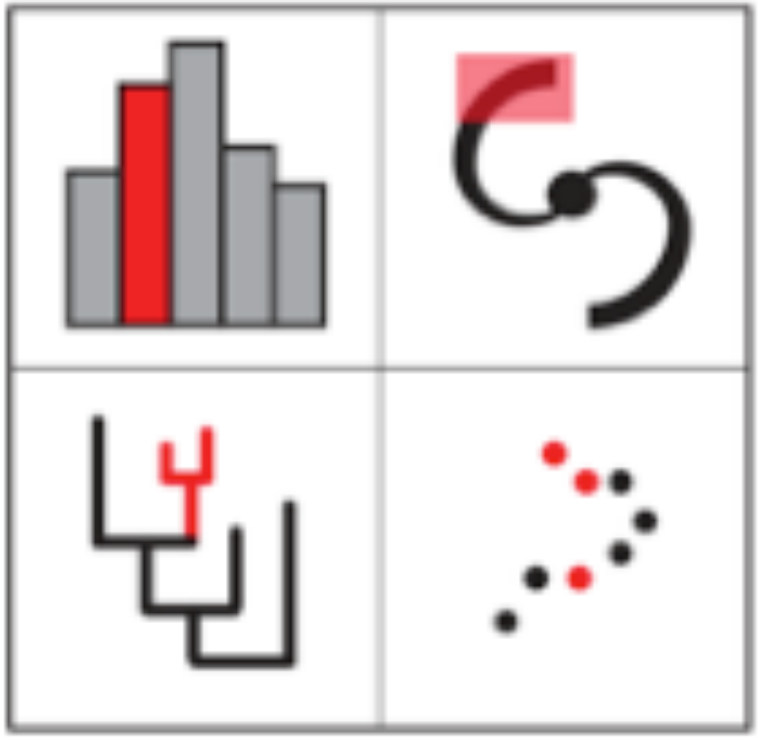
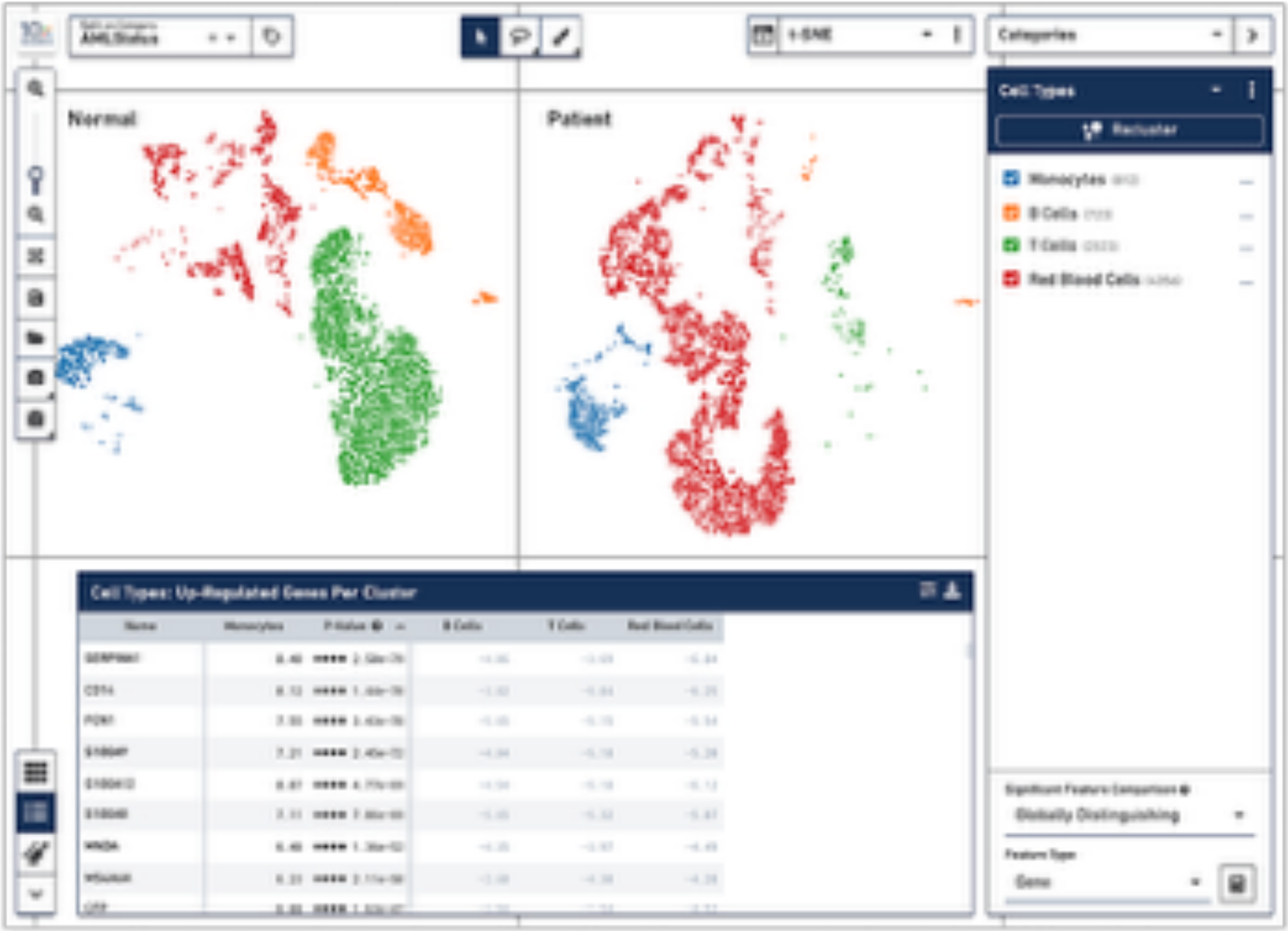


