

Integrating gene expression, spatial location and histology to identify spatial domains and spatially variable genes by graph convolutional network

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1 **Integrating gene expression, spatial location and histology to identify spatial**
2 **domains and spatially variable genes by graph convolutional network**

3

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22 **Key words:** spatial transcriptomics; histology; spatial domains; spatially variable genes; graph
23 convolutional network.

24 **Abstract**

25

26 Recent advances in spatial transcriptomics technologies have enabled comprehensive characterization of
27 gene expression patterns in the context of tissue microenvironment. To elucidate spatial gene expression
28 variation, we present SpaGCN, a graph convolutional network approach that integrates gene expression,
29 spatial location and histology in spatial transcriptomics data analysis. Through graph convolution, SpaGCN
30 aggregates gene expression of each spot from its neighboring spots, which enables the identification of
31 spatial domains with coherent expression and histology. The subsequent domain guided differential
32 expression analysis then detects genes with enriched expression patterns in the identified domains.
33 Analyzing five spatially resolved transcriptomics datasets using SpaGCN, we show it can detect genes with
34 much more enriched spatial expression patterns than existing methods. Furthermore, genes detected by
35 SpaGCN are transferrable and can be utilized to study spatial variation of gene expression in other
36 datasets. SpaGCN is computationally fast, making it a desirable tool for spatial transcriptomics studies.

37 Introduction

38

39 Recent advances in spatial transcriptomics technologies have enabled gene expression profiling with
40 spatial information in tissues¹. Knowledge of the relative locations of different cells in a tissue is critical
41 for understanding disease pathology because spatial information helps in understanding how the gene
42 expression of a cell is influenced by its surrounding environment and how neighboring regions interact at
43 the gene expression level. Experimental methods to generate spatial transcriptomics data can be broadly
44 classified into two categories: 1) single-molecule fluorescence *in situ* hybridization (smFISH) based
45 techniques, such as MERFISH² and seqFISH³, which measure expression level for hundreds of genes with
46 subcellular spatial resolution in a single cell; and 2) spatial barcoding followed by next generation
47 sequencing based techniques, such as SLIDE-seq⁴ and 10X Genomics Visium, which measure the
48 expression level for thousands of genes in captured locations, referred to as spots. These different spatial
49 transcriptomics techniques have made it possible to uncover the complex transcriptional architecture of
50 heterogenous tissues and enhanced our understanding of cellular mechanisms in diseases^{5,6}.

51

52 In spatial transcriptomics studies, an important step is identifying spatial domains defined as regions that
53 are spatially coherent in both gene expression and histology. Identifying spatial domains requires methods
54 that can jointly consider gene expression, spatial location, and histology. Traditional clustering methods
55 such as K-means and Louvain's method⁷ can only take gene expression data as input, and the resulting
56 clusters may not be contiguous due to the lack of consideration of spatial information and histology. To
57 account for spatial dependency of gene expression, new methods have been developed. For example,
58 stLearn⁸ uses features extracted from histology image as well as expression of neighboring spots to
59 spatially smooth gene expression data before clustering; BayesSpace⁹ employs a Bayesian approach for
60 clustering analysis by imposing a prior that gives higher weight to spots that are physically close; Zhu *et*

61 *al.*¹⁰ uses a Hidden-Markov random field approach to model spatial dependency of gene expression.
62 Although these methods can cluster spots or cells into distinct groups, they do not provide biological
63 interpretations of the identified spatial domains.

64

65 To link spatial domains with biological functions at the gene expression level, it is crucial to identify genes
66 that show enriched expression in the identified domains. Due to spatial variation of cell types in tissue,
67 the difference of gene expression between different domains is mainly driven by cell type composition
68 variation. On the other hand, information on spatial location and the corresponding histology allows the
69 construction of an anatomy-based taxonomy of the tissue, which provides a useful perspective on cell
70 type composition. Although stLearns integrates gene expression, spatial location, and histology
71 information in clustering, the putative correspondence between cell type difference and organizational
72 structure of the tissue remains unclear. As reported in Saiselet *et al.*¹¹, many spatial regions are highly
73 intermixed in terms of cell types. Without further downstream gene-level analysis, the spatial domains
74 detected by stLearn still suffer from the lack of interpretability. Recently, new methods such as
75 Trendsceek¹², SpatialDE¹³, and SPARK¹⁴ have been developed to detect spatially variable genes (SVGs).
76 These methods examine each gene independently and return a p-value to represent the spatial variability
77 of a gene. However, due to the lack of consideration of tissue taxonomy, genes detected by these methods
78 do not have a guaranteed spatial expression pattern, making it difficult to utilize these genes for further
79 biological investigations.

80

81 Rather than considering spatial domain identification and SVG detection as separate problems, we
82 developed SpaGCN, a graph convolutional network-based approach that considers these two problems
83 jointly. Using a graph convolutional network with an added iterative clustering layer, SpaGCN first
84 identifies spatial domains by integrating gene expression, spatial location, and histology together through

85 the construction of an undirected weighted graph that represents the spatial dependency of the data. For
86 each spatial domain, SpaGCN then detects SVGs that are enriched in the domain against its surrounding
87 regions by differential expression analysis guided by domain information. SpaGCN also has the option to
88 detect meta genes that are uniquely expressed in a given domain. The spatial domains and the
89 corresponding SVGs and meta genes detected for these domains provide a comprehensive picture on the
90 spatial gradients in gene expression in tissue.

91

92 **Results**

93

94 **Overview of SpaGCN and evaluation**

95 SpaGCN is applicable to both sequencing-based and smFISH-based data. As shown in Fig. 1a, SpaGCN first
96 builds a graph to represent the relationship of all samples (spots in sequencing-based or cells in smFISH-
97 based data) considering both spatial location and histology information. Next, SpaGCN utilizes a graph
98 convolutional layer to aggregate gene expression information from neighboring samples. Then, SpaGCN
99 uses the aggregated gene expression matrix to cluster samples using an unsupervised iterative clustering
100 algorithm¹⁵. Each cluster is considered as a spatial domain from which SpaGCN then detects SVGs that are
101 enriched in a domain by differential expression analysis (Fig. 1b). When a single gene cannot mark
102 expression pattern of a spatial domain, SpaGCN will construct a meta gene, formed by the combination
103 of multiple SVGs, to represent gene expression of the domain. Since the expression profile of a spot/cell
104 is heavily influenced by its local microenvironment, SpaGCN also offers the option of subcluster detection
105 within each spatial domain. SVGs can also be detected to help in understanding the function of each sub-
106 spatial domain.

107

108 To showcase the strength and scalability of SpaGCN, we applied it to five publicly available datasets,

109 including four datasets generated by sequencing-based techniques and one dataset generated by
110 MERFISH (Supplementary Table 1). The spatial domains identified by SpaGCN agree better with known
111 tissue layer structure than K-means and Louvain's clustering. We also compared SVGs detected by SpaGCN
112 with those detected by SPARK¹⁴ and SpatialDE¹³, and found that the SVGs detected by SpaGCN have more
113 coherent expression patterns and better biological interpretability than the other two methods. The
114 specificity of spatial expression patterns revealed by SpaGCN detected SVGs were further confirmed by
115 Moran's *I* statistic¹⁶, a metric that quantifies the spatial autocorrelation of detected genes.

116

117 **Application to mouse olfactory bulb data**

118 To evaluate the performance of SpaGCN, we first analyzed a mouse olfactory bulb (MOB) dataset¹⁷, which
119 consists of 16,218 genes measured in 262 spots. The main olfactory bulb has five layers, ordered from
120 surface to the center as follows: glomerular layer, external plexiform layer, mitral cell layer, internal
121 plexiform layer, and granule cell layer. We compared SpaGCN's clustering results to K-means and Louvain
122 by setting the number of clusters at 5 for all three methods. As shown in Fig. 2a, K-means only identified
123 3 main spatial domains, with only few spots assigned to domains 1 and 3. Louvain's method identified 5
124 main spatial domains. However, since it does not consider spatial and histology information, domains 2,
125 3, and 4 have blurred boundaries and more outliers than SpaGCN. By contrast, the domains detected by
126 SpaGCN agree better with the biologically known 5-layer structure of the MOB.

127

128 To understand the functions of the SpaGCN identified spatial domains, we next detected SVGs for each
129 spatial domain. In total, SpaGCN detected 60 SVGs. Fig. 2b-f shows a randomly selected SVG for each
130 domain, and all genes show strong specificity for the corresponding domain. The *In Situ* Hybridization
131 labelling of these genes from the Allen Brain Institute further confirmed the correspondence of the spatial
132 domains detected by SpaGCN. Additional SVGs detected by SpaGCN are shown in Supplementary Fig. 1.

133

134 As a comparison, we also detected SVGs using SpatialDE and SPARK. SpatialDE identified 67 SVGs, but only
135 12 of them overlapped with SpaGCN results (Supplementary Fig. 2). We further looked into the 55 genes
136 detected exclusively by SpatialDE and found many of the genes are expressed in only a few spots or are
137 highly expressed in most of the spots, leading to false detections of significant spatial patterns
138 (Supplementary Fig. 3). By contrast, SpaGCN avoided this issue by filtering out genes using minimum
139 within group expression fraction and maximum between group expression fraction. SPARK detected 772
140 genes, with 49 overlapping with SpaGCN (Supplementary Fig. 2). However, we found that the SPARK
141 results indicate that 274 genes have FDR-adjusted p-values less than 0.00001 with 14 of them having the
142 smallest identical FDR-adjusted p-value of 4.42e-13. As a result, the SPARK p-values are not informative
143 in differentiating the degree of spatial variability between different genes. Of note, none of these 14 genes
144 were detected by SpaGCN. Further examination revealed that some of these genes show spatial variability,
145 but more than half of them are only expressed in a few spots or highly expressed in most of the spots
146 (Supplementary Fig. 4). The FDR-adjusted p-value distribution of SPARK and q-value distribution of
147 SpatialDE are highly skewed toward 0, making it challenging to select informative SVGs based on their p-
148 values or q-values alone (Supplementary Fig. 5).

