Glue

Open Session | Export Session | Import Data | Export Data/Subsets | Link Data | x² 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_ENCF

color

opacity

Plot Options - Genome Track Viewer

Limits | Axes | Legend

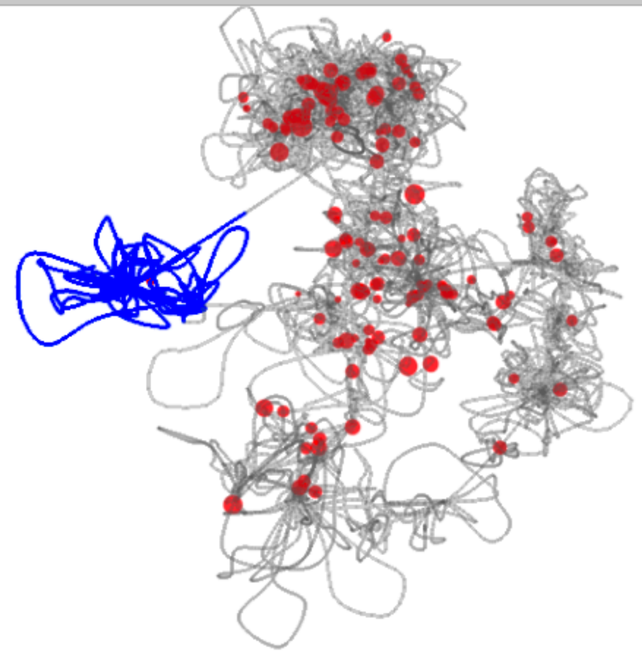
Chrom 3

Range -64848.6 5922e+07

Loops