glue

multidimensional data exploration


AML Status
t-SNE
Categories
Normal
Patient
Cell Types
Reclusterer
Monocytes
B Cells
T Cells
Red Blood Cells
Cell Types: Up-Regulated Genes Per Cluster
Name
Monocytes
P-Value
B Cells
T Cells
Red Blood Cells
Significant Feature Comparison
Globally Distinguishing
Feature Type
Gene

10x GENOMICS

“glue genes”

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

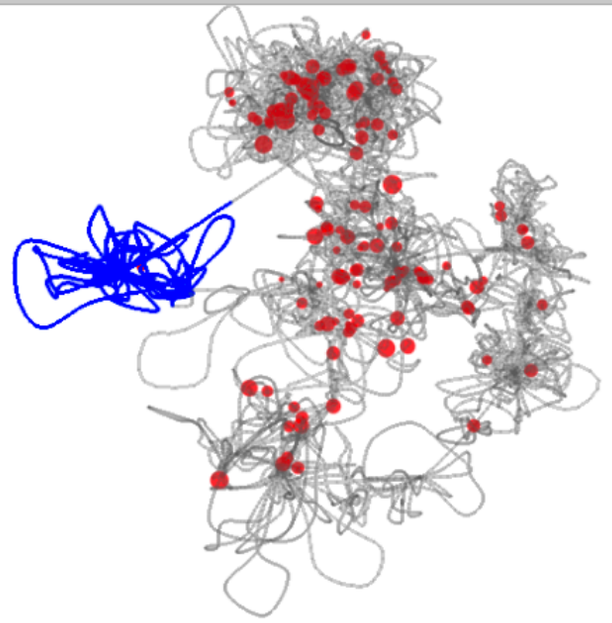
Chrom 3