149

150 To compare SVGs detected by different methods quantitatively, we calculated the Moran's I statistic,
151 which measures the spatial autocorrelation for each gene. Fig. 2g shows the distribution of Moran's I .
152 Although all SpaGCN detected SVGs have clear spatial patterns, their Moran's I values are not significantly
153 higher than the SVGs detected by SPARK and SpatialDE (median of 0.20 for SpaGCN against 0.18 for SPARK
154 and 0.25 for SpatialDE). Further examination revealed that many SVGs detected by SPARK and SpatialDE
155 are expressed in multiple adjacent spatial domains. For example, the gene *PCP4* uniquely detected by
156 SpatialDE is expressed in two adjacent layers (domains 2 and 4 defined by SpaGCN) (Supplementary Fig.

157 6). By contrast, all the SVGs detected by SpaGCN are domain specific, offering interpretation in alignment
158 with our knowledge of layer structure. We note that less informative SVGs with clear, but non-domain
159 specific, spatial patterns, such as *PCP4*, can also be detected by SpaGCN if the user combines domains 2
160 and 4 as the target domain in SVG detection.

161

162 **Application to mouse posterior brain data**

163 Next, we analyzed a dataset generated from mouse posterior cerebrum, cerebellum and brainstem by
164 10X Genomics that includes 3,353 spots and 31,053 genes¹⁸. We compared the clustering results of
165 SpaGCN with K-means and Louvain's clustering. The number of clusters in K-means and resolution in
166 Louvain were set to generate the same number of clusters as SpaGCN (10 clusters). Fig. 3a shows that
167 Louvain's clustering is similar to SpaGCN, but the spatial domains detected by SpaGCN are more spatially
168 contiguous than Louvain's results. The integrity of SpaGCN's spatial domains stems from the aggregation
169 of gene expression based on spatial information and histology, which ensures that the genes detected by
170 differential expression analysis have clear spatial expression patterns.

171

172 SpaGCN detected 523 SVGs for the 10 spatial domains while SPARK and SpatialDE detected 9,678 and
173 12,676 SVGs, respectively (Supplementary Fig. 7). We hypothesized that the substantially larger number
174 of SVGs detected by SPARK and SpatialDE are due to the lack of spatial expression patterns that exist in
175 the data. To confirm this hypothesis, we calculated the Moran's *I* statistic for all detected SVGs (Fig. 3b).
176 The Moran's *I* values of SpaGCN detected SVGs are much higher than those detected by SPARK and
177 SpatialDE (median of 0.50 for SpaGCN against 0.21 for SPARK and 0.16 for SpatialDE). Closer examination
178 of the SVGs detected by SPARK and SpatialDE revealed that most of the SVGs suffer from one of the two
179 problems observed previously in the MOB dataset: they are (1) only expressed in a few spots or highly
180 expressed in most of the spots, suggesting high false positive rates for SPARK and SpatialDE or (2) spatially

181 variable, but expressed in multiple adjacent spatial domains, making it difficult to interpret. Another
182 limitation of these two methods is that the FDR-adjusted p-value from SPARK and q-value from SpatialDE
183 are not informative. Genes with similar p-values/q-values do not necessarily show similar spatial pattern
184 and a smaller p-value/q-value does not guarantee a better spatial pattern (Supplementary Fig. 8 and
185 Supplementary Fig. 9). The p-value and q-value distributions of SPARK and SpatialDE are highly skewed
186 toward 0 (Supplementary Fig. 10). By contrast, the SVGs detected by SpaGCN were enriched in specific
187 spatial domains (Supplementary Fig. 11) and their expression patterns are transferable to an adjacent
188 tissue slice in the mouse posterior brain (Supplementary Fig. 12). Further, multiple domain adaptive
189 filtering criteria implemented in SpaGCN allow it to eliminate false positive SVGs and ensure all detected
190 SVGs have clear spatial expression patterns.

191
192 To illustrate why appropriate filtering is important, we use domains 1, 5, and 8 as an example. For each of
193 these domains, SpaGCN detected a single SVG enriched in that region. As shown in Fig. 3c, *PVALB* is
194 enriched in domain 1, and *TRM62* is enriched in domain 8. Although domains 1 and 8 are adjacent to each
195 other, these two SVGs can still well mark these domains. *NRGN* is a SVG that SpaGCN detected for domains
196 5 and 7. The high expression of *NRGN* in domains 5 and 7 also indicate that these two domains are
197 neuroanatomically similar – both consisting of cortex and the pyramidal layer of the hippocampus. Both
198 the cortex and hippocampus are regions that are on the curved surface of the brain. This posterior brain
199 tissue section has the top part of the curved surface in domain 5 and the bottom part of the curved surface
200 in domain 7. Domains 5 and 7, which would be contiguous in a complete 3D reconstruction, are
201 artifactually separated due to the way the section was cut. Therefore, it is not surprising that in addition
202 to *NRGN*, SpaGCN also detected many other SVGs, such as *APP*, *ATP6V1G2*, *CALM2*, *CHN1*, *CLSTN1*,
203 *ARPP21*, *CYP46A1*, *DCLK1*, *LINGO1*, and *MARCKS*, that are highly expressed in both domains 5 and 7

204 (Supplementary Fig. 11). The unique and powerful SVG detection procedure in SpaGCN ensures that genes
205 like these are not missed.

206

207 SpaGCN did not identify any SVGs for domain 0. However, we reason that a meta gene, formed by the
208 combination of multiple genes, may better reveal spatial patterns than any single genes. We used domain
209 0 as an example to show how SpaGCN can create informative meta genes to mark a spatial domain (Fig.
210 3d). First, by lowering the filtering thresholds, SpaGCN identified *KLK6* which is highly expressed in the
211 lower part of domain 0. Using *KLK6* as a starting gene, SpaGCN used a novel approach to find a log-linear
212 combination of gene expression of *KLK6*, *MBP* and *ATP1B1*, which accurately marked the spatial domain
213 0. In this meta gene, *KLK6* and *MBP* are considered as positive markers because they are highly expressed
214 in some spots in domain 0, whereas *ATP1B1* is considered a negative marker as it is mainly expressed in
215 regions other than domain 0. Previous studies have shown that *KLK6* and *MBP* expression is restricted to
216 oligodendrocytes, while *ATP1B1* is mainly expressed in neurons and astrocytes¹⁹. This resonates the fact
217 that domain 0 represents white matter which is dominated by oligodendrocytes and has few neuronal cell
218 bodies. Therefore, the genes that make up this meta gene have meaningful biological interpretation.
219 Using this meta gene detection procedure, we also detected meta genes for domains 2, 7, 8 and 9, and
220 found that these meta genes are transferrable to an adjacent tissue slice (Supplementary Fig. 13).

221

222 The expression profile and biological function of a spot is heavily influenced by its neighboring spots. The
223 surrounding spots can trigger a response pathway or signal the spot to perform certain tasks. Although
224 the spots in one spatial domain detected by SpaGCN are spatially coherent and have similar gene
225 expression patterns, they may still have different functions since their surrounding spots are different. For
226 instance, spots located near the boundary of a spatial domain may have different functions compared to
227 spots located in the inner part of the domain. To learn more about the effect of different neighborhoods

228 on the spots, we performed sub-domain detection. For example, domain 2 is located in the center of the
229 tissue slice and surrounded by multiple other spatial domains. As a result, the neighboring environment
230 for spots in domain 2 varies. As shown in Fig. 3e, domain 2 was separated into 5 sub-domains which are
231 located either in the center or different boundary regions of domain 2, suggesting that differences in the
232 neighborhoods of spots contribute to within-domain heterogeneity. SVGs detected for each sub-domain
233 can help us understand the gene expression variability of spots within each sub-domain.

234

235 **Application to LIBD human dorsolateral prefrontal cortex data**

236 In addition to the datasets described previously, SpaGCN also showed advantage over competing methods
237 when evaluated on the LIBD human dorsolateral prefrontal cortex (DLPFC) data²⁰. The LIBD study
238 sequenced 12 slices from DLPFC that spans six neuronal layers plus white matter. We started from
239 analyzing slice 151673, which includes 3,639 spots and 33,538 genes. As the original publication manually
240 annotated the tissue into 7 layers, for fair comparison, the number of clusters was also set at 7 for SpaGCN,
241 K-means, and Louvain. As shown in Fig. 4a, K-means and Louvain failed to separate the tissue into layers
242 with clear boundary. By contrast, SpaGCN successfully identified layer structures with clear boundaries.
243 The Adjusted Rand Indexes (ARIs) for the SpaGCN, K-means, and Louvain identified domains are 0.42, 0.24,
244 and 0.33, respectively, suggesting that the SpaGCN results better agree with the manually curated layer
245 structure reported in the original study.

246

247 To further validate the identified spatial domains, we then detected SVGs. In total, SpaGCN detected 61
248 SVGs, with 53 of them specific to domain 4, which corresponds to the white matter region (Supplementary
249 Fig. 14). Patterns of SVGs for other domains are not very clear. These results indicate that gene expression
250 profiles of spots from white matter are distinct from spots in the neuronal layers, while gene expression
251 differences among the six neuronal layers are much smaller and more difficult to distinguish using

252 individual marker genes. SVGs detected by SPARK and SpatialDE also suffered from the same problem.
253 SPARK detected 3,187 SVGs with 1,131 of them having FDR-adjusted p-values equal to 0, most of which
254 only marked the white matter region. We also found that the SVGs detected by SPARK lack domain
255 specificity (Supplementary Fig. 15). SpatialDE detected 3,654 SVGs with 806 of them having q-values equal
256 to 0, but these genes do not necessarily show better spatial pattern than genes with larger q-values
257 (Supplementary Fig. 16). Although SPARK and SpatialDE detected much larger numbers of SVGs than
258 SpaGCN (Supplementary Fig. 17), the genes detected by these two methods lack ability to distinguish
259 different degrees of spatial variability in expression as their p-value and q-value distributions are highly
260 skewed toward 0 (Supplementary Fig. 18). Fig. 4b shows that the Moran's I values for SpaGCN detected
261 SVGs are significantly higher than those detected by SpatialDE and SPARK (median of 0.39 for SpaGCN
262 against 0.09 for SPARK and 0.08 for SpatialDE). For 3 out of the 6 neuronal layers, SpaGCN detected a
263 single SVG to mark that region (Fig. 4c). For example, *NEFM* is enriched in domain 0 (layer 3) and *PCP4* is
264 enriched in domain 1 (layer 4). Although it is difficult to identify single genes to mark the other neuronal
265 layers, SpaGCN was able to find layer-specific meta genes. As shown in Fig. 4c, the meta gene formed by
266 *KRT19*, *MYL9*, *MBP*, *GFAP*, and *SNAP25* for domain 5 is specific to layer 1. Since layer 1 only has few spots,
267 it is difficult to find a highly enriched gene. However, by adding depleted genes like *MBP* and *SNAP25*, the
268 expression pattern in this region is strengthened. Furthermore, the SVGs and meta genes detected by
269 SpaGCN are transferrable to slice 151676 obtained from the same study (Supplementary Fig. 19 and
270 Supplementary Fig. 20).

