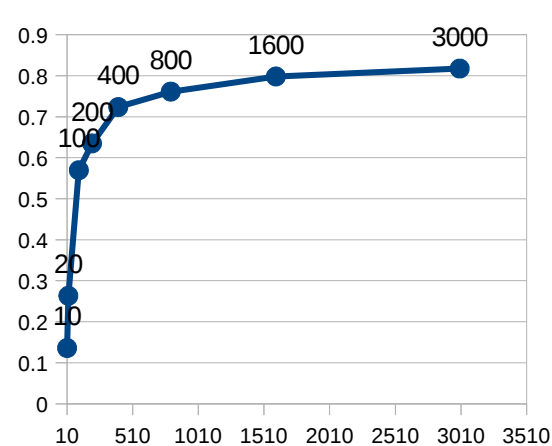
### 22 finer classes



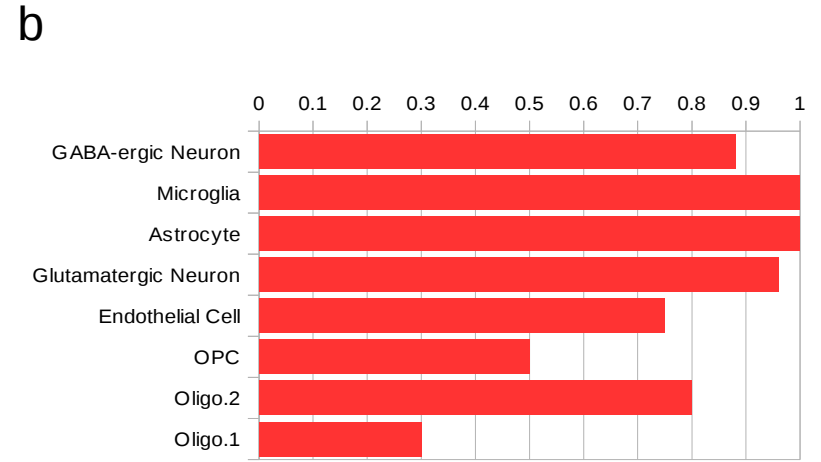
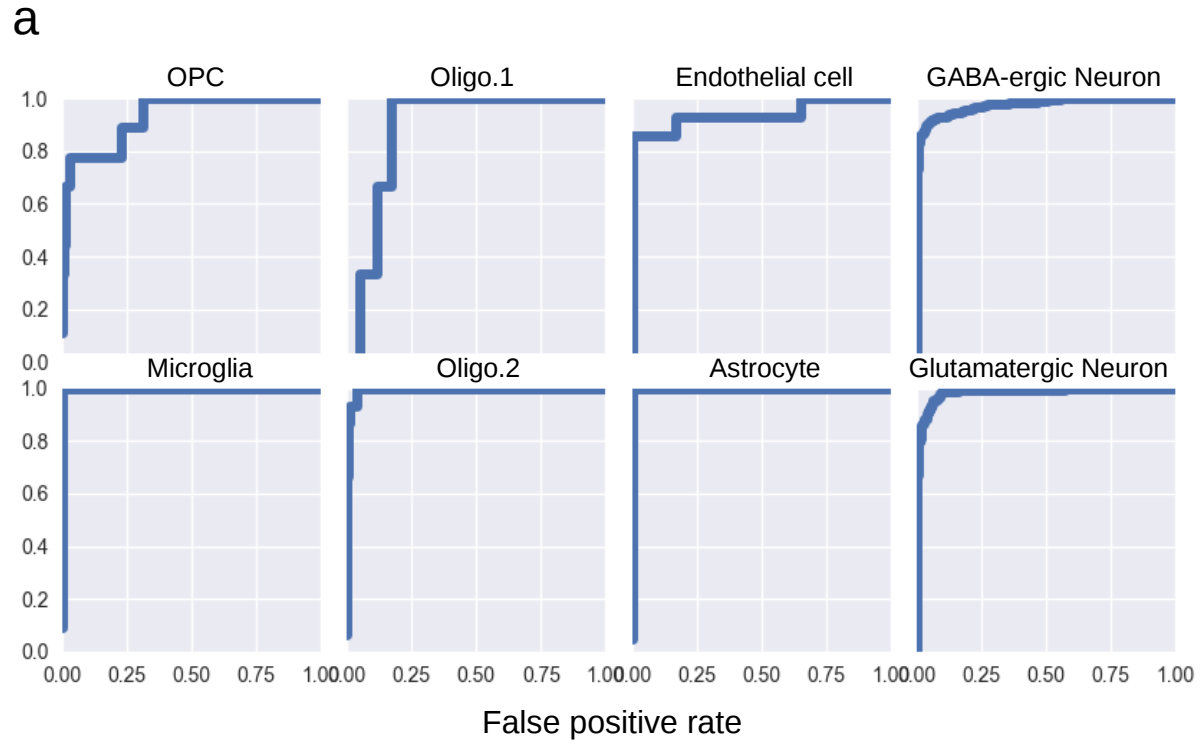
# random DE genes used for multiclass SVM