Range -64848.6 6922e+07

Loops

Show Genes

3D Scatter



Genome Track Viewer

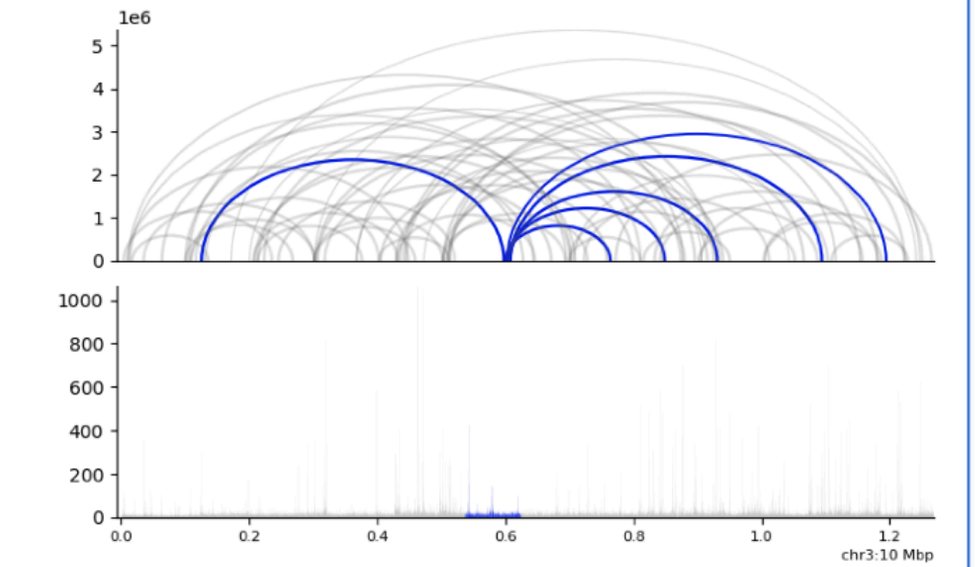
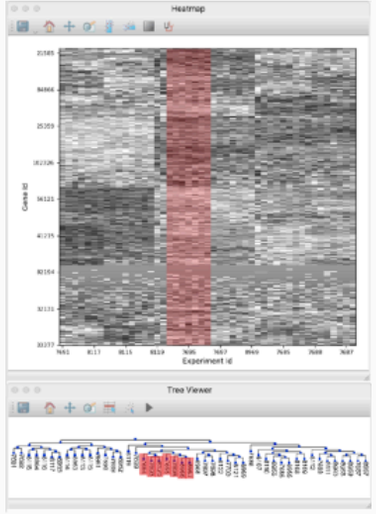
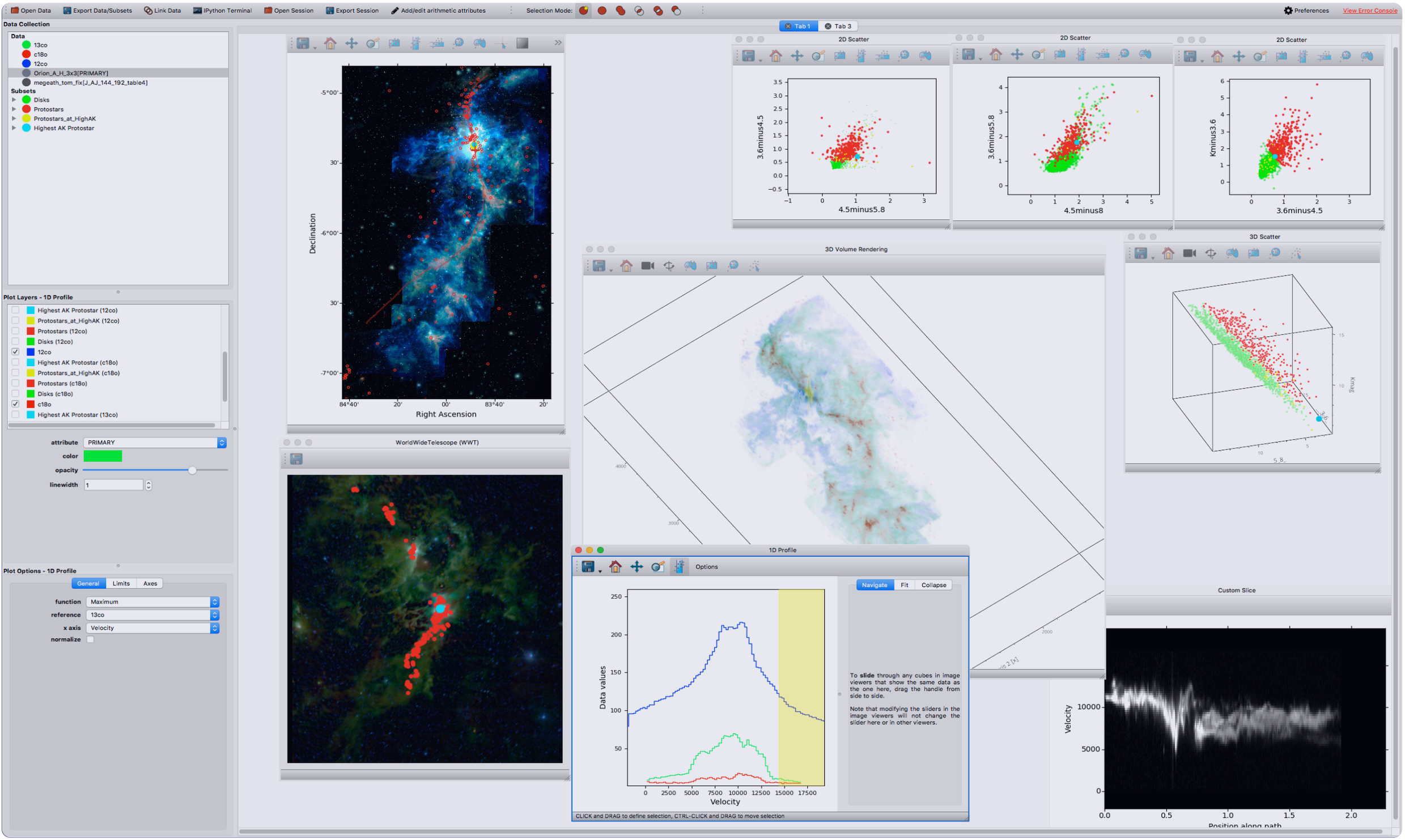
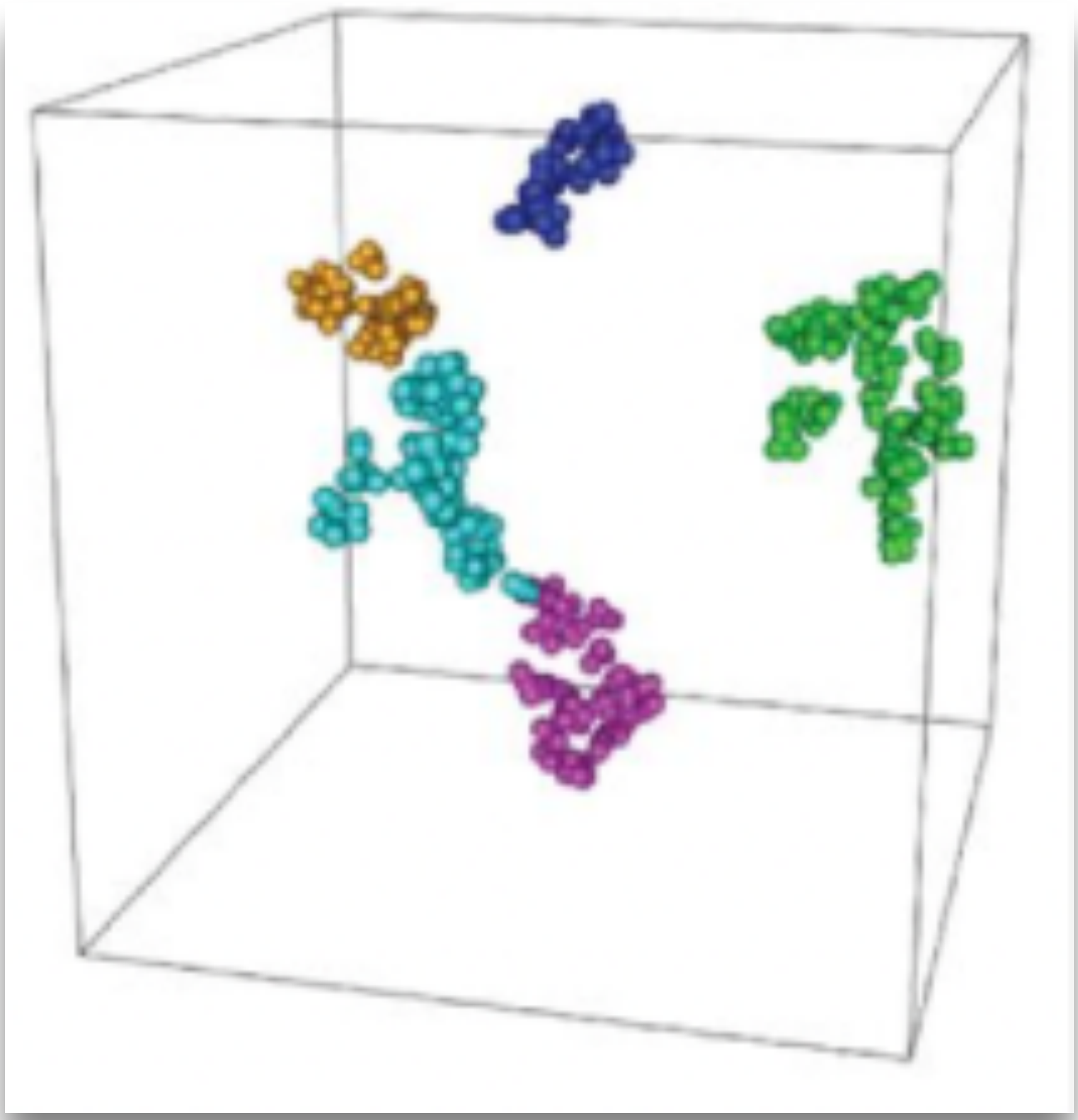