271
272 To show the SVGs and meta genes detected by SpaGCN are useful for downstream analysis, we performed
273 K-means clustering on slice 151676 using SVGs and meta genes detected from slice 151673 by SpaGCN.
274 Specifically, we selected 2 SVGs or meta genes detected by SpaGCN for each spatial domain, resulting in
275 14 features (18 unique genes involved in total) used in K-means clustering. Comparing with manually

276 curated layer assignment reported in the original study, this clustering analysis had an ARI of 0.25 (Fig.
277 4d). We performed similar clustering analysis using SVGs detected by SpatialDE and SPARK. When only
278 using their top 18 SVGs, the ARI is only 0.07 for SpatialDE and 0.05 for SPARK. Even when using the 806
279 most significant SpatialDE detected SVGs, the ARI is only 0.14. When using the 1,114 most significant
280 SPARK detected SVGs, the ARI is 0.15 (Fig. 4e). The ARIs of both SpatialDE and SPARK are much lower than
281 SpaGCN, even though both used many more SVGs than SpaGCN, which further confirmed the lack of
282 spatial expression specificity for genes detected by these methods.

283

284 **Application to human primary pancreatic cancer tissue**

285 We also analyzed a human primary pancreatic cancer tissue dataset⁵, which includes 224 spots and 16,448
286 genes across 3 manually annotated sections, to show SpaGCN's ability in detecting tumorous regions. The
287 original study identified and annotated the cancer region on the histology image. However, the cancer
288 region detected by their clustering method based on gene expression information alone did not closely
289 match the pathologist annotated cancer region (Fig. 5a). Since the cancer region in the histology image is
290 darker in color than non-cancer regions, it is informative for clustering. To give histology information
291 higher weight, we increased the scaling parameter s in SpaGCN from 1 to 2 when calculating distance
292 between each spot pair. This step ensured that spots in the same dark region in the histology are more
293 likely to be clustered together. Fig. 5a shows that domain 2 detected by SpaGCN has a better
294 correspondence to the cancer region than clusters reported in the original study. In total, SpaGCN
295 detected 12 SVGs, with 3, 8, and 1 SVGs for domains 0, 1, and 2, respectively (Fig. 5b; Supplementary Fig.
296 21). Furthermore, a meta gene using *KRT17*, *MMP11*, and *SERPINA1* marked the cancer region better than
297 the originally identified SVG *KRT17* (Fig. 5c). *KRT17* functions as a tumor promoter and regulates
298 proliferation in pancreatic cancer²¹, and *MMP11* has been found to be a prognostic biomarker for
299 pancreatic cancer²². Our identification of *KRT17* and *MMP11* as the two positive genes for the cancer

300 region agree well with pancreatic cancer biology. SPARK and SpatialDE detected 203 and 163 SVGs,
301 respectively (Supplementary Fig. 22). However, the Moran's I values for their SVGs are much lower than
302 those detected by SpaGCN, suggesting their lack of spatial expression patterns (Fig. 5d).

303

304 **Application to MERFISH mouse hypothalamus data**

305 Next, we show that SpaGCN can also be applied to smFISH-based data. To this end, we analyzed a MERFISH
306 dataset generated from the preoptic region of hypothalamus in mouse brain², which includes 5,665 cells
307 and 161 genes. One important difference between MERFISH and sequencing-based spatial
308 transcriptomics data is that the captured tissue area is much smaller and less genes are measured, making
309 it difficult to detect spatial domains since the cells within such a small area are more similar to each other.
310 Thus, when utilizing these types of data, we suggest increasing the contribution of neighboring cells when
311 calculating the weighted gene expression of each cell. Using this approach, SpaGCN detected spatial
312 domains that agreed well with the annotated hypothalamic nuclei (Fig. 6a), with domain 2 corresponding
313 to ACA, domain 3 corresponding to PS, and domain 7 corresponding to MnPo. By contrast, the domains
314 identified from the Hidden Markov Random Field (HMRF) approach showed little overlap with the
315 hypothalamic region annotation. Using SpaGCN, we further detected 19 SVGs including *DGKK*, *ERMN*, and
316 *SLN* that showed enriched expression patterns for domains 2, 3, and 7 (Fig. 6b; Supplementary Fig. 23).

317

318 **Discussion**

319 Identification of spatial domains and detection of SVGs are important steps in spatial transcriptomics data
320 analysis. In this paper, we presented SpaGCN, a graph convolutional network-based approach that
321 integrates gene expression, spatial location, and histology to model spatial dependency of gene
322 expression for clustering analysis of spatial domains and identification of domain enriched SVGs or meta
323 genes. Through the use of a convolutional layer in an undirected weighted graph, SpaGCN aggregates

324 gene expression of each spot from its neighboring spots, which enables the identification of spatial
325 domains with coherent gene expression and histology. The subsequent domain guided differential
326 expression analysis also enables the detection of SVGs or meta genes with enriched expression patterns
327 in the identified domains. SpaGCN has been extensively tested on datasets from different species, regions,
328 and tissues generated using both sequencing- and smFISH-based techniques. The results consistently
329 showed that SpaGCN can identify spatial domains with coherent gene expression and histology and detect
330 SVGs and meta genes that have much clearer spatial expression patterns and biological interpretations
331 than genes detected by SPARK and SpatialDE. Additionally, the SpaGCN detected SVGs and meta genes
332 are transferrable and can be utilized for downstream analyses in independent tissue sections.

333

334 The spatial domain detection step in SpaGCN is flexible. For datasets with clear layer structure in histology
335 image, such as the mouse posterior brain data and human primary pancreatic cancer data, higher weight
336 can be given to histology by increasing the scaling parameter s in SpaGCN when calculating distance
337 between each spot pair, which results in spatial domains that are more similar to the anatomy-based
338 taxonomy in the histology image. Another important scaling parameter in SpaGCN is the characteristic
339 length scale l , which controls the relative contribution from other spots when aggregating gene
340 expression. By varying l , users can get spatial domain separations with different patterns in which a higher
341 l will result in spatial domains with higher contiguity.

342

343 The SVG detection procedure in SpaGCN is also flexible. While we mainly demonstrated SVG detection for
344 a single domain, SpaGCN also allows users to combine multiple domains as one target domain or specify
345 which neighboring domains to be included in DE analysis. Additionally, SpaGCN allows the users to
346 customize SVG filtering criteria based on p-value and three additional metrics, i.e., in-fraction, in/out

347 fraction ratio, and fold change, to select SVGs. The resulting genes can be ranked by any of these metrics
348 to select SVGs with desired spatial expression patterns.

349
350 SpaGCN is computationally fast and memory efficient. To showcase the computational advantage of
351 SpaGCN, we recorded its run time and memory usage for the mouse posterior brain data and compared
352 with SPARK and SpatialDE. All analyses were conducted on Mac OS 10.13.6 with single Intel® Core(TM) i5-
353 8259U CPU @2.30GHz and 16GB memory. As shown in Supplementary Fig. 24, SpaGCN completed spatial
354 domain and SVG detection in less than one minute, whereas the computing time is ~13 minutes for
355 SpatialDE and more than 18 hours for SPARK. Furthermore, SpaGCN only required 1.3 GB of memory,
356 whereas SpatialDE and SPARK required more than 3.1 GB and 7.2 GB of memory, respectively. With the
357 increasing popularity of spatial transcriptomics in biomedical research, we expect SpaGCN will be an
358 attractive tool for large-scale spatial transcriptomics data analysis. Results from SpaGCN will enable
359 researchers to accurately identify spatial domains and SVGs in their studies.

360

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365

366 **Author contributions**

367 This study was conceived of and led by M.L.. J.H. designed the model and algorithm. J.H. implemented the
368 SpaGCN software and led the data analysis with input from M.L., X.L., K.C., A.S., D.I., E.L., and R.T.S.. J.H.
369 and M.L. wrote the paper with feedback from all other coauthors.

370

371 **Competing financial interests**

372 The authors declare no competing interests.

373 **Figure legends**

374

375 **Figure 1. Workflow of SpaGCN.** **a**, SpaGCN starts from integrating gene expression, spatial location and
376 histology information using a graph convolutional network (GCN), then separates spots into different
377 spatial domains using unsupervised iterative clustering. The GCN is based on an undirected weighted
378 graph in which the edge weight between every two spots is determined by Euclidean distance between
379 the two spots, defined by the spatial coordinates (x, y) and the 3-rd dimensional coordinate z , obtained
380 from the RGB values in the histology image. **b**, For each detected spatial domain, SpaGCN identifies SVGs
381 or meta genes by domain guided differential expression analysis.