## d

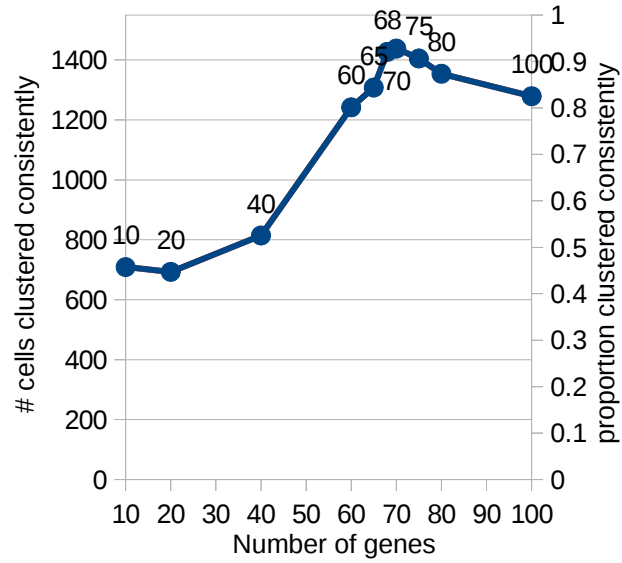
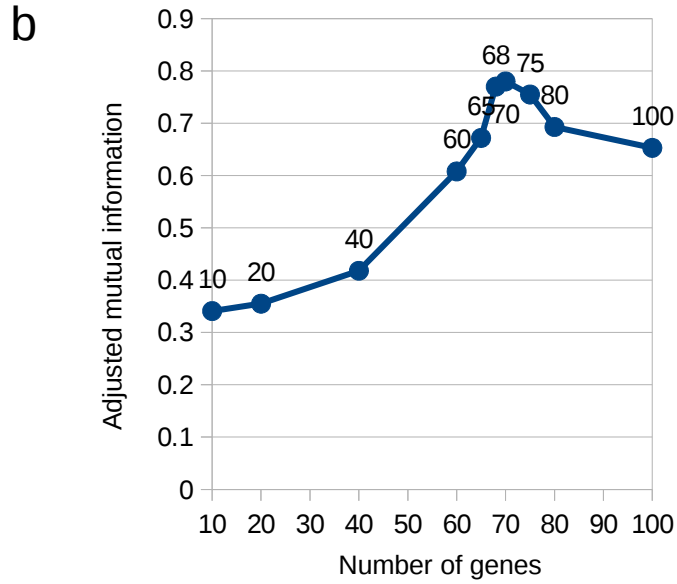
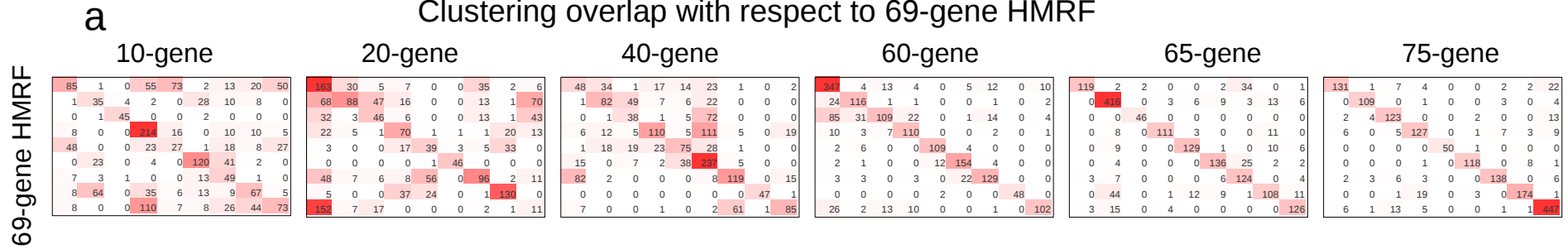
### 49 minor classes



