glueviz File Edit View Canvas Data Manager Plugins Help

Glue

Open Session | Export Session | Import Data | Export Data/Subsets | Link Data | x^2 Arithmetic attributes | Active Subset: Subset 1 | Mode:

Tab 1

Data Collection

Data
- HE_Rep1
- HE_Rep8_MOB

Subsets
- Subset 1

Plot Layers - 2D Image

- Subset 1 (HE_Rep1)
- HE_Rep1 (red)
- HE_Rep1 (green)
- HE_Rep1 (blue)

attribute: blue

limits: Min/Max | Linear

22 | 255

color/opacity | Sync

contrast/bias | Reset

Plot Options - 2D Image

General | Limits | Axes | Legend

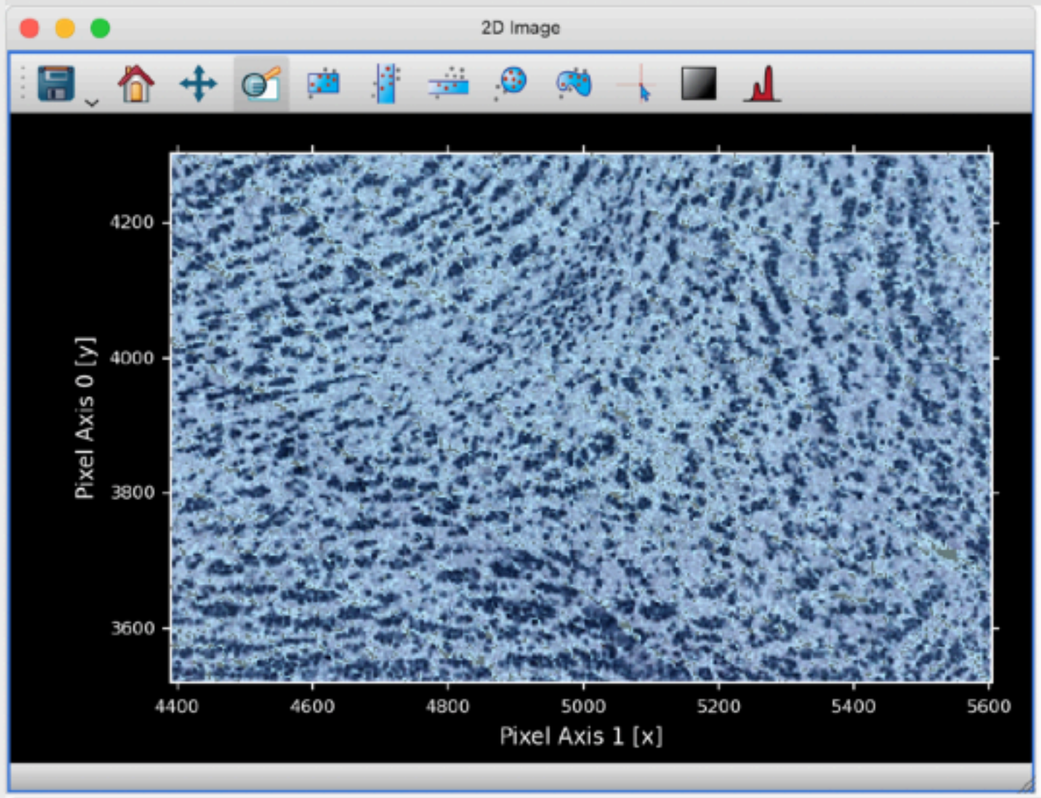
mode: One color per layer

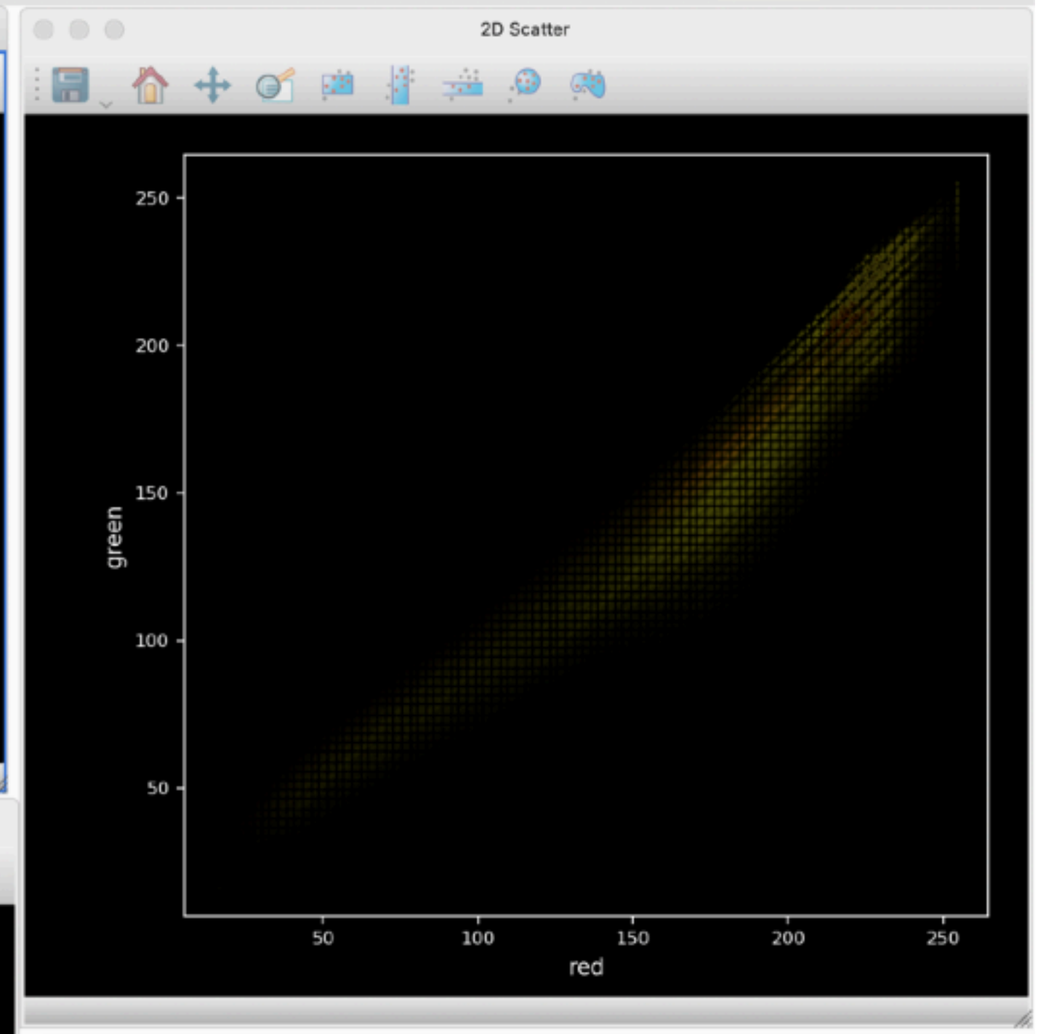
aspect: Square Pixels

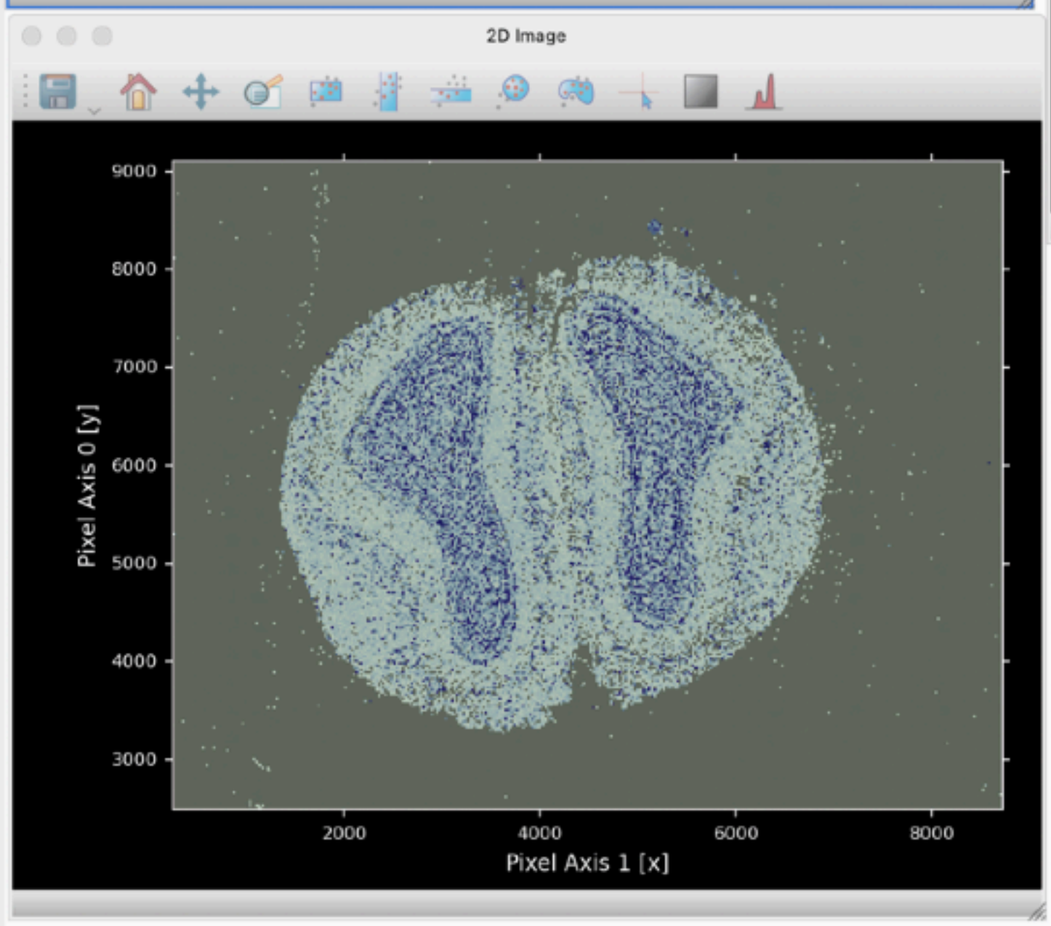
reference: HE_Rep1

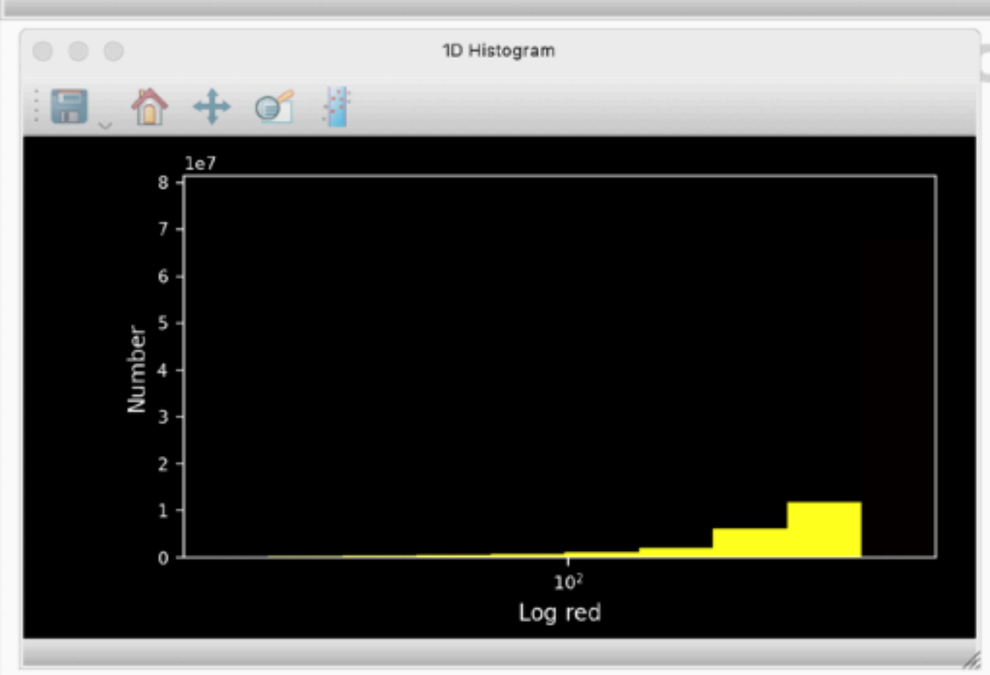
x axis: Pixel Axis 1 [x]

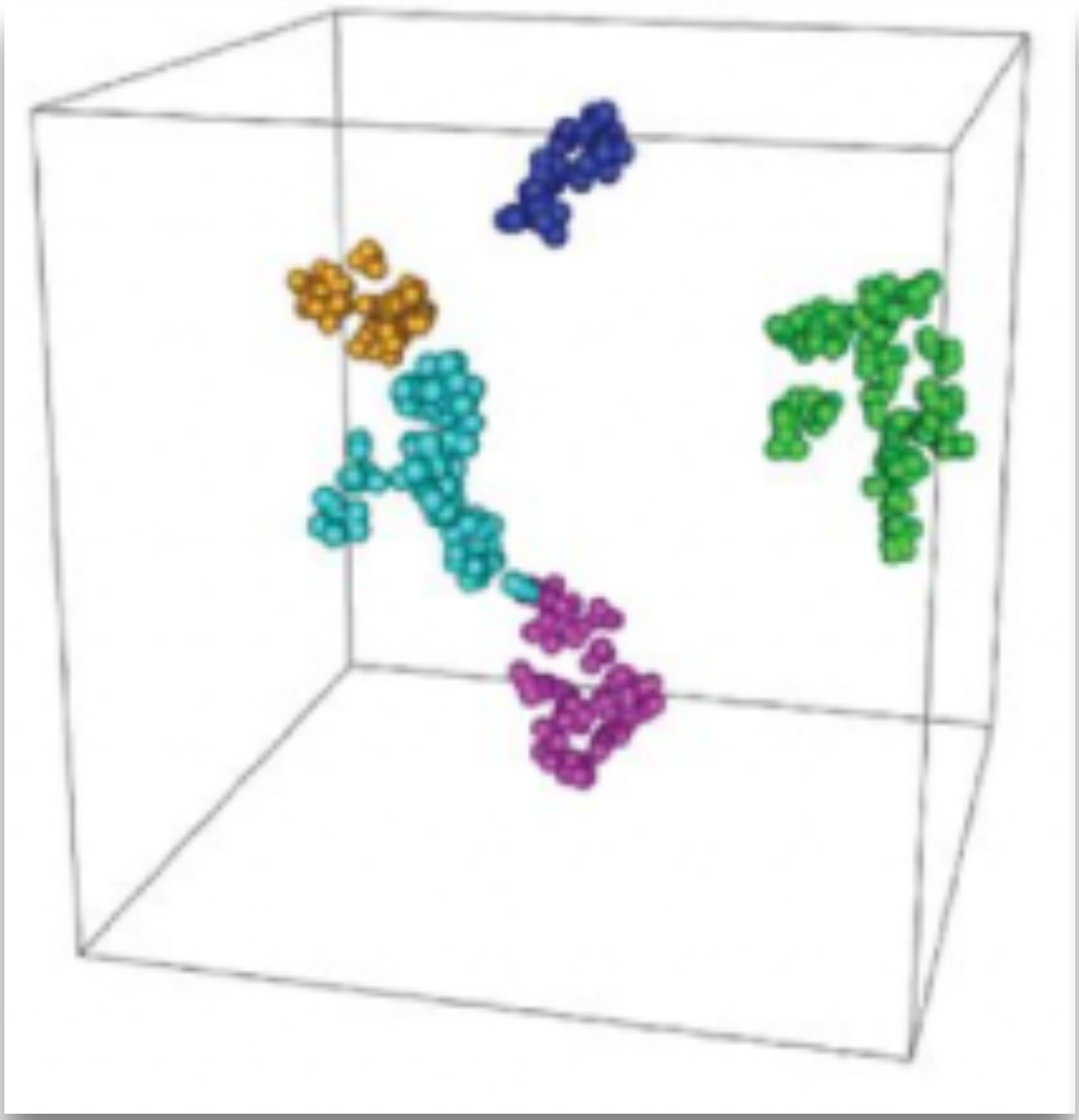
y axis: Pixel Axis 0 [y]