Show Genes

3D Scatter



Genome Track Viewer

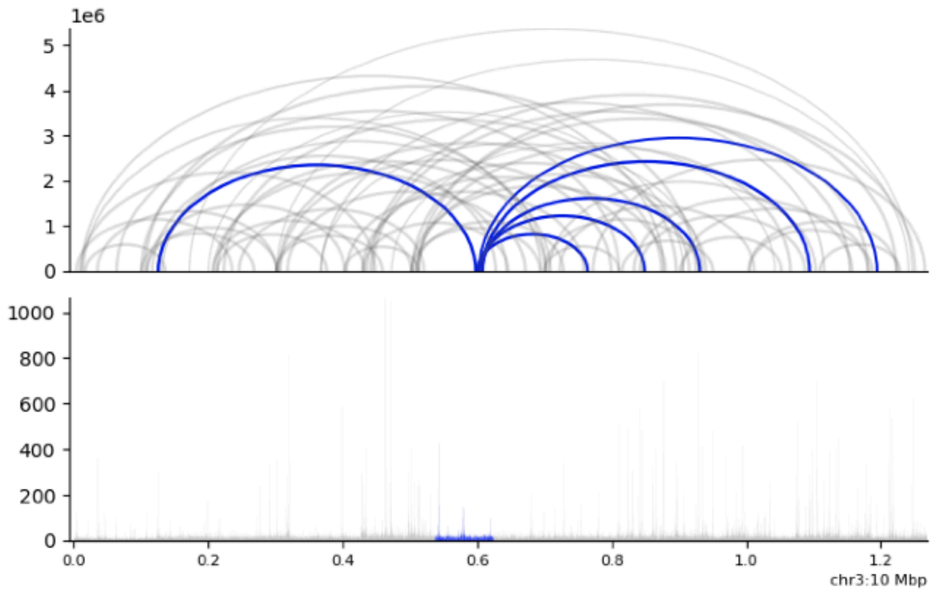
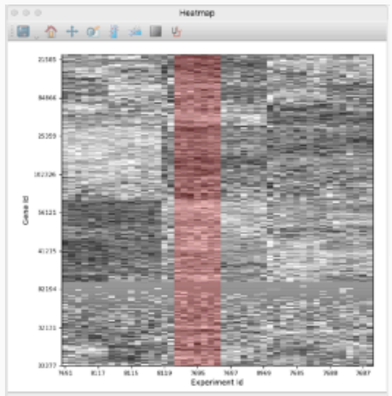
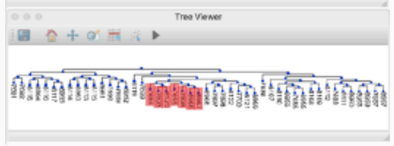
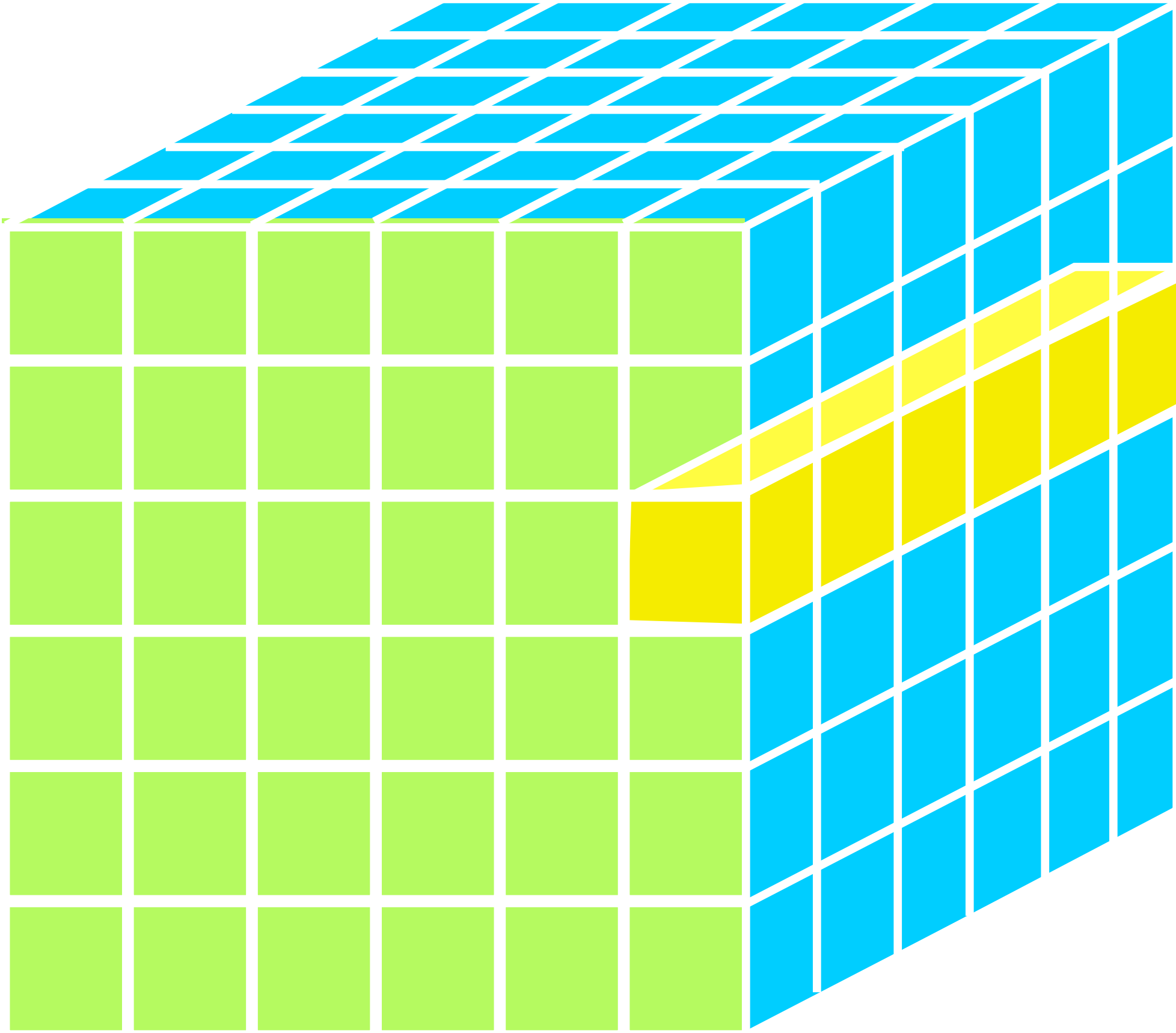


Table: ChIA-PET_Rep1_peaks_ENCFF578RML.chr3

	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.