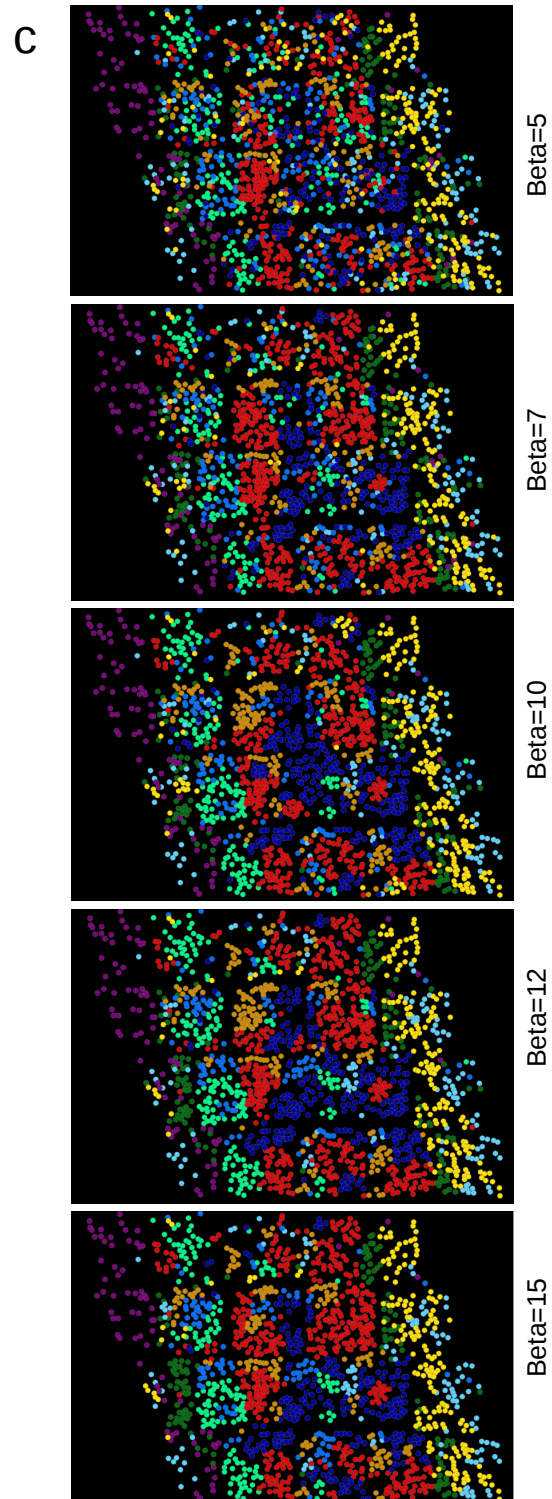
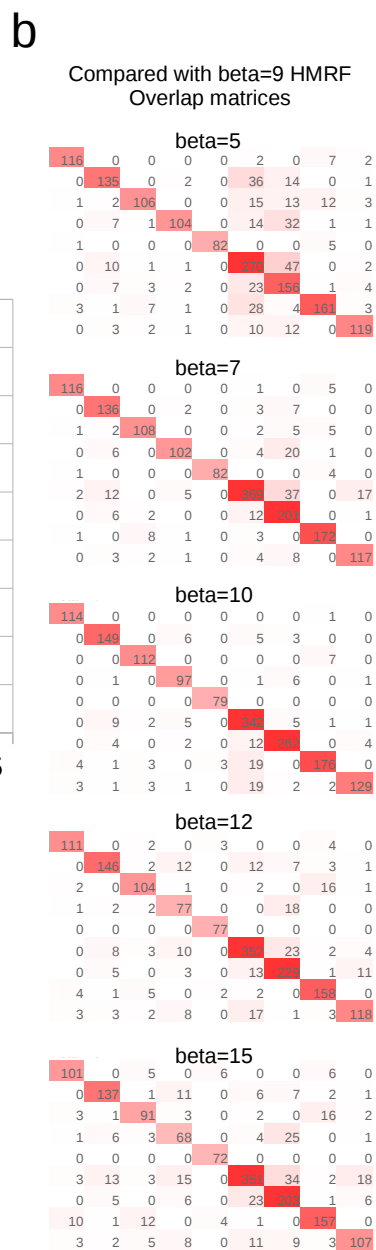