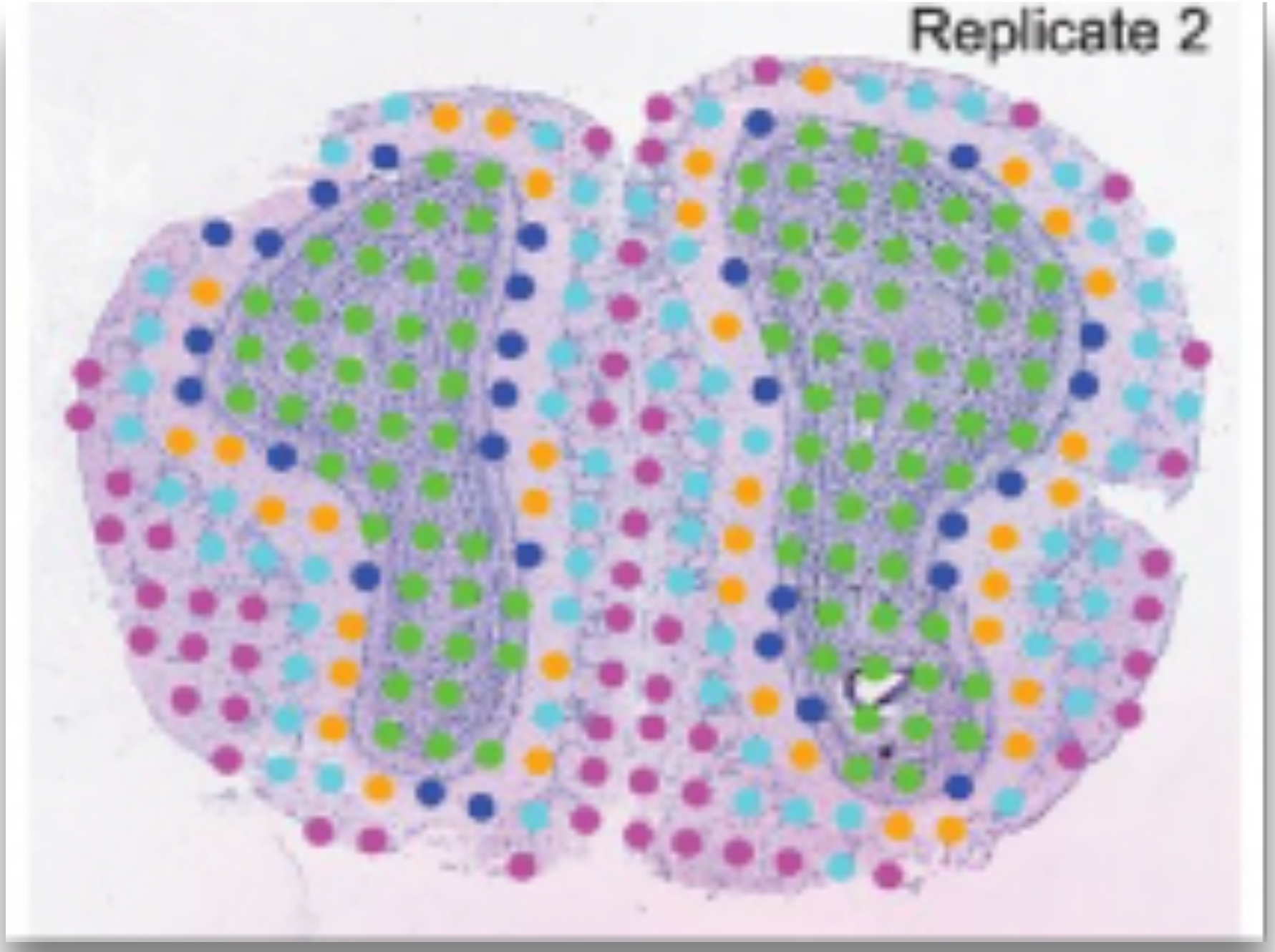


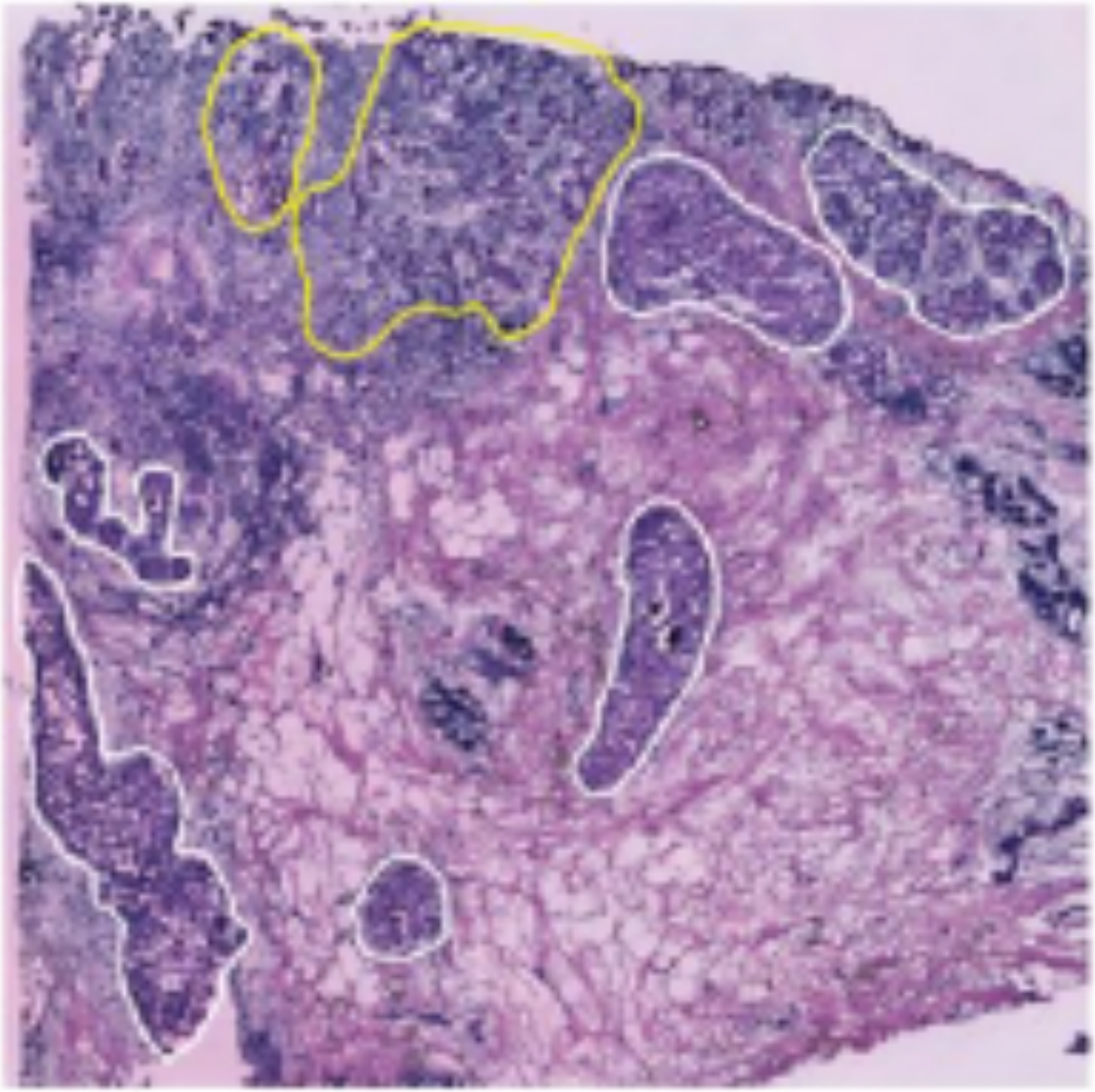


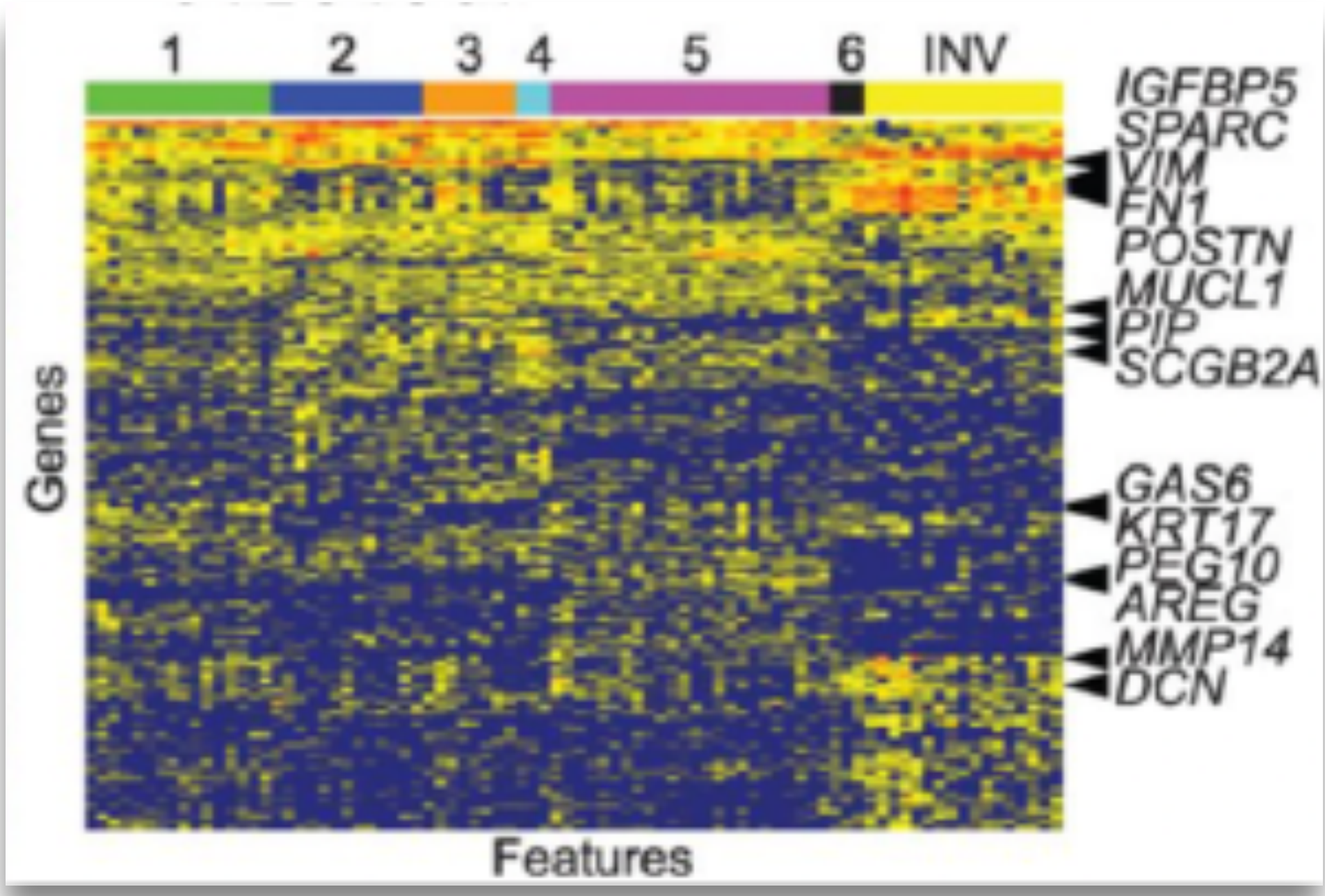







Replicate 2

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GAS6
KRT17
PEG10
AREG
MMP14
DCN
Genes
Features

gluegenes

TRANSCRIPTION

Visualization and analysis of gene expression in tissue sections by spatial transcriptomics