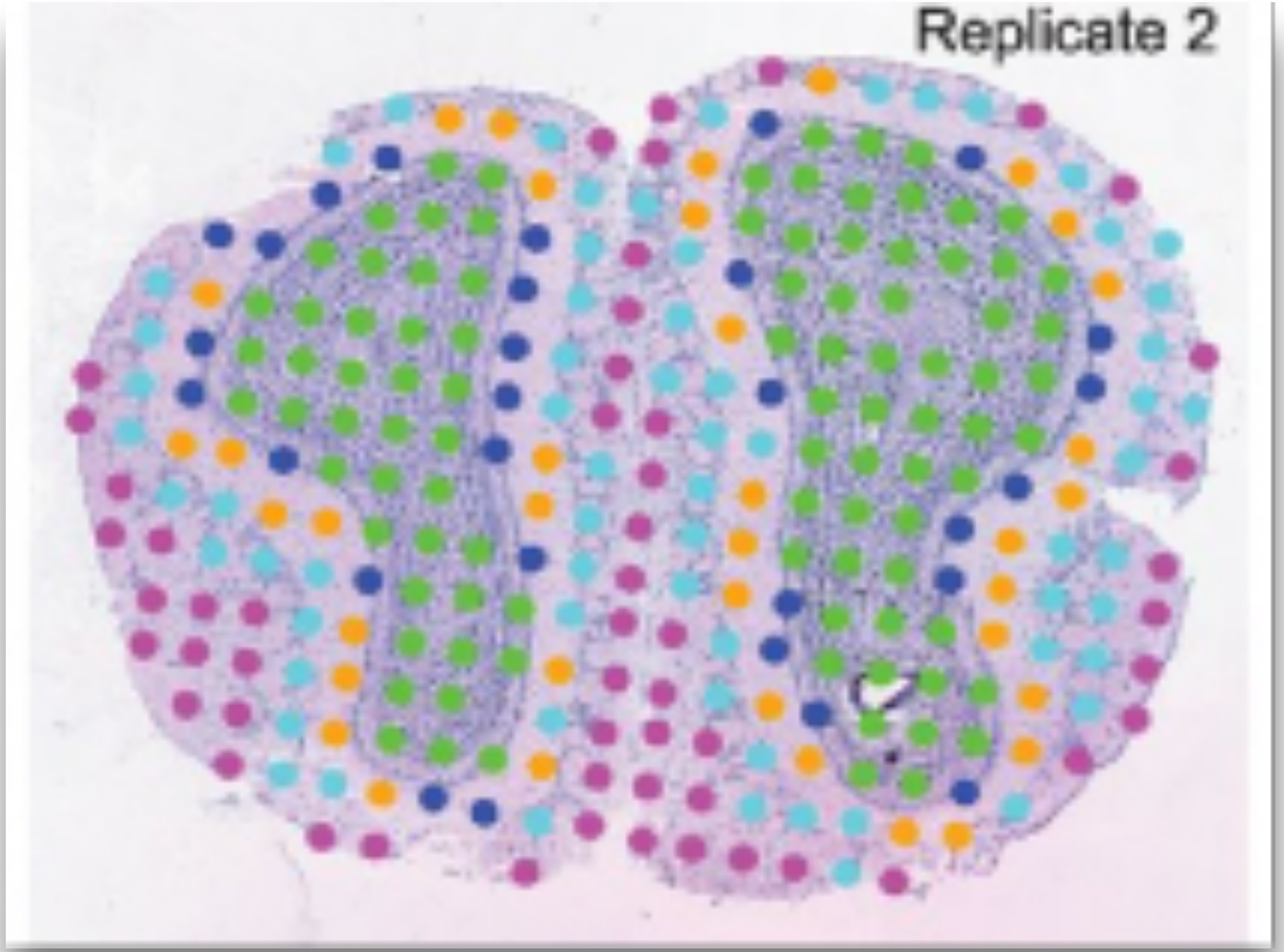
Table: ChIA-PET_Rep1_peaks_ENCFF578RML.chr3