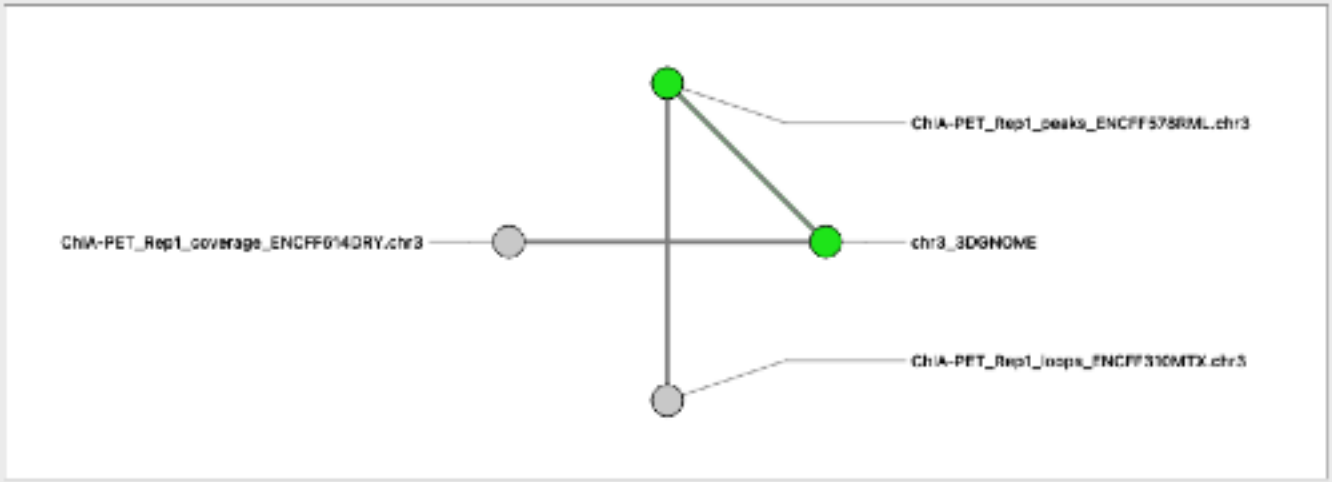




“High-dimensional Data”: Genomics

Link Editor

Click on two datasets to set up links or click on an existing connection to edit links. Selected datasets are shown in green. When one dataset is selected, the colors show directly and indirectly linked (blue) and inaccessible (red) datasets.



Dataset 1

ChIA-PET_I

Main compo
chr
end
start
ucol3
ucol4
ucol5
ucol6

≠

Dataset 2

chr3_3DGN

Main compo
chr
cx
cy
cz
genome_pos
Coordinate c
Pixel Axis 0

Links between Dataset 1 and Dataset 2

identity(start <-> genome_position)
identity(chr <-> chr)