Patrik L. Ståhl,[1,2*] Fredrik Salmén,[2*] Sanja Vickovic,[2†] Anna Lundmark,[2,3†] José Fernández Navarro,[1,2] Jens Magnusson,[1] Stefania Giacomello,[2] Michaela Asp,[2] Jakub O. Westholm,[4] Mikael Huss,[4] Annelie Mollbrink,[2] Sten Linnarsson,[5] Simone Codeluppi,[5,6] Åke Borg,[7] Fredrik Pontén,[8] Paul Igor Costea,[2] Pelin Sahlén,[2] Jan Mulder,[9] Olaf Bergmann,[1] Joakim Lundeberg,[2‡] Jonas Frisén[1]

Analysis of the pattern of proteins or messenger RNAs (mRNAs) in histological tissue sections is a cornerstone in biomedical research and diagnostics. This typically involves the visualization of a few proteins or expressed genes at a time. We have devised a strategy, which we call "spatial transcriptomics," that allows visualization and quantitative analysis of the transcriptome with spatial resolution in individual tissue sections. By positioning histological sections on arrayed reverse transcription primers with unique positional barcodes, we demonstrate high-quality RNA-sequencing data with maintained two-dimensional positional information from the mouse brain and human breast cancer. Spatial transcriptomics provides quantitative gene expression data and visualization of the distribution of mRNAs within tissue sections and enables novel types of bioinformatics analyses, valuable in research and diagnostics.

“Instant” Spatial Transcriptomics . . .

Glue

Open Session | Export Session | Import Data | Export Data/Subsets | Link Data | Arithmetic attributes | Active Subset: None/Create New (the next selection will create a subset) | Terminal | Preferences

Data Collection

Data
- chr3_3DGNOME
- ChIA-PET_Rep1_coverage_ENC...
- ChIA-PET_Rep1_loops_ENCFF3...
- ChIA-PET_Rep1_peaks_ENCFF...

Subsets
- Isolated Region

Plot Layers - Genome Track Viewer
- ChIA-PET_Rep1_loops_ENCFF310
- Isolated Region (ChIA-PET_Rep1_
- Isolated Region (ChIA-PET_Rep1_
- ChIA-PET_Rep1_coverage_ENCFF

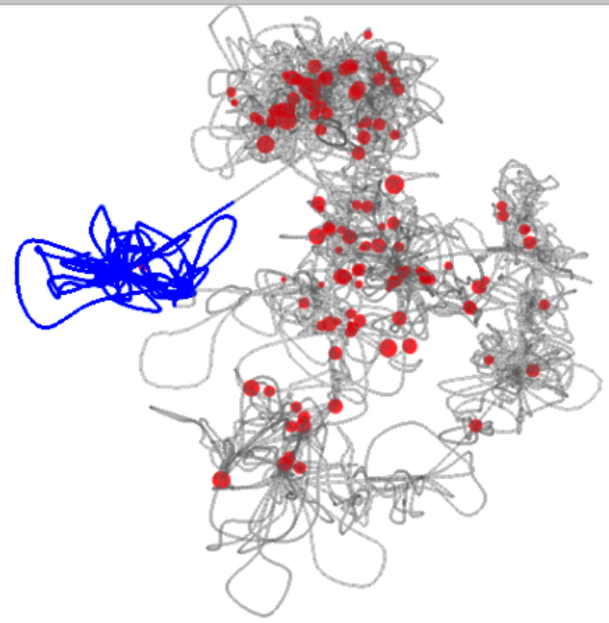
color
opacity

Plot Options - Genome Track Viewer

Limits | Axes | Legend

Chrom 3
Range -64848.6 3922e+07
Loops
Show Genes

3D Scatter



Genome Track Viewer

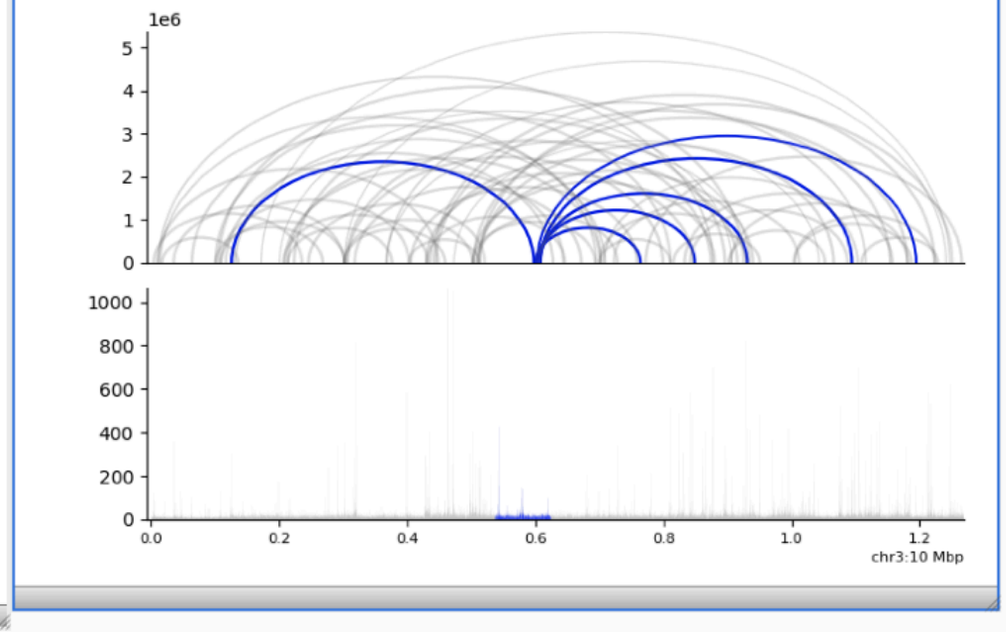
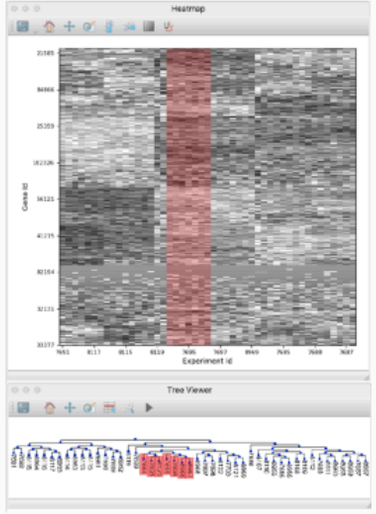
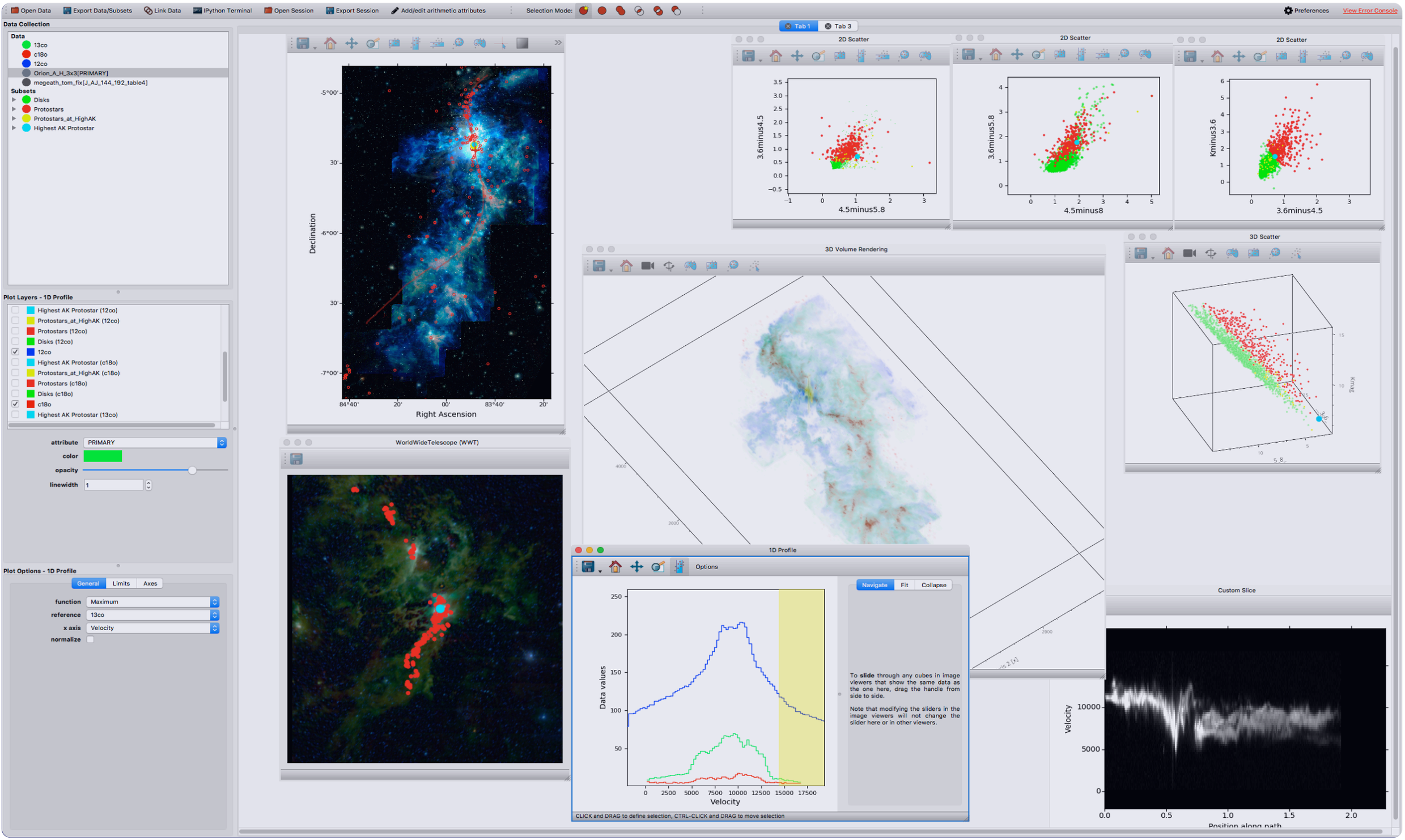