382

383 **Figure 2. Spatial domains and SVGs detected in the mouse olfactory bulb dataset.** **a**, Histology image of
384 the tissue section and spatial domains detected by SpaGCN, Louvain's method, and K-means clustering.
385 **b-f**, Spatial expression patterns of SVGs detected by SpaGCN for domains 0 (*LCAT*), 1 (*NR2F2*), 2 (*CACNB3*),
386 3 (*SLC17A7*), and 4 (*NECAB2*), and the corresponding *in situ* hybridization of these SVGs obtained from the
387 Allen Brain Atlas. **g**, Boxplot of Moran's I values for SVGs detected by SpaGCN, SPARK, and SpatialDE.

388

389 **Figure 3. Spatial domains and SVGs detected in the mouse brain posterior brain dataset.** **a**, Histology
390 image of the tissue section and spatial domains detected by SpaGCN, Louvain's method, and K-means
391 clustering. **b**, Boxplot of Moran's I values for SVGs detected by SpaGCN, SPARK, and SpatialDE. **c**, Spatial
392 expression patterns of SVGs detected by SpaGCN for domain 1 (*PVALB*), 8 (*TRIM62*), and 5 (*NRGN*). **d**,
393 Spatial expression patterns of genes *KLK6*, *MBP*, *ATP1B1*, which form the specific marker meta gene for
394 domain 0 (*KLK6 + MBP - ATP1B1*). **e**, Clustering results for 5 sub-domains detected by SpaGCN for domain
395 2, and the spatial expression patterns of SVGs for sub-domains 0 (*KCNC3*), 1 (*CAMK2A*), and 2 (*NRSN2*).

396

397 **Figure 4. Spatial domains and SVGs detected in the LIBD human dorsolateral prefrontal cortex dataset.**

398 **a**, Manually annotated layer structure for slice 151673 from the original study²⁰, and spatial domains
399 detected by SpaGCN, Louvain's method, and K-means clustering. **b**, Boxplot of Moran's *I* values for SVGs
400 detected by SpaGCN, SPARK, and SpatialDE for slice 151673. **c**, Spatial expression patterns of SVGs for
401 domain 0 (*NEFM*) and domains 1 (*PCP4*), and a meta gene formed by *KRT19*, *MYL9*, *MBP*, *GFAP*, and
402 *SNAP25* for domain 5 (*KRT19 + MYL9 – MBP + GFAP – SNAP25*). **d**, Manually annotated layer structure for
403 slice 151676 from the original study²⁰, and K-means clustering results for slice 151676 using 18 genes
404 selected by SpaGCN, SPARK, and SpatialDE. For SpaGCN, we selected the following genes, domain 0 (*NEFL*,
405 *NEFM*), domain 1 (*PCP4*, *TMSB10 + PCP4 – KRT19*), domain 2 (*CCK + KRT17 – MT-ND1*, *CPLX2 + KRT17 –*
406 *MT-ND2*), domain 3 (*CAMK2N1*, *ENC1*), domain 4 (*MBP*, *FTL*), domain 5 (*KRT19 + MYL9 – MBP + GFAP –*
407 *PLP1*, *KRT8 + MYL9 – MBP + GFAP – PLP1*), and domain 6 (*GFAP*, *MBP*), resulting in 18 unique genes in
408 total. For SPARK and SpatialDE, the 18 SVGs with the smallest FDR-adjusted p-value or q-value were
409 randomly selected. **e**, ARIs between manually annotated layers and K-means' clustering using SVGs
410 selected by different methods. For SpaGCN, we only used the selected SVGs and meta genes, with 18
411 genes involved in total while for SPARK and SpatialDE, we used top 18, 100, 200, 500 and all SVGs with
412 the identical smallest FDR-adjusted p-value or q-value.

413

414 **Figure 5. Spatial domains and SVGs detected in the human primary pancreatic cancer tissue dataset. a,**

415 Histology image of the tissue section with manually annotated regions from the original study⁵, spatial
416 domains detected by SpaGCN, and clustering results from the original study. **b**, Spatial expression pattern
417 of SVGs detected by SpaGCN for domain 0 (*AEBP1*) and domain 1 (*SERPINA1*). **c**, Spatial expression
418 patterns of genes *KRT17*, *MMP11*, *SERPINA1*, which form the specific marker meta gene for domain 2
419 (*KRT17 + MMP11 - SERPINA1*). **d**, Boxplot of Moran's *I* values for SVGs detected by SpaGCN, SPARK, and
420 SpatialDE.

421

422 **Figure 6. Spatial domains and SVGs detected in the MERFISH mouse brain hypothalamus dataset. a,**

423 Spatial domains detected by SpaGCN and the HMRF method overlaid with annotated hypothalamic

424 nuclei from the original study², and cell type distribution from the original study. **d,** Spatial expression

425 patterns of SVGs detected by SpaGCN for domain 2 (*ERMN*), domain 3 (*DGKK*), and domain 7 (*SLN*).

426 **Methods**

427

428 **Data preprocessing**

429 SpaGCN takes spatial gene expression and histology image data (when available) as input. The spatial gene
430 expression data are stored in an $N \times D$ matrix of unique molecular identifier (UMI) counts with N samples
431 and D genes, along with the (x, y) 2-dimensional spatial coordinates of each sample. In sequencing-based
432 data, each sample represents a spot containing multiple cells, whereas in single-molecule fluorescence *in*
433 *situ* hybridization (smFISH)-based data, each sample represents a single cell. For simplicity, we will use
434 ‘spot’ to refer to a sample, as most of the data analyzed in this paper are sequencing based. Genes
435 expressed in less than three spots are eliminated. The gene expression values in each spot are normalized
436 such that the unique molecular identifier (UMI) count for each gene is divided by the total UMI count
437 across all genes in a given spot, multiplied by 10,000, and then transformed to a natural log scale.

438

439 **Conversion of spatial transcriptomics data into graph-structured data**

440 After preprocessing, SpaGCN converts the gene expression and histology image data into a weighted
441 undirected graph, $G(V, E)$. In this graph, each vertex $v \in V$ represents a spot and every two vertices in V
442 are connected via an edge with a specified weight. We focus our analysis on spatial transcriptomics data
443 with histology information, but the method can be easily adapted to analyze smFISH-based data, for which
444 histology information is not available.

445

446 Calculation of distance between two vertices

447 The distance between any two vertices u and v in the graph reflects the relative similarity of the two
448 corresponding spots. This distance is determined by two factors: 1) the physical locations of spots u and
449 v in the tissue slice, and 2) the corresponding histology information of these two spots. Although some

450 spots are physically close to each other in the tissue, the histology image may reveal that they belong to
 451 different tissue layers. Therefore, SpaGCN considers two spots to be close if and only if 1) the two spots
 452 are physically close, and 2) they have similar pixel features as shown in the histology image. To define a
 453 distance metric considering both aspects, SpaGCN extends the 2-dimensional space in the tissue slice into
 454 a 3-dimensional space that incorporates histology information. For spot v , its physical location in the
 455 tissue slice is represented by 2-dimensional coordinates (x_v, y_v) . To determine the corresponding pixel in
 456 the histology image for spot v , SpaGCN maps spot v to the histology image according to its pixel
 457 coordinates (x_{pv}, y_{pv}) . Instead of using the color of the pixel at (x_{pv}, y_{pv}) , SpaGCN draws a square
 458 centered on (x_{pv}, y_{pv}) containing 50×50 pixels and calculates the mean color value for the RGB
 459 channels, (r_v, g_v, b_v) , of all pixels that fall in the square. This step smooths the color value and ensures
 460 that the color is not dominated by a single pixel. To derive a single value to represent the histology image
 461 features, SpaGCN uses a weighted sum of the RGB values as follows,

462

$$463 \quad z_v = \frac{r_v \times V_r + g_v \times V_g + b_v \times V_b}{V_r + V_g + V_b},$$

464

465 where $V_r = \text{Variance}(r_v)$, $V_g = \text{Variance}(g_v)$, and $V_b = \text{Variance}(b_v)$ for all $v \in V$. In this
 466 transformation, higher weight is given to the channel with larger variance so that this combined value z_v
 467 captures an accurate representation of the patterns in the histology image.

468

469 Next, SpaGCN rescales z_v as

470

$$471 \quad z_v^* = \frac{z_v - \mu_z}{\sigma_z} \times \max(\sigma_x, \sigma_y) \times s,$$

472

473 where μ_z is the mean of z_v , $\sigma_x, \sigma_y, \sigma_z$ are the standard deviations of x_v, y_v and z_v , respectively, for $v \in$
 474 V , and s is a scaling factor. In our analysis, s is usually set at 1 to make sure that z_v^* has the same scale
 475 variance as x_v and y_v , and we set s to a value larger than 1 when the goal is to increase the weight of
 476 histology. The coordinates of spot v are set to be (x_v, y_v, z_v^*) in the extended 3-dimensional space. Finally,
 477 the Euclidean distance between every two spots u and v is calculated as

478

$$479 \quad d(u, v) = \sqrt{(x_u - x_v)^2 + (y_u - y_v)^2 + (z_u^* - z_v^*)^2}.$$

480

481 Calculation of weight for each edge and construction of graph

482 The weight of each edge (u, v) measures the degree of relatedness between spots u and v and is
 483 negatively associated with their distance. The graph structure G is stored in an $N \times N$ adjacency matrix
 484 $\mathbf{A} = [w(u, v)]$, where the edge weight between spot u and spot v and is defined as

485

$$486 \quad w(u, v) = \exp\left(-\frac{d(u, v)^2}{2l^2}\right).$$

487

488 The hyperparameter l , also known as the characteristic length scale, determines how rapidly the weight
 489 decays as a function of distance. A similar function has been employed in SpatialDE¹³. Let \mathbf{I} denote the
 490 identity matrix. For spot v , the corresponding row sum of $\mathbf{A} - \mathbf{I}$, denoted by a_v , can be interpreted as the
 491 relative contribution of other spots to its gene expression. We choose the value of l such that the average
 492 of a_v across all spots is equal to a pre-specified value, e.g. 0.5.