Link details

Link conceptually identical components

Dataset 1 attributes

x chr

Dataset 2 attributes

y chr

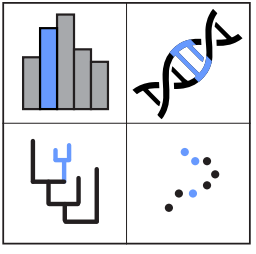
Glue attributes

Create advanced link

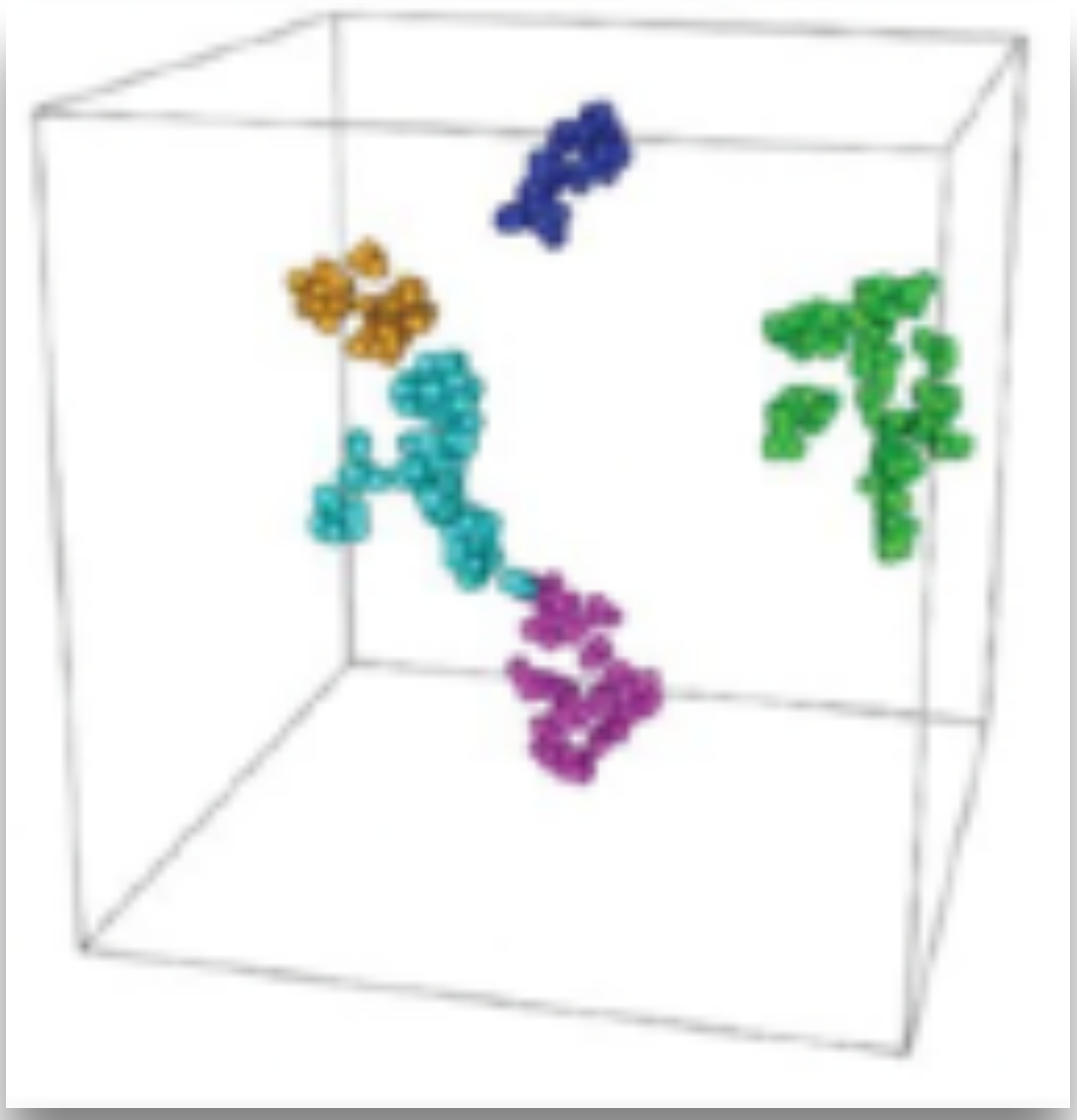
Remove link

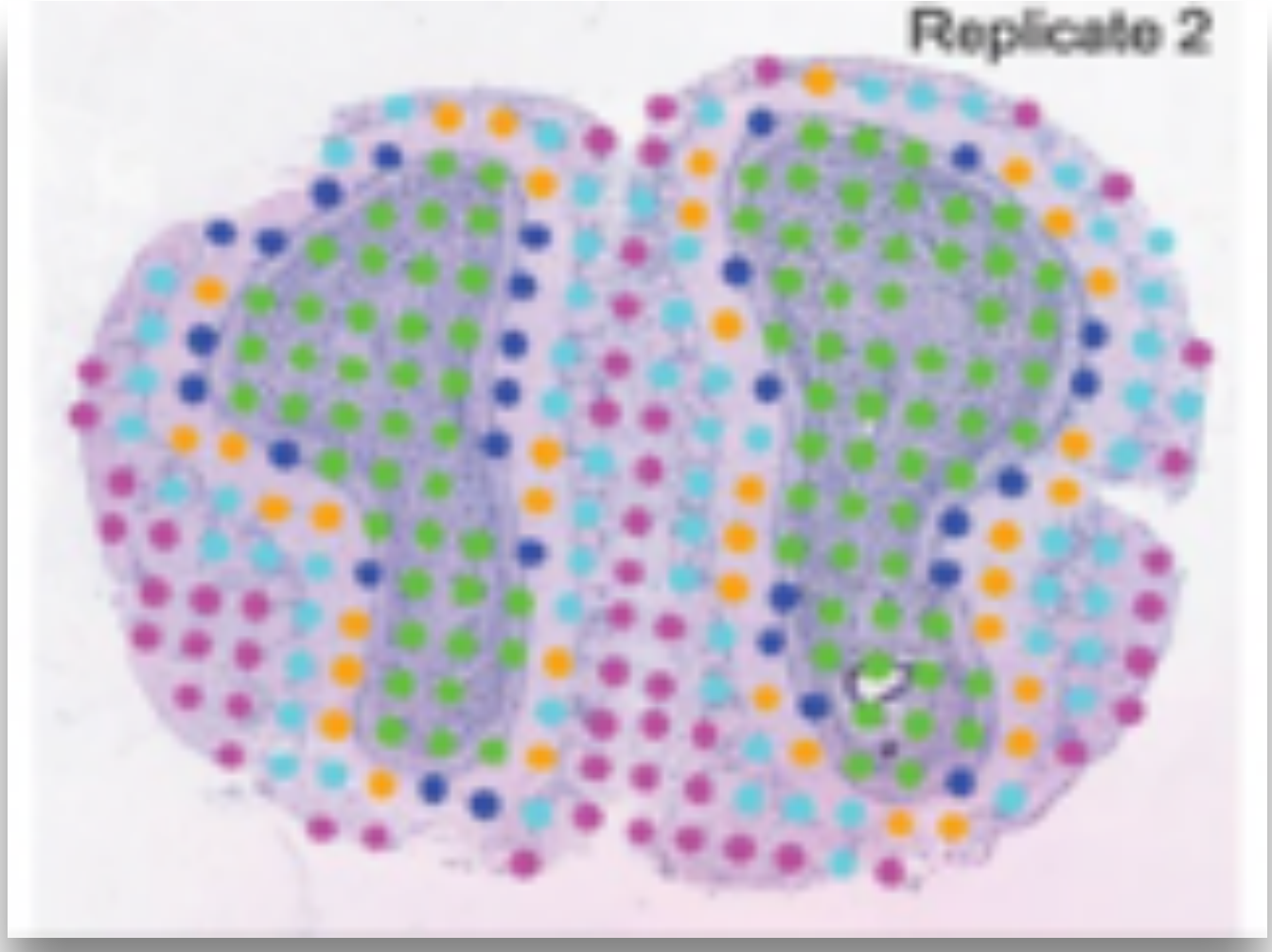