Table: ChIA-PET_Rep1_peaks_ENCFF578RML.chr3

	chr	end	start	peak_intensity	x	y
26	chr3	5027016	5026505	4.87089987...	-16.95555...	-20.22317.
27	chr3	5027804	5027264	4.79005547...	-15.96221...	-20.38275.
28	chr3	5058836	5057743	4.06550913...	-29.73126...	-18.92818.
29	chr3	5121954	5121471	3.4065460...	-12.510781...	-14.179771
30	chr3	5122810	5122272	4.781716172...	-12.42688...	-10.85097.
31	chr3	5123968	5123002	3.9530344...	-12.511697...	-7.803144.
32	chr3	5137283	5136938	2.99992079...	-24.46438...	-5.097149.
33	chr3	5426373	5425735	3.2009293...	-41.73639...	33.330951
34	chr3	5427401	5426635	3.73743405...	-41.83707...	32.817504.
35	chr3	6994724	6994337	4.35688817...	9.6423483...	-7.427244.




Open Data
Export Data/Subsets
Link Data
IPython Terminal
Open Session
Export Session
Add/edit arithmetic attributes
Selection Mode:
Preferences
View Error Console
Tab 1
Tab 3
Data Collection
Data
13co
c18o
12co
Orion_A_H_3x3[PRIMARY]
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Subsets
Disks
Protostars
Protostars_at_HighAK
Highest AK Protostar
Plot Layers - 1D Profile
Highest AK Protostar (12co)
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Protostars (12co)