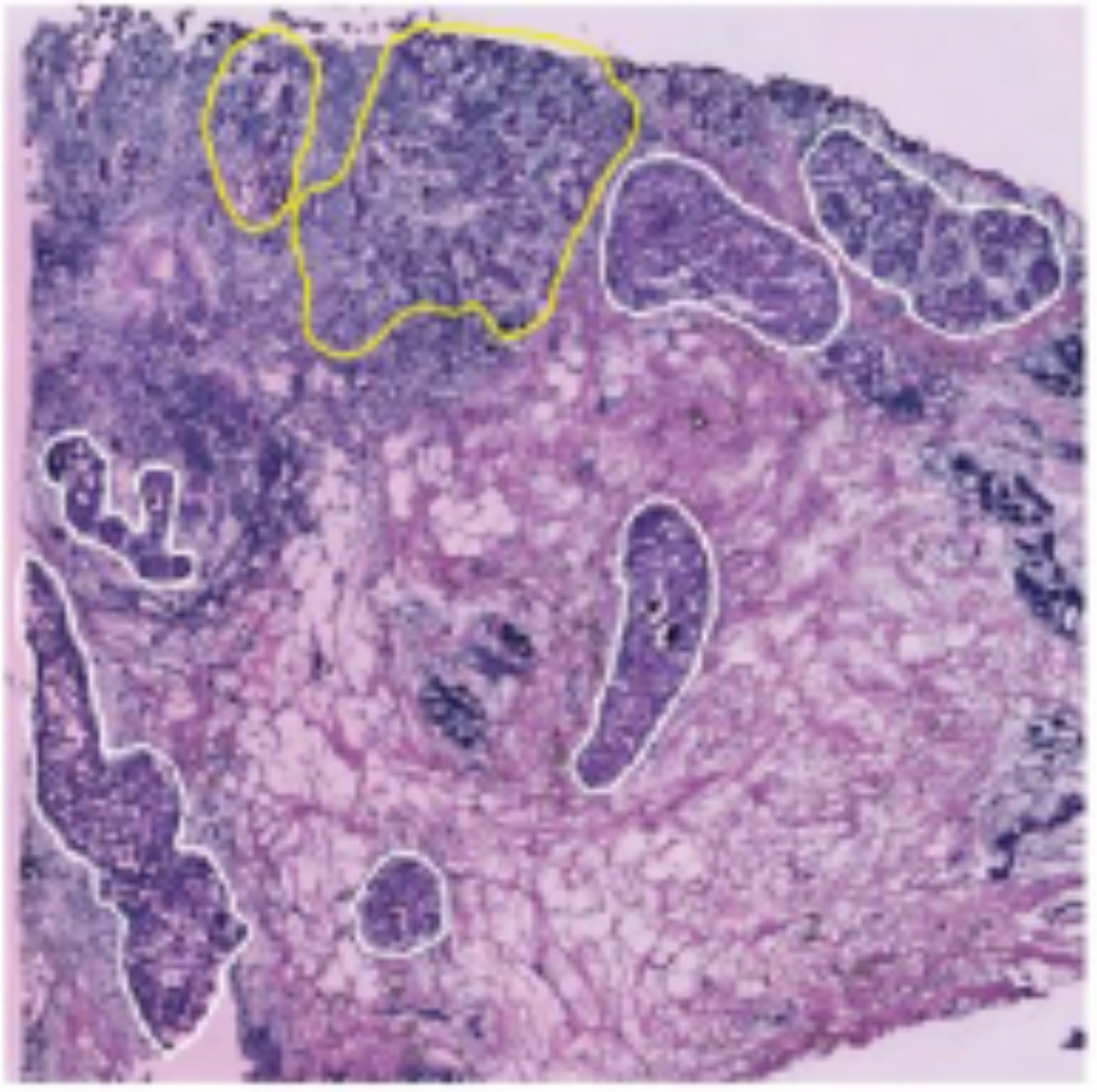
	chr	end	start	peak_intensity	x	y
26	chr3	5027016	5026505	4.87089987...	-16.95555...	-20.22317.
27	chr3	5027804	5027264	4.79005547...	-15.96221...	-20.38275.
28	chr3	5058836	5057743	4.06550913...	-29.73126...	-18.92818.
29	chr3	5121954	5121471	3.4065460...	-12.510781...	-14.179771
30	chr3	5122810	5122272	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.