Cancel

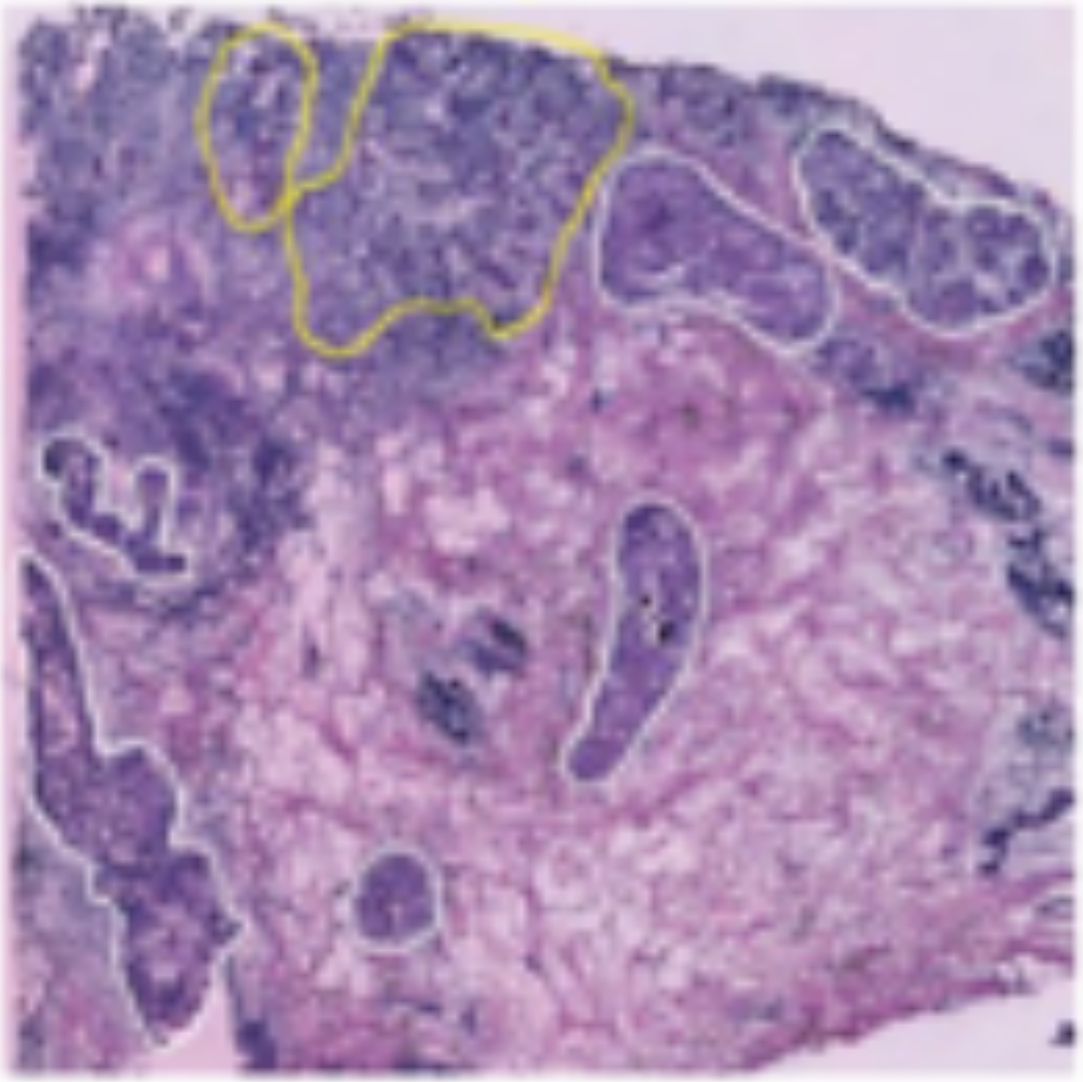
OK

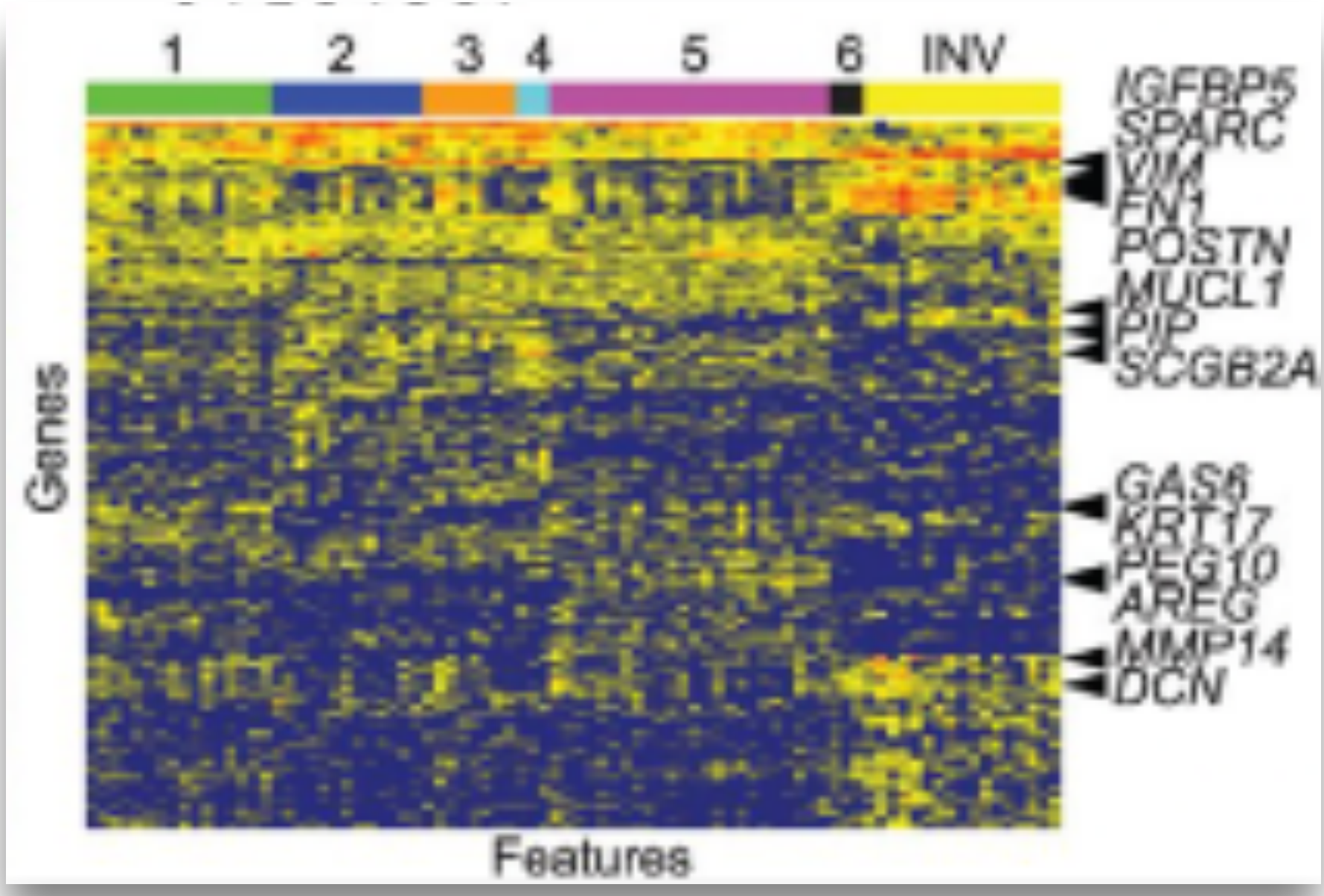


gluegenes




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

Ståhl PL, Salmén F, Vickovic S, Lundmark A, Navarro JF, Magnusson J, Giacomello S, Asp M, Westholm JO, Huss M, Mollbrink A, Linnarsson S, Codeluppi S, Borg Å, Pontén F, Costea PI, Sahlén P, Mulder J,

Bergmann O, Lundeberg J, Frisén J (2016) Visualization and analysis of gene expression in tissue sections by spatial transcriptomics. *Science*, 353(6294):78–82. https://doi.org/10.1126/science.aaf2403