493

494 **Graph convolutional layer**

495 SpaGCN reduces the dimension of the preprocessed gene expression matrix using principal component
496 analysis (PCA). The top 50 principal components are used as input, which work well for all datasets
497 analyzed in this paper. Next, utilizing the power of a graph convolutional network, SpaGCN concatenates
498 the gene expression information and edge weights in G to cluster the nodes. Following Kipf and Welling²³,
499 the graph convolutional layer can be written as

500

$$501 \quad f(\mathbf{X}, \mathbf{A}) = \delta(\mathbf{A}\mathbf{X}\mathbf{B}),$$

502

503 where \mathbf{X} is the $N \times 50$ embedding matrix obtained from PCA, \mathbf{B} is a 50×50 matrix representing filter
504 parameters of the convolutional layer, and $\delta(\cdot)$ is a non-linear activation function such as ReLU. The graph
505 convolutional layer ensures that a corresponding row of parameters in \mathbf{B} will control the aggregation of
506 neighborhood information for each feature in \mathbf{X} , thus offering the flexibility of feature specific aggregation
507 of information provided by neighboring spots. The filter parameters in \mathbf{B} are shared across all vertices in
508 the graph and are automatically updated during an iterative training progress. Through graph convolution,
509 SpaGCN has aggregated the gene expression information according to the edge weights specified in G .
510 The output of this layer is an aggregated matrix that includes information on gene expression, spatial
511 location, and histology. The graph convolutional layer was implemented based on Kipf and Welling²³,
512 where the backpropagation is operated via a localized first-order approximation of spectral graph
513 convolution.

514

515 **Spatial domain identification by clustering**

516 Next, based on the output from the above graph convolutional layer, SpaGCN employs an unsupervised
517 clustering algorithm to iteratively cluster the spots into different spatial domains¹⁵. Each cluster identified
518 from this analysis is considered to be a spatial domain, which contains spots that are coherent in gene

519 expression and histology. To initialize cluster centroids, we use Louvain’s method⁷ on the aggregated
 520 output matrix from the graph convolutional layer. If the number of domains in the tissue is known, the
 521 resolution parameter in Louvain will be set to generate the same number of spatial domains. Otherwise,
 522 we vary the resolution parameter from 0.2 to 1.0 and select the resolution that gives the highest
 523 Silhouette score²⁴.

524

525 To update the cluster assignments iteratively, we define a metric to measure the distance from a spot to
 526 a cluster centroid using the Student’s t -distribution as a kernel. The distance between the embedded
 527 point h_i for spot i and centroid μ_j for cluster j

528

$$529 \quad q_{ij} = \frac{(1 + \|h_i - \mu_j\|^2)^{-1}}{\sum_{j'=1}^K (1 + \|h_i - \mu_{j'}\|^2)^{-1}},$$

530

531 can be interpreted as the probability of assigning cell i to cluster j .

532

533 Next, we iteratively refine the clusters by defining an auxiliary target distribution P based on q_{ij}

534

$$535 \quad p_{ij} = \frac{q_{ij}^2 / \sum_{i=1}^N q_{ij}}{\sum_{j'=1}^K (q_{ij'}^2 / \sum_{i=1}^N q_{ij'})},$$

536

537 which upweights spots assigned with high confidence, and normalizes the contribution of each centroid
 538 to the overall loss function to prevent large clusters from distorting the hidden feature space. Now that
 539 we have the soft assignment q_{ij} and the auxiliary distribution p_{ij} , we can define the objective function as
 540 a Kullback-Leibler (KL) divergence loss,

541

542

$$L = KL(P||Q) = \sum_{i=1}^N \sum_{j=1}^K p_{ij} \log \frac{p_{ij}}{q_{ij}}.$$

543

544 The network parameters and cluster centroids are simultaneously optimized by minimizing L using
545 stochastic gradient descent with momentum. This unsupervised iterative clustering algorithm has been
546 previously utilized for scRNA-seq analysis and showed superior performance over Louvain's method^{25,26}.

547

548 **Detection of spatially variable genes**

549 We are interested in detecting spatially variable genes (SVGs) that are enriched in each spatial domain.

550 We note that some genes may be expressed in multiple but disconnected domains. Although they are not
551 uniquely expressed in a particular domain, these genes are still useful for understanding spatial variation
552 of gene expression and can be used to form meta genes that are uniquely expressed in a specific domain.

553 Therefore, rather than doing differential expression (DE) analysis using spots from a target domain versus

554 all other spots, we first select spots to form a neighboring set of the target domain. The goal is to detect

555 genes that are highly expressed in the target domain but are not expressed or are expressed at low levels

556 in the neighboring spots. To determine which spots should be considered as neighbors, we draw a circle

557 with a prespecified radius around each spot in the target domain. All spots from non-target domains that

558 reside in the circle are considered its neighbors. The radius is set such that all spots in the target domain

559 have approximately 8 neighbors on average. Next, neighbors of all spots in the target domain are collected

560 and form a neighboring set. For each non-target domain, if more than 50% (default) of its spots are in the

561 neighboring set, this domain is then selected as a neighboring domain. This criterion is set to avoid the

562 situation when a domain is selected as a neighboring domain, but only a small proportion of its spots are

563 adjacent to the target domain.

564

565 After neighboring domains are determined, SpaGCN then performs DE analysis between spots in the
566 target domain and the neighboring domain(s) using Wilcoxon rank-sum test. Genes with a false discovery
567 rate (FDR) adjusted p-value <0.05 are selected as SVGs. To ensure only genes with enriched expression
568 patterns in the target domain are selected, we further require a gene to meet the following three criteria:
569 1) the percentage of spots expressing the gene in the target domain, i.e., in-fraction, is $>80\%$; 2) for each
570 neighboring domain, the ratio of the percentages of spots expressing the gene in the target domain and
571 the neighboring domain(s), i.e., in/out fraction ratio, is >1 ; and 3) the expression fold change between the
572 target and neighboring domain(s) is >1.5 . If a user is interested in finding SVGs for a particular combination
573 of spatial domains, SpaGCN offers the option to do so.

574

575 **Detection of spatially variable meta genes**

576 The spatial domain-specific DE analysis described above typically detects SVGs with enriched expression
577 for the majority of the domains. For domains in which no such SVGs are detected, we aim to identify a set
578 of genes that, when combined to form a meta gene, shows an enriched expression pattern in the given
579 domain. To identify genes to form a meta gene, we employ a multi-step approach. First, we lower the
580 thresholds for SVG filtering, e.g., change the minimum fold change threshold from 1.5 to 1.2, to identify
581 genes showing weaker enriched expression pattern in the target domain. In the presence of multiple such
582 weaker SVGs, we randomly select one of them as the base gene and denote it as $gene_0$. Second, we aim
583 to aggregate expression from other genes to the base gene to enhance the spatial pattern for the target
584 domain. To achieve this goal, we first calculate the mean expression level of $gene_0$ for spots in the target
585 domain as e_0 . Then, all spots from non-target domains with $gene_0$'s expression level higher than e_0 are
586 extracted to form a control group. Next, we perform DE analysis using spots from the target domain
587 against spots in the control group using Wilcoxon rank-sum test. The gene with the smallest FDR-adjusted
588 p-value and higher expression in the target domain is selected as $gene_{0+}$. Similarly, we perform DE

589 analysis using spots from the control group against those from the target domain and select a gene with
590 the smallest FDR-adjusted p-value and higher expression in the control group as $gene_{0-}$. The meta gene's
591 expression is calculated as

592

$$593 \quad \log(meta_gene_1) = \log(gene_0) + \log(gene_{0+}) - \log(gene_{0-}) + C_0,$$

594

595 where C_0 is a constant to make $\log(meta_gene_1)$ non-negative. The log transformation is used to rescale
596 expression and make the expression levels comparable across different genes. We have found that
597 including negative genes can strengthen spatial expression pattern for domains that do not have enriched
598 positive marker genes. This algorithm can be used iteratively to find additional genes to form an updated
599 meta gene with a clearer spatial pattern for the target domain. For the $(t + 1)^{th}$ iteration, the meta gene
600 expression is calculated as

601

$$602 \quad \log(meta_gene_{t+1}) = \log(meta_gene_t) + \log(gene_{t+}) - \log(gene_{t-}) + C_t$$

603

604 In the $(t + 1)^{th}$ iteration, after adding $gene_{t+}$ and subtracting $gene_{t-}$, SpaGCN will select the $(t + 1)^{th}$
605 control group based on $meta_gene_{t+1}$. The size of the new control group, which is the number of spots
606 not in the target domain but have higher expression of $meta_gene_{t+1}$ than spots in the target domain,
607 should be smaller than the size of the t^{th} control group, to ensure that $meta_gene_{t+1}$ has a clearer
608 spatial pattern than $meta_gene_t$. Also, $meta_gene_{t+1}$ is expected to have a larger difference of mean
609 expression between the target and control groups than $meta_gene_t$. Therefore, at each iteration,
610 SpaGCN checks whether both criteria are met, and the search of additional genes will stop otherwise. An
611 illustration of this iterative meta gene search is shown in Supplementary Fig. 25.

612

613 **Evaluation of spatially variable genes using Moran's I statistic**

614 The Moran's I statistic¹⁶ is a measure of spatial autocorrelation, which can be used to measure the degree
615 of spatial variability in gene expression²⁷. The Moran's I value ranges from -1 to 1 , where a value close to
616 1 indicates a clear spatial pattern, a value close to 0 indicates random spatial expression, and a value close
617 to -1 indicates a chess board like pattern. To evaluate the spatial variability of a given gene, we calculate
618 the Moran's I using the following formula,

619

$$620 \quad I = \frac{N \sum_i \sum_j [w_{ij} (x_i - \bar{x})(x_j - \bar{x})]}{\sum_i (x_i - \bar{x})^2},$$

621

622 where x_i and x_j are gene expression of spots i and j , \bar{x} is the mean expression of the gene, N is the total
623 number of spots, w_{ij} is spatial weight between spots i and j calculated using the 2-dimensional spatial
624 coordinates of the spots, and W is the sum of w_{ij} . For each spot, we select the k nearest neighbors using
625 spatial coordinates. Moran's I statistic is robust to the choice of k and is set at 4 in our analysis. We assign
626 $w_{ij} = 1$ if spot j is in the nearest neighbors of spot i , and $w_{ij} = 0$ otherwise.