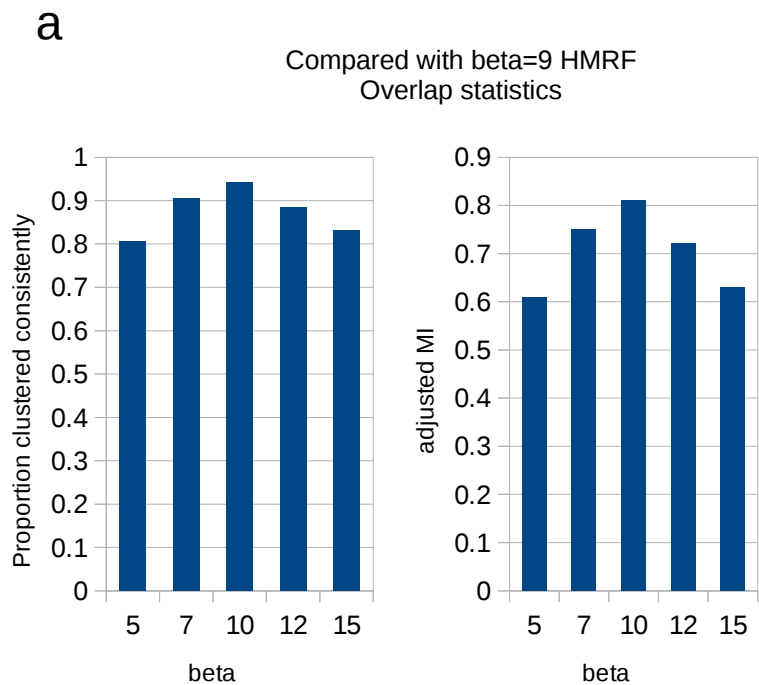
# SFig 22