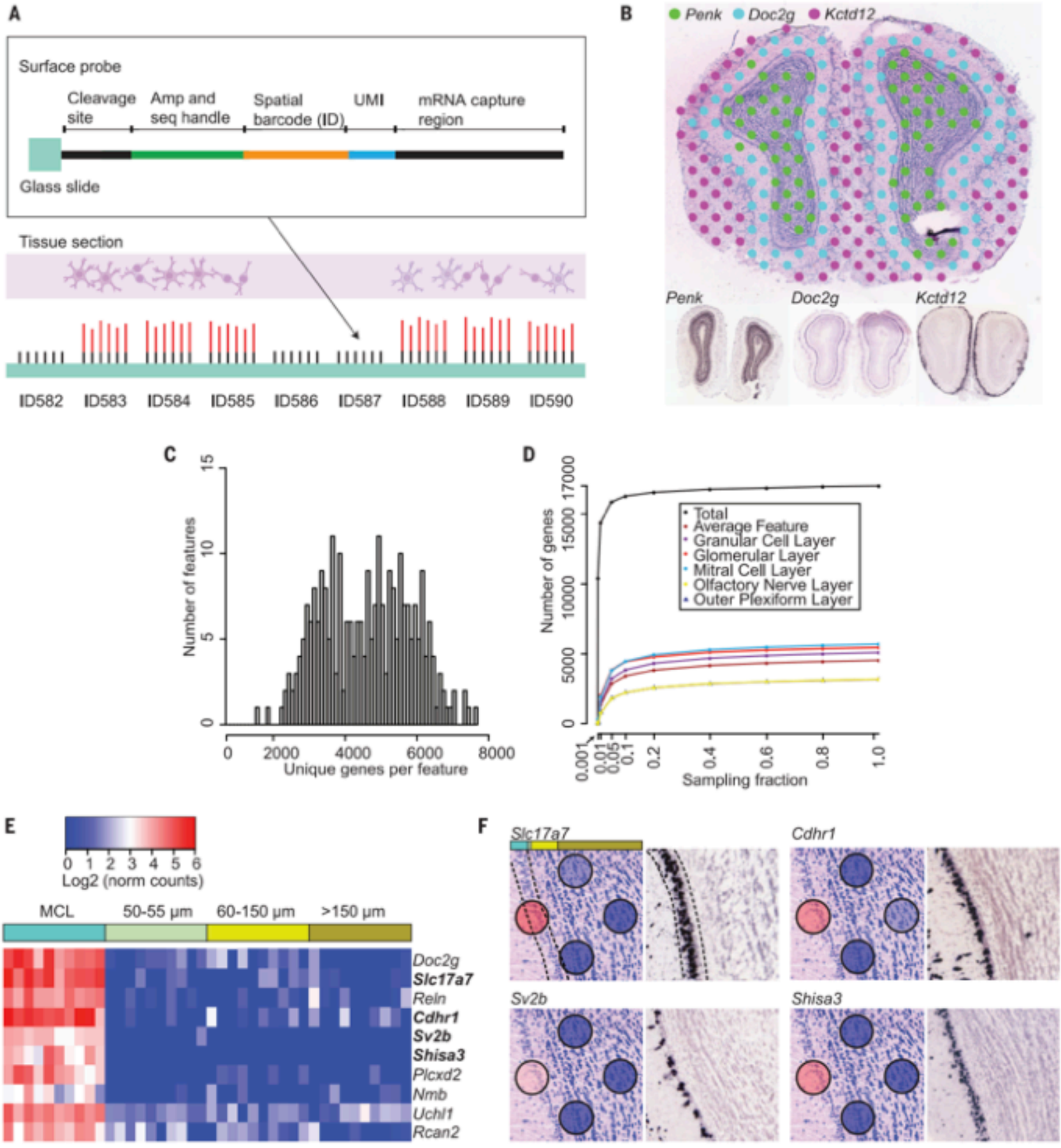


Fig. 2. Spatially resolved gene expression. (**A**) Each array feature contains unique DNA-barcoded probes containing a cleavage site, a T7 amplification and sequencing handle, a spatial barcode, a unique molecular identifier (UMI), and an oligo(dT) VN-capture region, where V is anything but T and where N is any nucleotide. cDNA (red) is generated from captured mRNA by reverse transcription. (**B**) Visualization of the expression of three genes by spatial transcriptomics (top) and in situ hybridization (bottom). *Penk* and *Kctd12* in situ images are from the Allen Institute. Cutoff normalized counts, *Penk*, 8; *Doc2g*, 13; and *Kctd12*, 19. (**C**) Distribution of unique genes per feature under the tissue. (**D**) Number of genes detected for different layers and entire tissue over sequencing depth. (**E**) Lateral diffusion of transcripts from genes enriched in MCL. The genes are expressed in MCL features but are not separable from the background in features adjacent to the MCL. (**F**) Spatial expression and in situ hybridization of four genes in (E). The leftmost feature overlaps the MCL, and the three rightmost features are situated in the GCL. The colored bar depicts the distances from feature center in (E).