627

628 **Detection of subclusters within a spatial domain**

629 To better characterize heterogeneity within a spatial domain due to the influence of its neighborhood,
630 SpaGCN can further detect sub-domains within each spatial domain by utilizing information from
631 neighboring spots. SpaGCN draws a circle around each spot with a pre-specified radius, and all spots that
632 reside in the circle are considered as neighbors of this spot. The value of the radius is set to ensure that
633 every spot in the target domain have ten neighbors on average. Next, SpaGCN records the number of
634 neighbors from different spatial domains for each spot and stores this information in a $T \times K$ matrix,
635 where T is the number of spots in the target domain and K is the total number of spatial domains

636 detected. The value for the i^{th} row and j^{th} column is the number of neighbors of spot i belonging to
637 domain j . Next, this matrix is fed into a K -means classifier to detect sub-clusters. Differential expression
638 analysis as described above can be performed to identify subcluster enriched genes.

639

640 **Data availability**

641 We analyzed multiple spatial transcriptomics datasets. Publicly available data were acquired from the
642 following websites or accession numbers: (1) mouse olfactory bulb
643 (https://drive.google.com/drive/folders/1C4I3IBaYI7uuV2AA2o0WDzO_mkc_b0pv?usp=sharing); (2)
644 mouse posterior brain ([https://support.10xgenomics.com/spatial-gene-
645 expression/datasets/1.0.0/V1_Mouse_Brain_Sagittal_Posterior](https://support.10xgenomics.com/spatial-gene-expression/datasets/1.0.0/V1_Mouse_Brain_Sagittal_Posterior)); (3) LIBD human dorsolateral prefrontal
646 cortex Dorsolateral pre-frontal cortex (<http://research.libd.org/spatialLIBD/>); (4) human primary
647 pancreatic cancer data (GSE111672); (5) MERFISH mouse hypothalamus data
648 (<https://datadryad.org/stash/dataset/doi:10.5061/dryad.8t8s248>). Details of the datasets analyzed in
649 this paper were described in **Supplementary Table 1**.

650

651 **Software availability**

652 An open-source implementation of the SpaGCN algorithm can be downloaded from
653 <https://github.com/jianhuupenn/SpaGCN>

654

655 **Life sciences reporting summary**

656 Further information on experimental design is available in the Life Sciences Reporting Summary.

657

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Figures

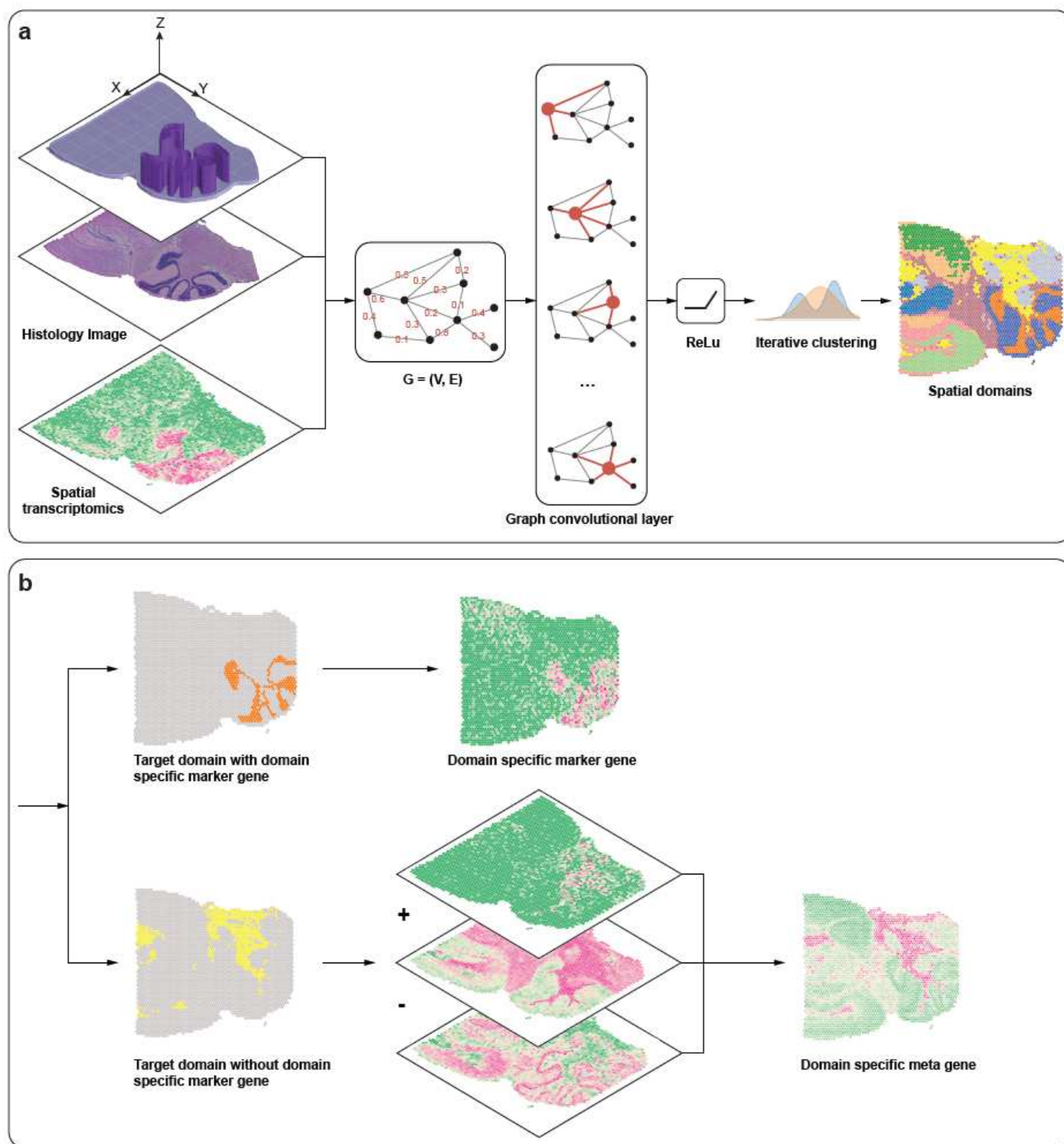


Figure 1

Workflow of SpaGCN. a, SpaGCN starts from integrating gene expression, spatial location and histology information using a graph convolutional network (GCN), then separates spots into different spatial domains using unsupervised iterative clustering. The GCN is based on an undirected weighted graph in

which the edge weight between every two spots is determined by Euclidean distance between the two spots, defined by the spatial coordinates (x, y) and the 3-rd dimensional coordinate z , obtained from the RGB values in the histology image. b, For each detected spatial domain, SpaGCN identifies SVGs or meta genes by domain guided differential expression analysis.

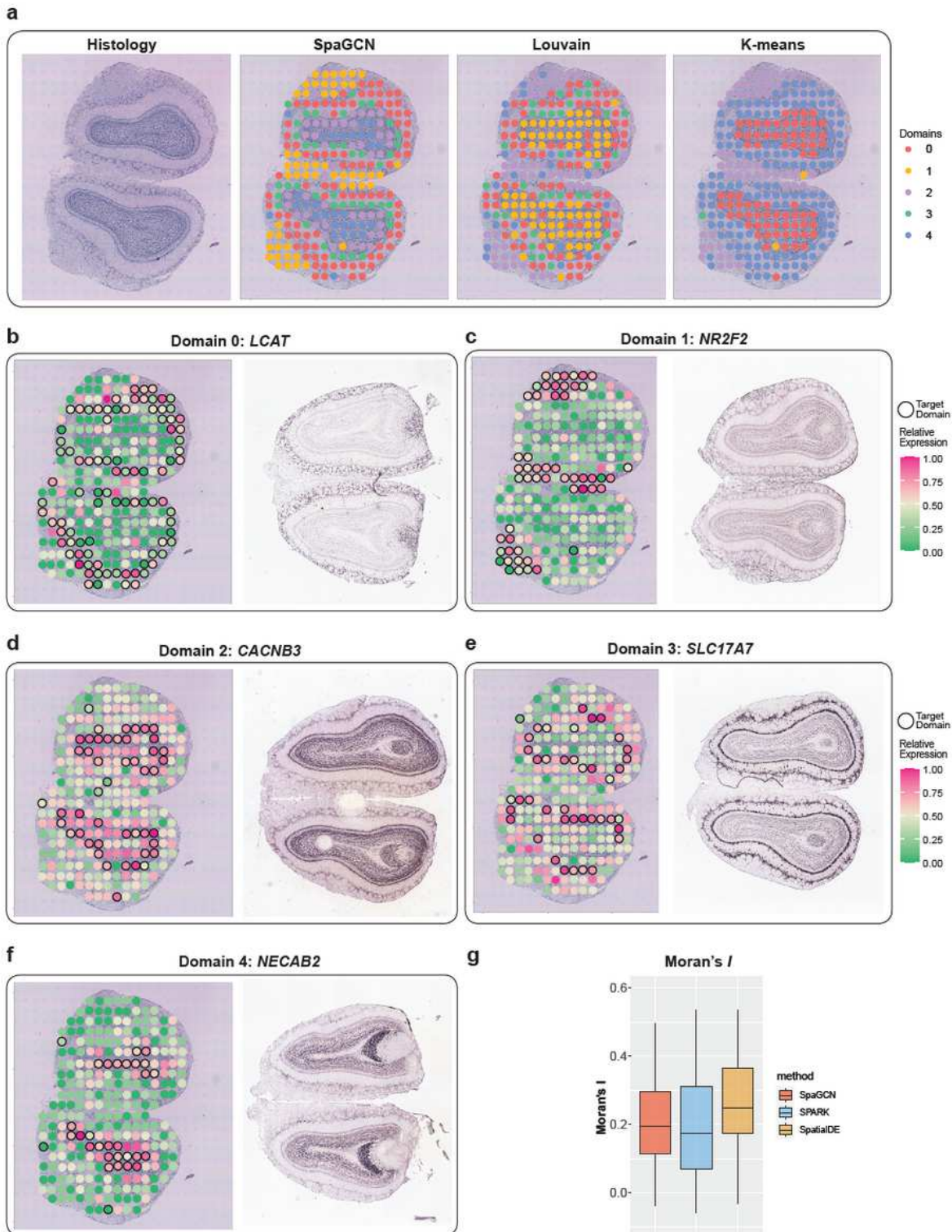


Figure 2

Spatial domains and SVGs detected in the mouse olfactory bulb dataset. a, Histology image of the tissue section and spatial domains detected by SpaGCN, Louvain's method, and K-means clustering. b-f, Spatial expression patterns of SVGs detected by SpaGCN for domains 0 (LCAT), 1 (NR2F2), 2 (CACNB3), 3 (SLC17A7), and 4 (NECAB2), and the corresponding in situ hybridization of these SVGs obtained from the Allen Brain Atlas. g, Boxplot of Moran's I values for SVGs detected by SpaGCN, SPARK, and SpatialDE.