Disks (12co)
12co
Highest AK Protostar (c18o)
Protostars_at_HighAK (c18o)
Protostars (c18o)
Disks (c18o)
c18o
Highest AK Protostar (13co)
attribute
PRIMARY
color
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Plot Options - 1D Profile
General
Limits
Axes
function
Maximum
reference
13co
x axis
Velocity
normalize
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Right Ascension
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2D Scatter
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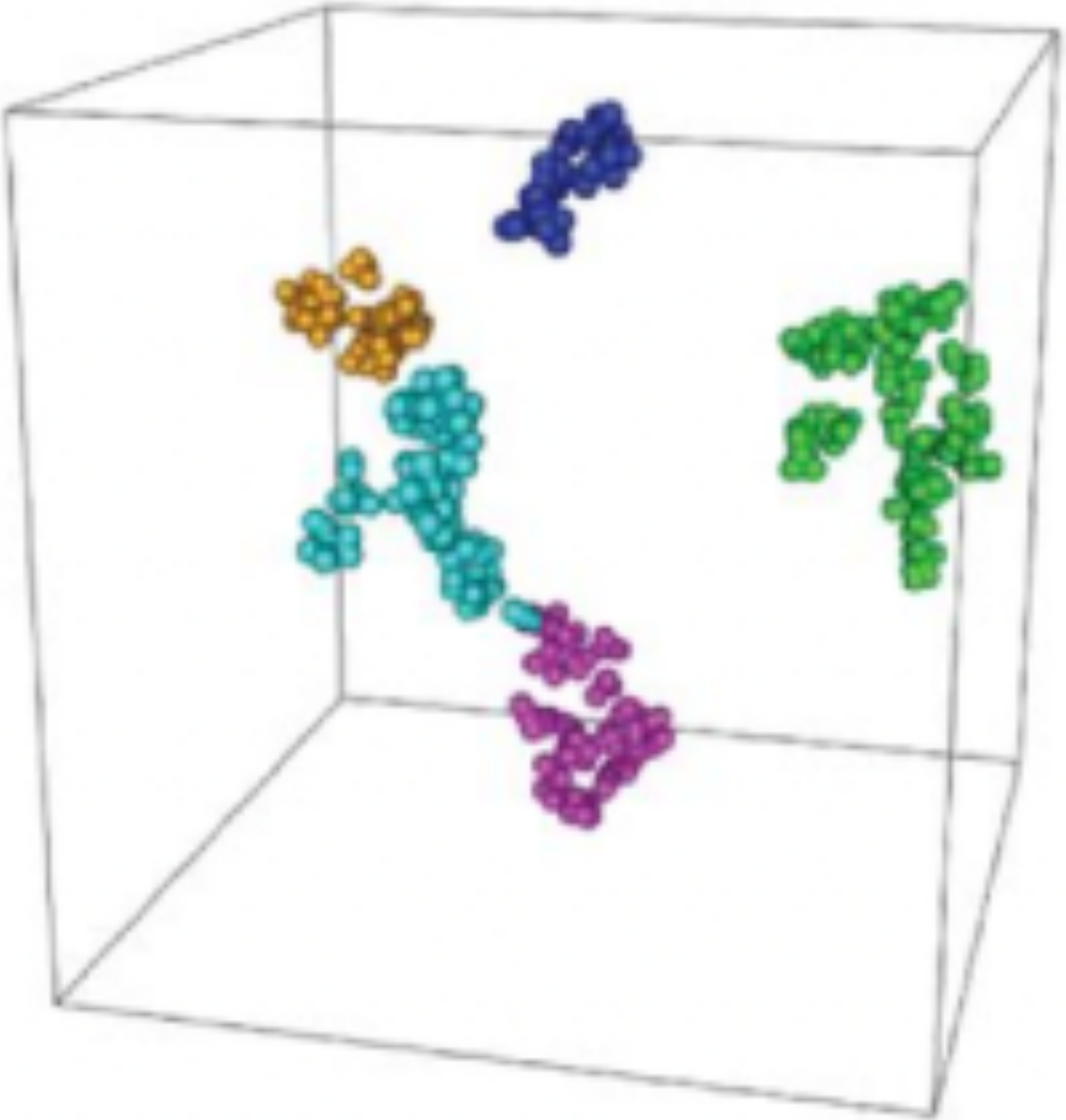
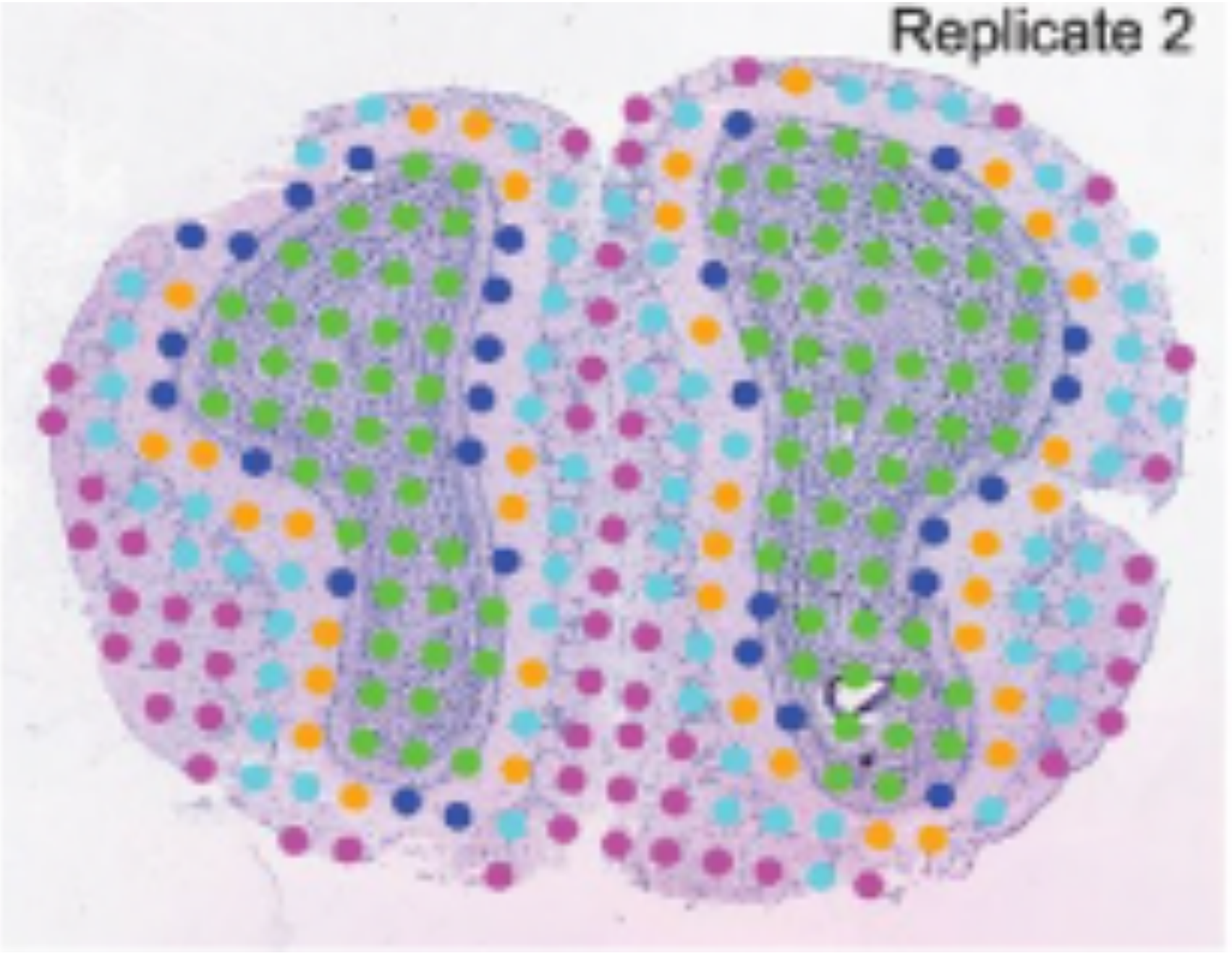
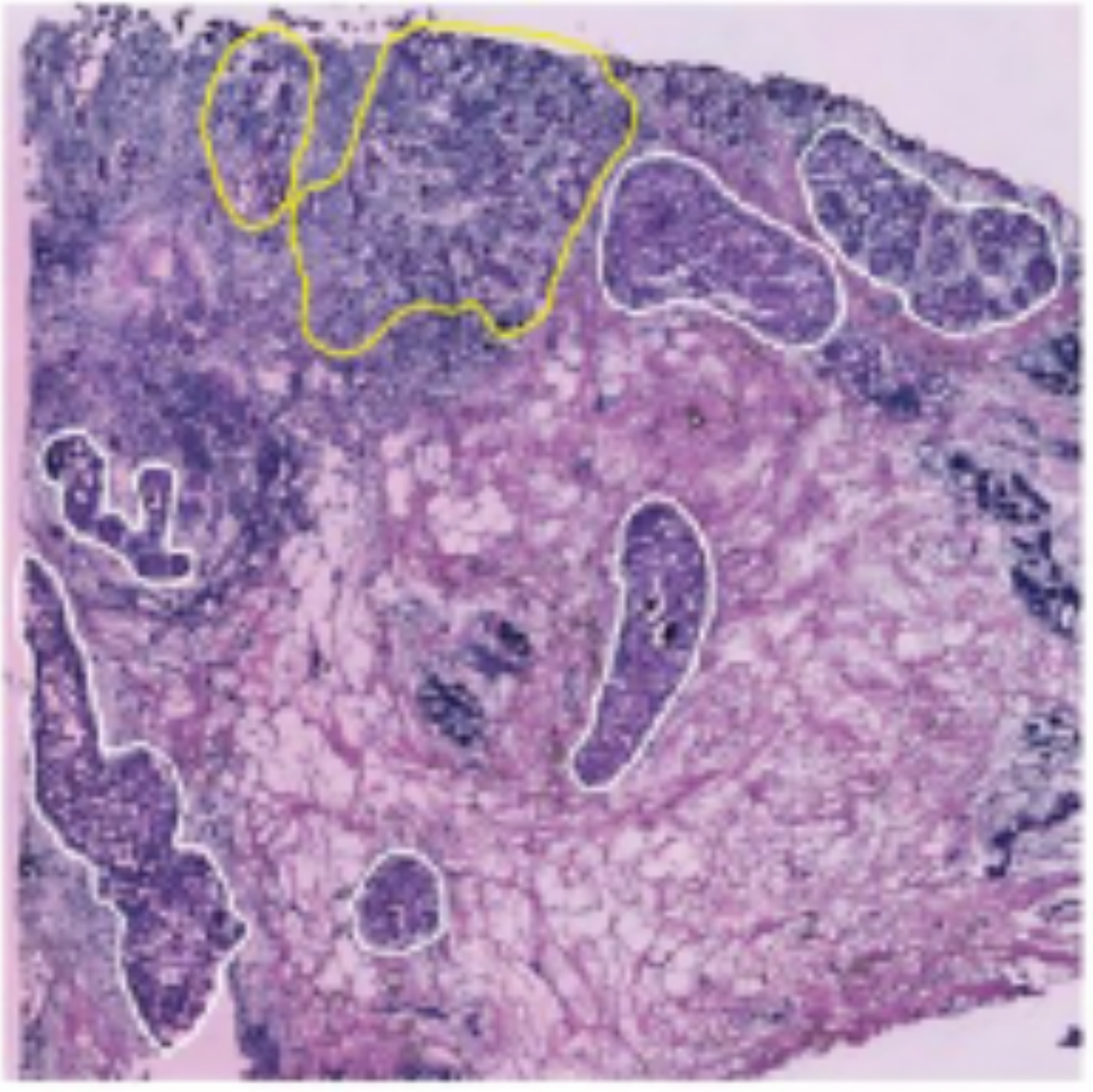
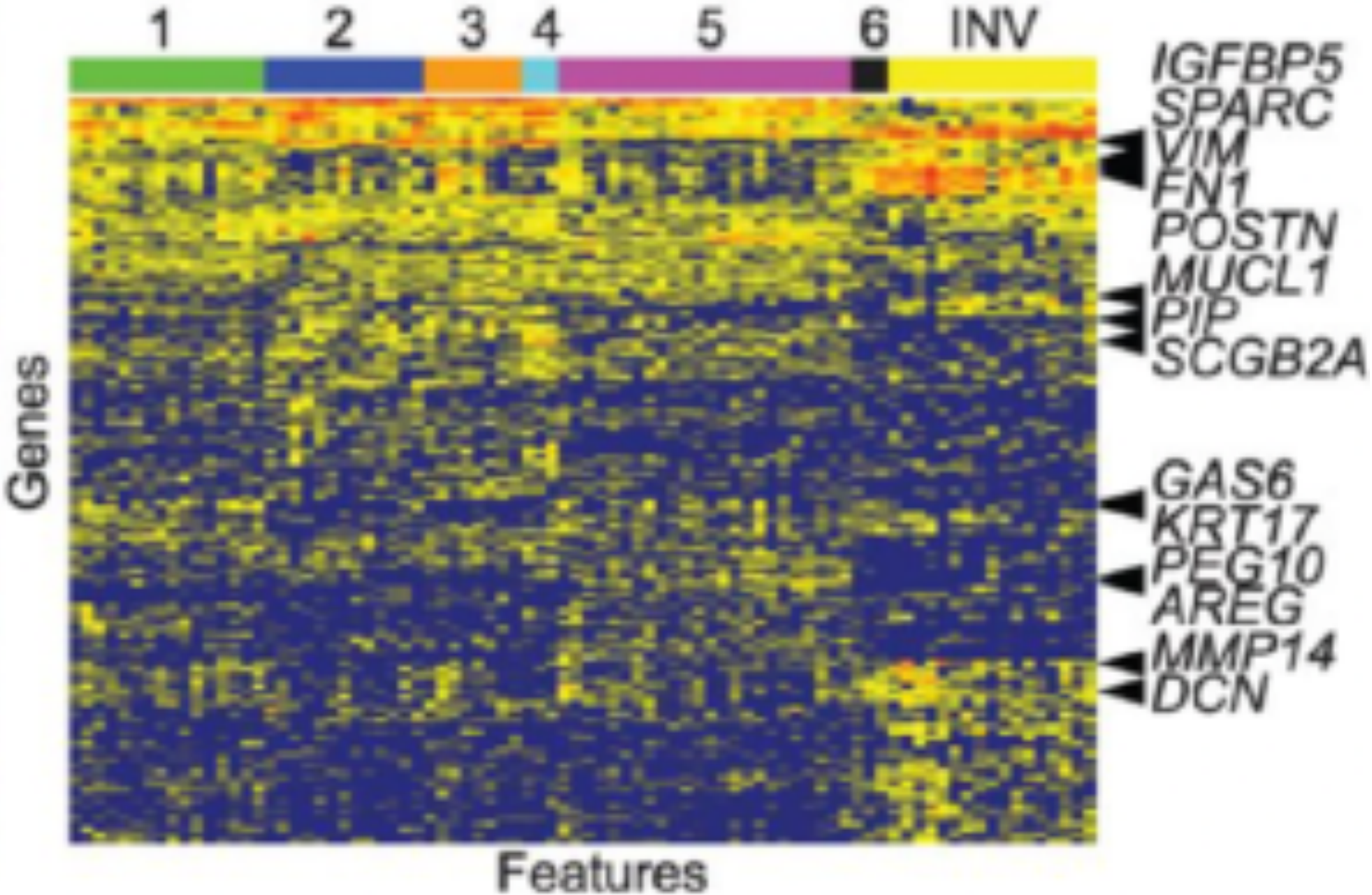
4.5minus5.8
3.6minus5.8
4.5minus8
Kminus3.6
3.6minus4.5
3D Volume Rendering
3D Scatter
Kmag
1D Profile
Options
Navigate
Fit
Collapse
Data values
Velocity
To slide through any cubes in image viewers that show the same data as the one here, drag the handle from side to side.
Note that modifying the sliders in the image viewers will not change the slider here or in other viewers.
CLICK and DRAG to define selection, CTRL-CLICK and DRAG to move selection
Custom Slice
Velocity
Position along path