Clustering overlap with respect to 69-gene HMRF

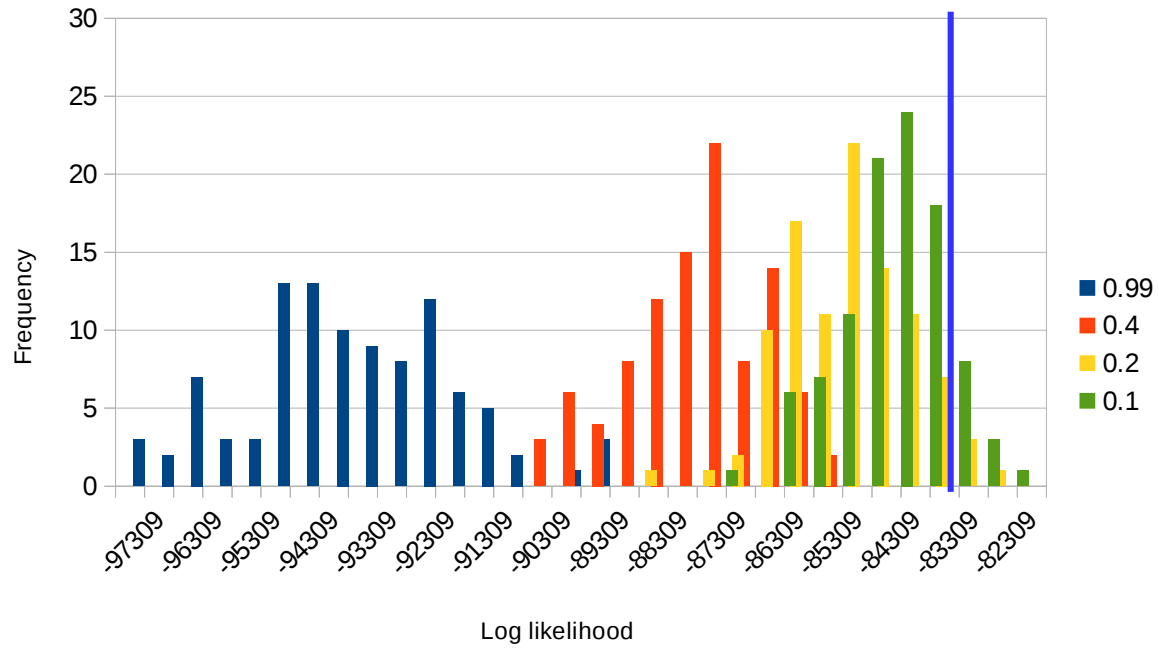


# SFig 24

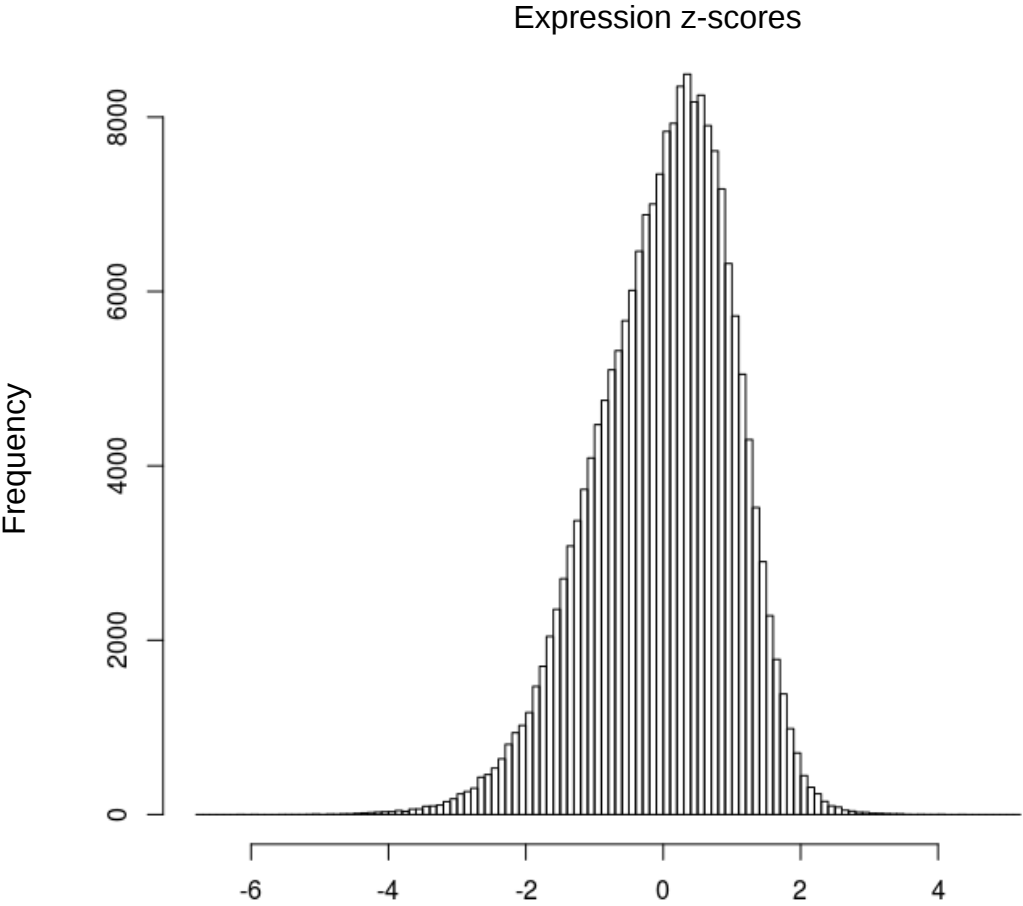




SFig 25



SFig 26



# SFig 27

## Mann Whitney U test