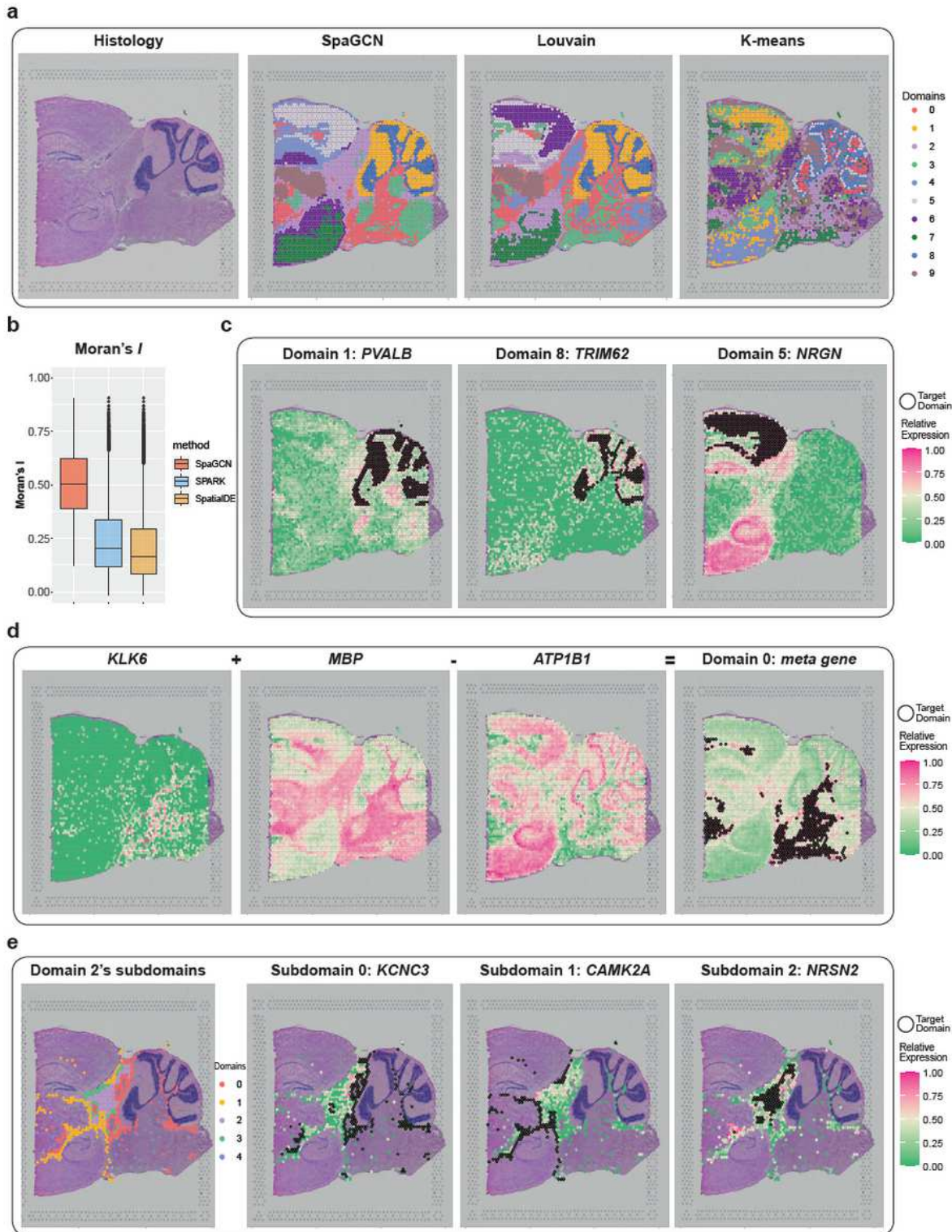


Figure 3

Spatial domains and SVGs detected in the mouse brain posterior brain dataset. a, Histology image of the tissue section and spatial domains detected by SpaGCN, Louvain's method, and K-means clustering. b, Boxplot of Moran's I values for SVGs detected by SpaGCN, SPARK, and SpatialDE. c, Spatial expression patterns of SVGs detected by SpaGCN for domain 1 (PVALB), 8 (TRIM62), and 5 (NRGN). d, Spatial expression patterns of genes KLK6, MBP, ATP1B1, which form the specific marker meta gene for domain 0 (KLK6 + MBP - ATP1B1). e, Clustering results for 5 sub-domains detected by SpaGCN for domain 2, and the spatial expression patterns of SVGs for sub-domains 0 (KCNC3), 1 (CAMK2A), and 2 (NRSN2).

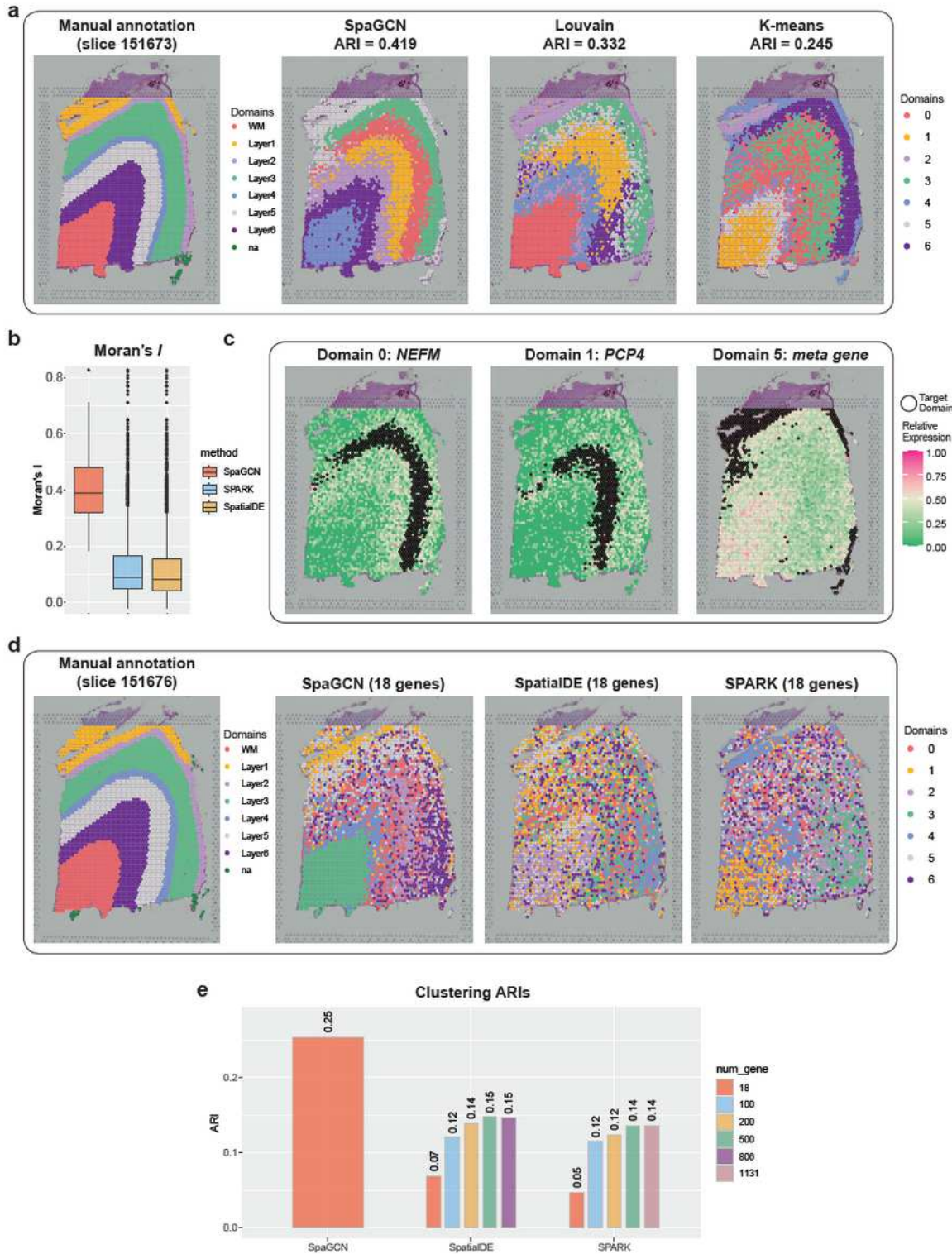


Figure 4

Spatial domains and SVGs detected in the LIBD human dorsolateral prefrontal cortex dataset. a, Manually annotated layer structure for slice 151673 from the original study²⁰, and spatial domains detected by SpaGCN, Louvain's method, and K-means clustering. b, Boxplot of Moran's I values for SVGs detected by SpaGCN, SPARK, and SpatialDE for slice 151673. c, Spatial expression patterns of SVGs for domain 0 (NEFM) and domains 1 (PCP4), and a meta gene formed by KRT19, MYL9, MBP, GFAP, and SNAP25 for domain 5 (KRT19 + MYL9 - MBP + GFAP - SNAP25). d, Manually annotated layer structure for slice 151676 from the original study²⁰, and K-means clustering results for slice 151676 using 18 genes selected by SpaGCN, SPARK, and SpatialDE. For SpaGCN, we selected the following genes, domain 0 (NEFL, NEFM), domain 1 (PCP4, TMSB10 + PCP4 - KRT19), domain 2 (CCK + KRT17 - MT-ND1, CPLX2 + KRT17 - MT-ND2), domain 3 (CAMK2N1, ENC1), domain 4 (MBP, FTL), domain 5 (KRT19 + MYL9 - MBP + GFAP - PLP1, KRT8 + MYL9 - MBP + GFAP - PLP1), and domain 6 (GFAP, MBP), resulting in 18 unique genes in total. For SPARK and SpatialDE, the 18 SVGs with the smallest FDR-adjusted p-value or q-value were randomly selected. e, ARIs between manually annotated layers and K-means' clustering using SVGs selected by different methods. For SpaGCN, we only used the selected SVGs and meta genes, with 18 genes involved in total while for SPARK and SpatialDE, we used top 18, 100, 200, 500 and all SVGs with the identical smallest FDR-adjusted p-value or q-value.