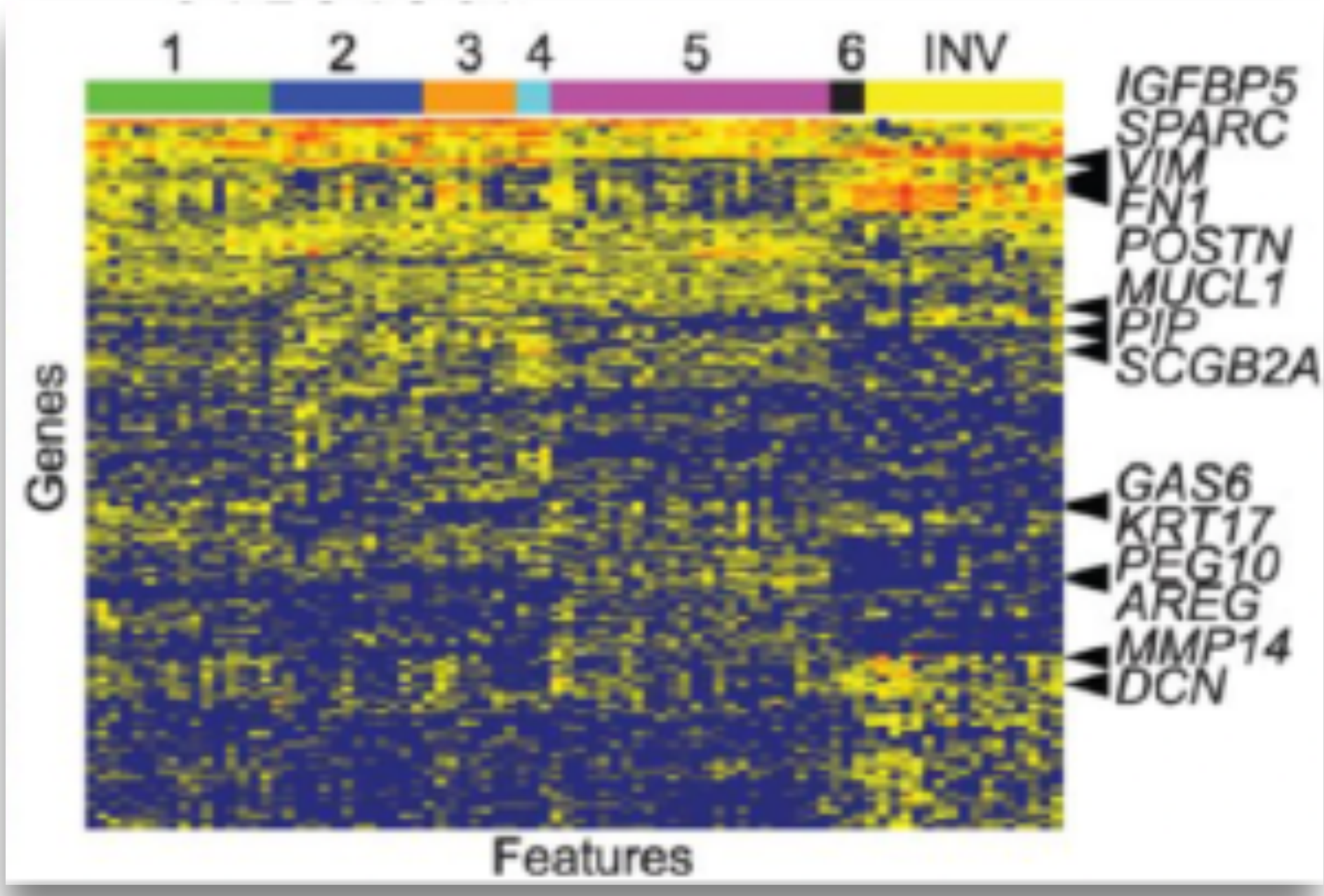



Open Data
Export Data/Subsets
Link Data
IPython Terminal
Open Session
Export Session
Add/edit arithmetic attributes
Selection Mode:
Preferences
View Error Console
Data Collection
Data
13co
c18o
12co
Orion_A_H_3x3[PRIMARY]
megeath_tom_fix[J_AJ_144_192_table4]
Subsets
Disks
Protostars
Protostars_at_HighAK
Highest AK Protostar
Plot Layers - 1D Profile
Highest AK Protostar (12co)
Protostars_at_HighAK (12co)
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
opacity
linewidth
1
Plot Options - 1D Profile
General
Limits
Axes
function
Maximum
reference
13co
x axis
Velocity
normalize
Tab 1
Tab 3
Declination
Right Ascension
2D Scatter
3.6minus4.5
4.5minus5.8
2D Scatter
3.6minus5.8
4.5minus8
2D Scatter
Kminus3.6
3.6minus4.5