Replicate 2

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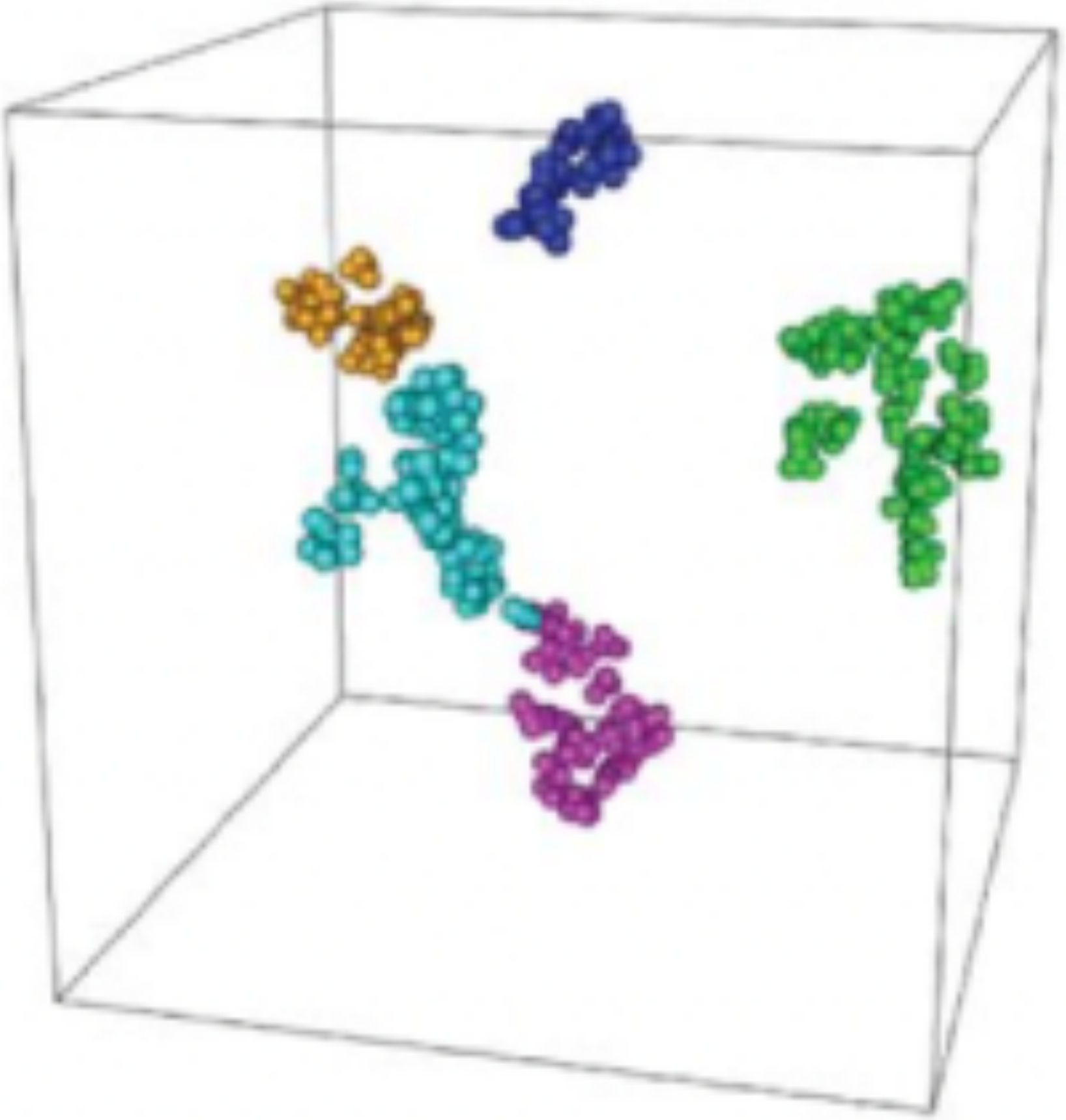
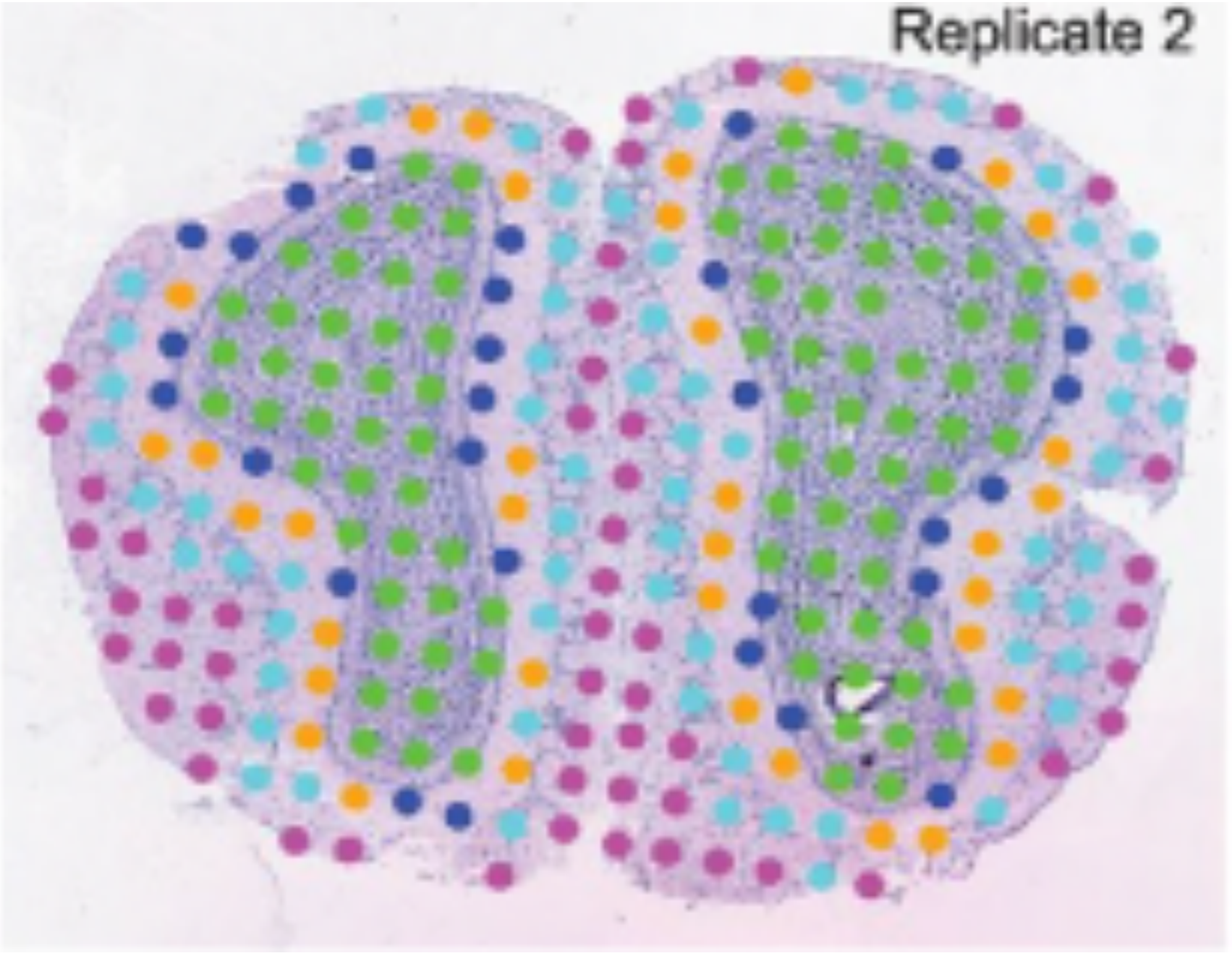
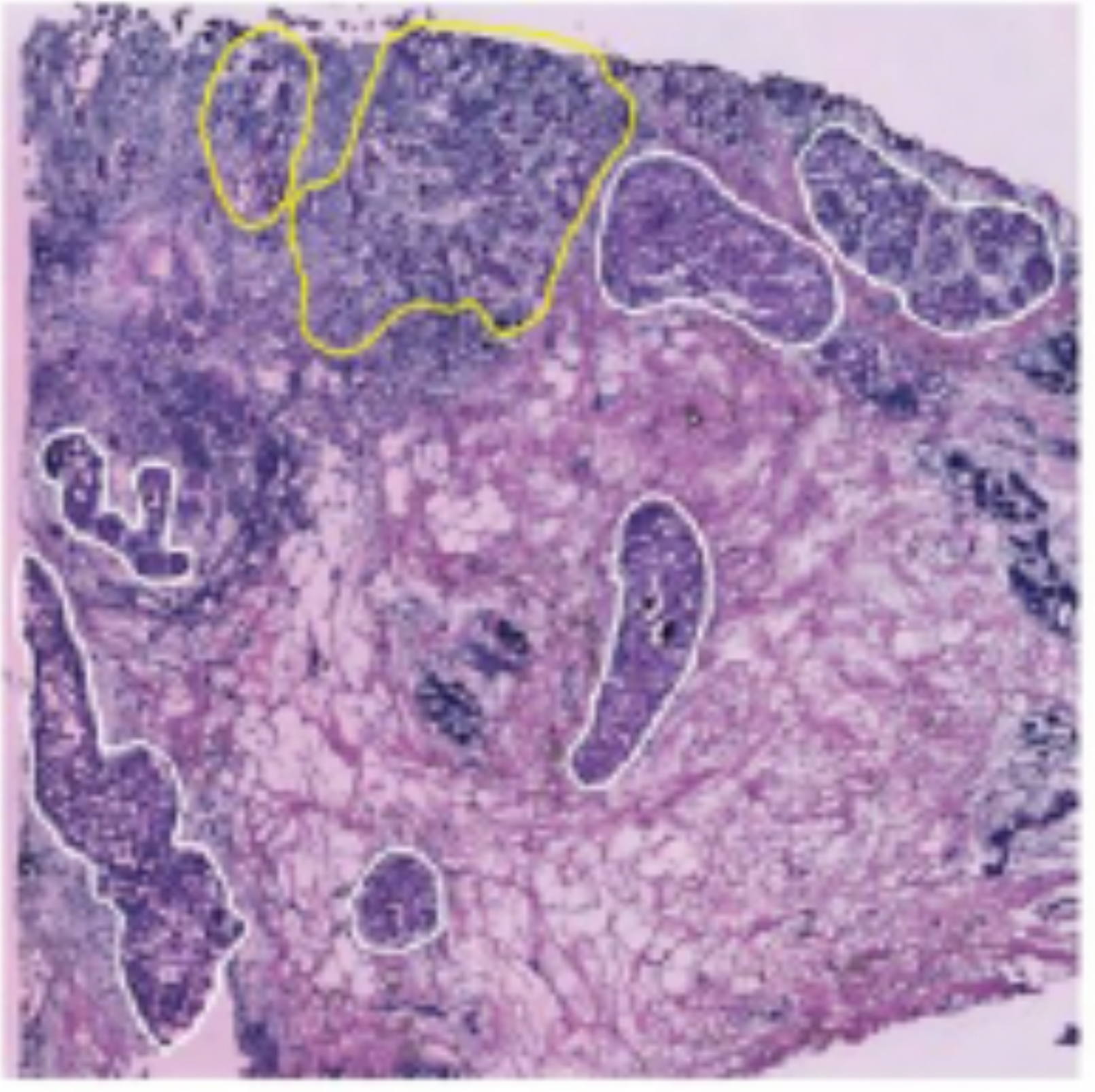
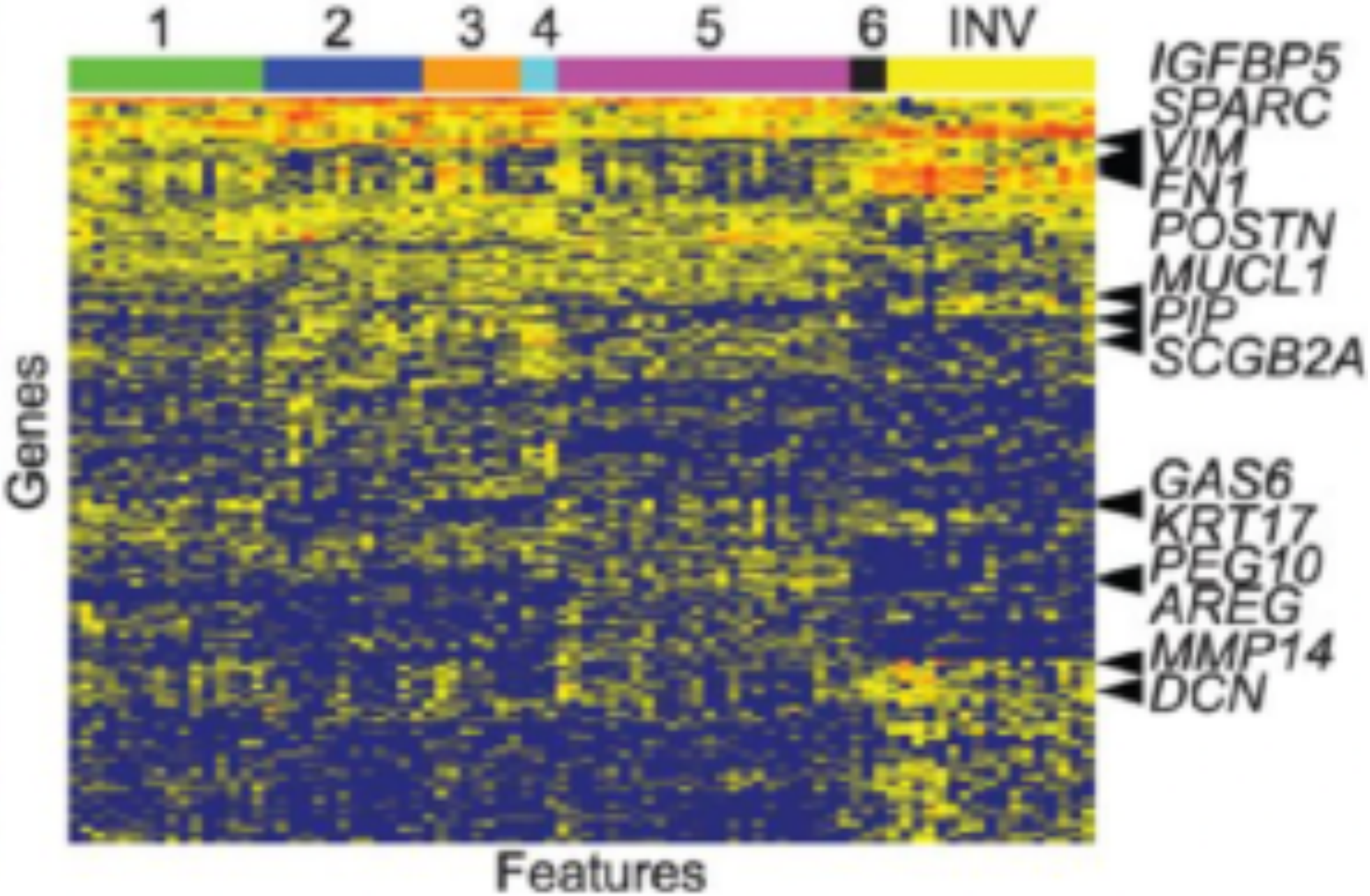



Replicate 2

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SCGB2A
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AREG
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Genes
Features