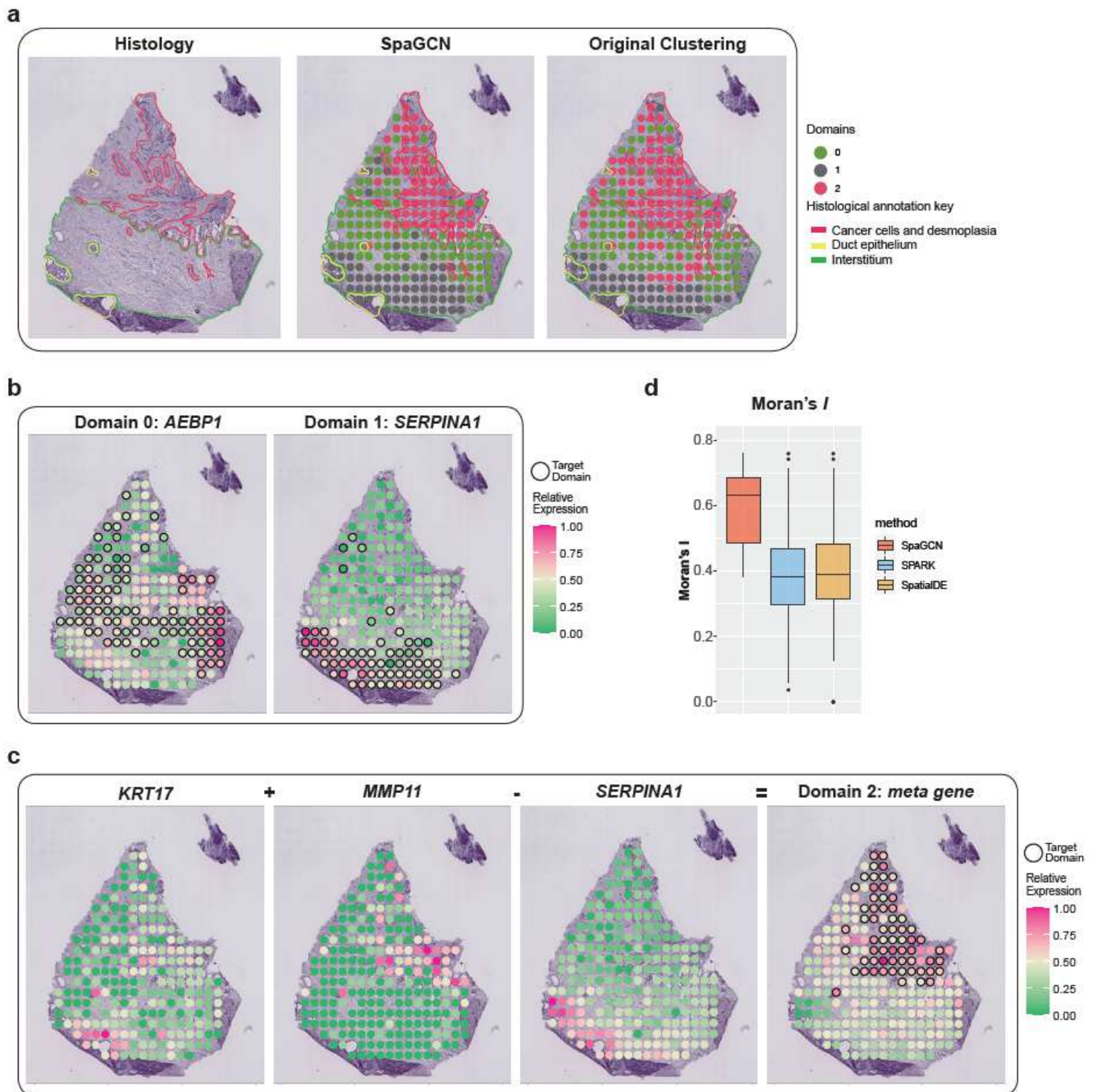


Figure 5

Spatial domains and SVGs detected in the human primary pancreatic cancer tissue dataset. a, Histology image of the tissue section with manually annotated regions from the original study⁵, spatial domains detected by SpaGCN, and clustering results from the original study. b, Spatial expression pattern of SVGs detected by SpaGCN for domain 0 (AEBP1) and domain 1 (SERPINA1). c, Spatial expression patterns of genes KRT17, MMP11, SERPINA1, which form the specific marker meta gene for domain 2 (KRT17 +

MMP11 - SERPINA1). d, Boxplot of Moran's I values for SVGs detected by SpaGCN, SPARK, and SpatialDE.

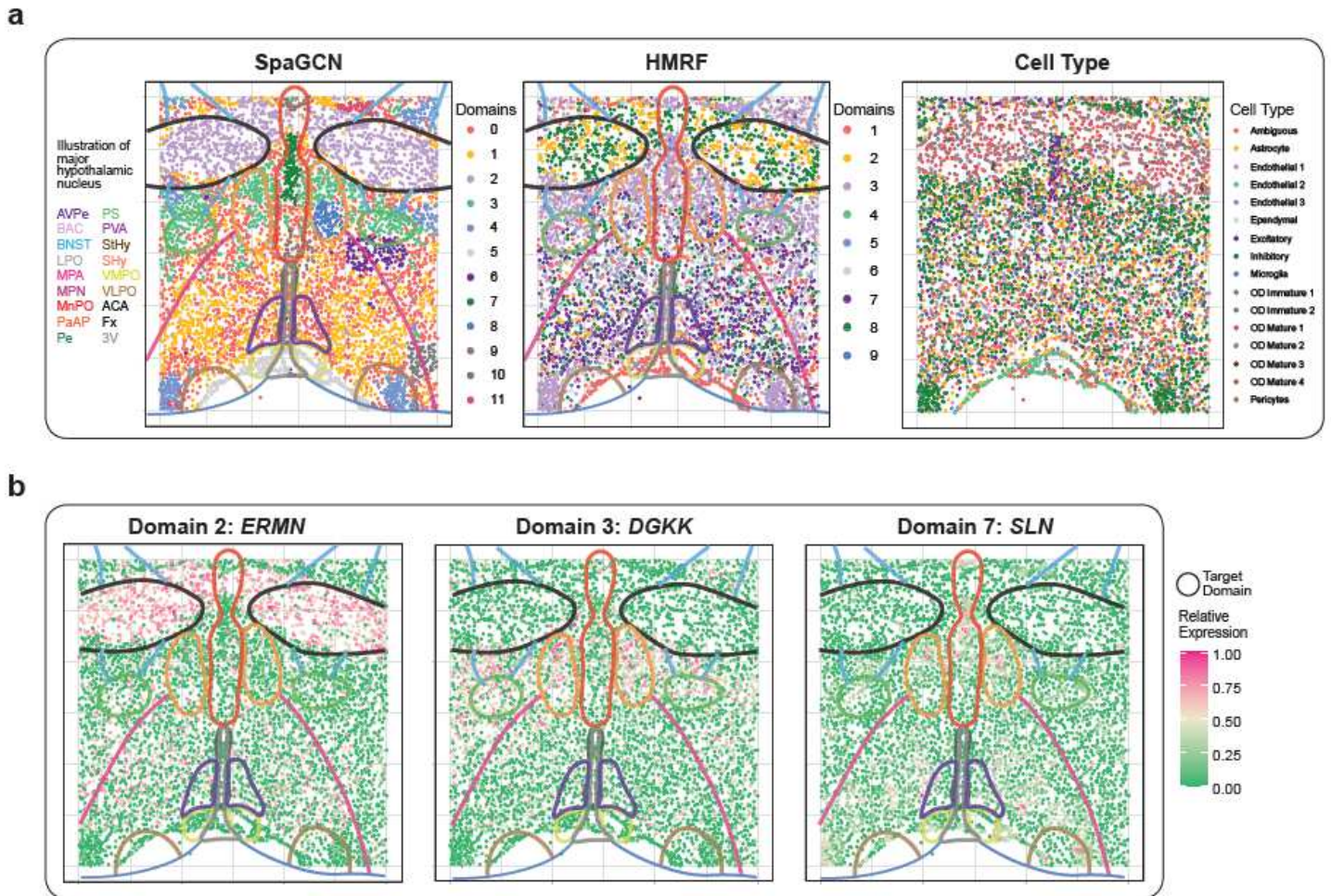


Figure 6

Spatial domains and SVGs detected in the MERFISH mouse brain hypothalamus dataset. a, Spatial domains detected by SpaGCN and the HMRf method overlaid with annotated hypothalamic nuclei from the original study², and cell type distribution from the original study. d, Spatial expression patterns of SVGs detected by SpaGCN for domain 2 (ERMN), domain 3 (DGKK), and domain 7 (SLN).

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- [SupplementaryInformation11302020.docx](#)