3D Volume Rendering
3D Scatter
WorldWideTelescope (WWT)
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




1
2
3
4
5
6
INV
IGFBP5
SPARC
VIM
FN1
POSTN
MUCL1
PIP
SCGB2A
GAS6
KRT17
PEG10
AREG
MMP14
DCN
Genes
Features

Jupyter, JupyterLab options

GUI and/or command line, python

all linked

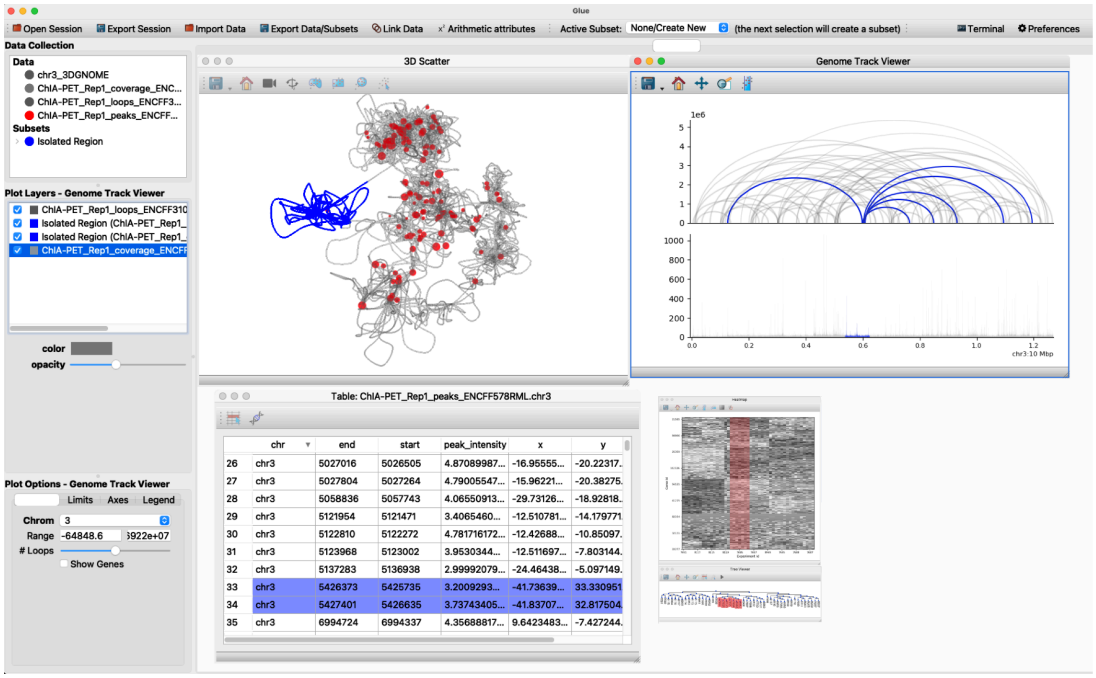
as many views as a user would like at once,

extensible via iPython terminal and plug-in

architecture for plot types, data types, analysis tools,

and external web tools

free, open source


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
1e6
chr3:1.0 Mbp
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...
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35 chr3 6994724 6994337 4.35688817... 9.6423483... -7.427244...