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.

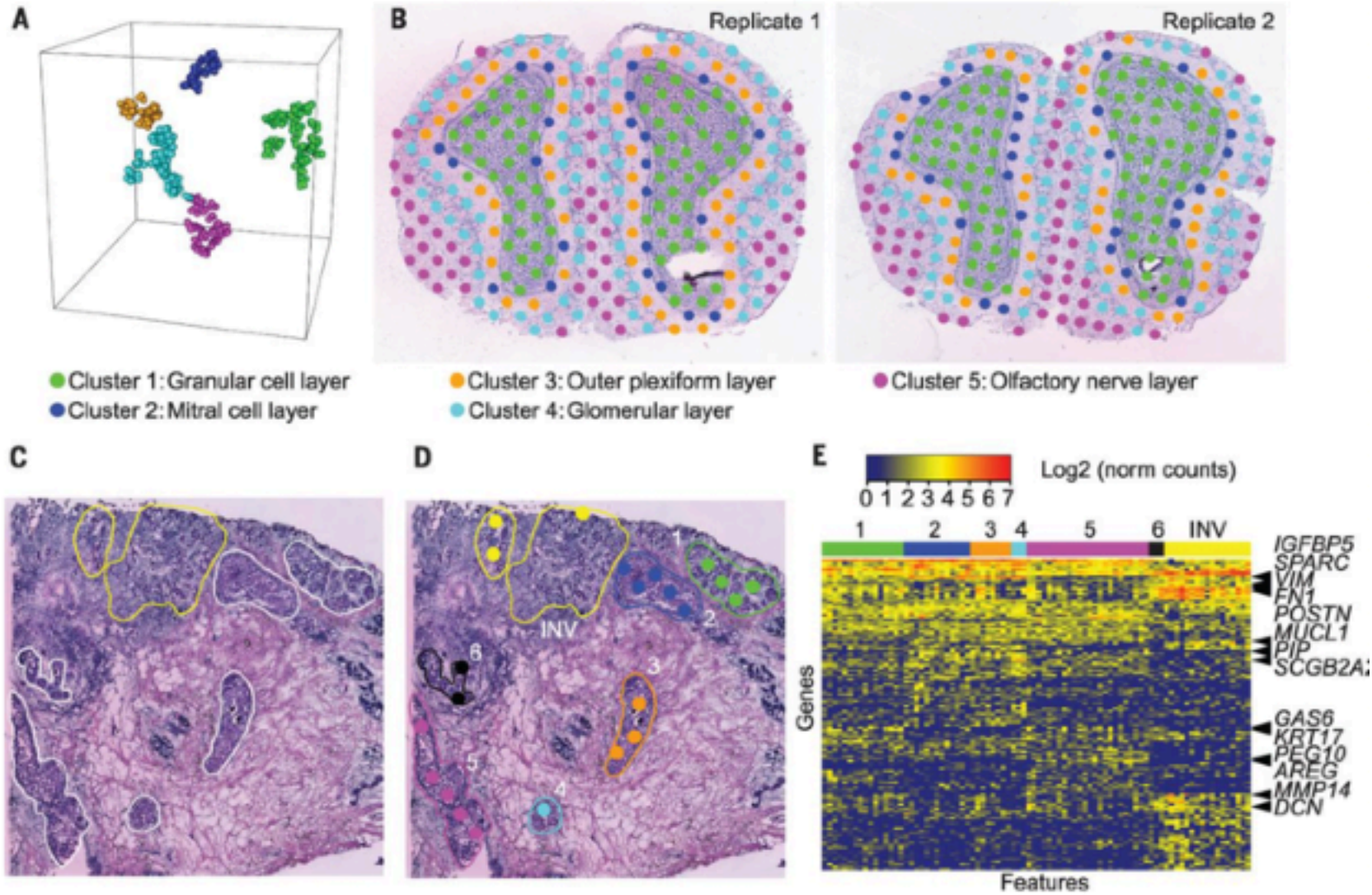


Fig. 4 Comparative analyses of tissue domains. (**A**) t-SNE analysis and hierarchical clustering of 551 features from two replicates creates five distinct clusters. (**B**) The features placed back onto the two tissue images. (**C** and **D**) Histological section of a breast cancer biopsy (C) containing invasive ductal cancer (INV) and six separate areas of ductal cancer in situ (1 to 6), with analyzed spatial transcriptomics features in (D). INV areas without, or with minimal, stromal infiltration were selected. (**E**) Gene expression heat map over the different areas in four adjacent sections (D) and (fig. S11).

“High-dimensional Data”: Genomics

Transcriptomics

Spatial