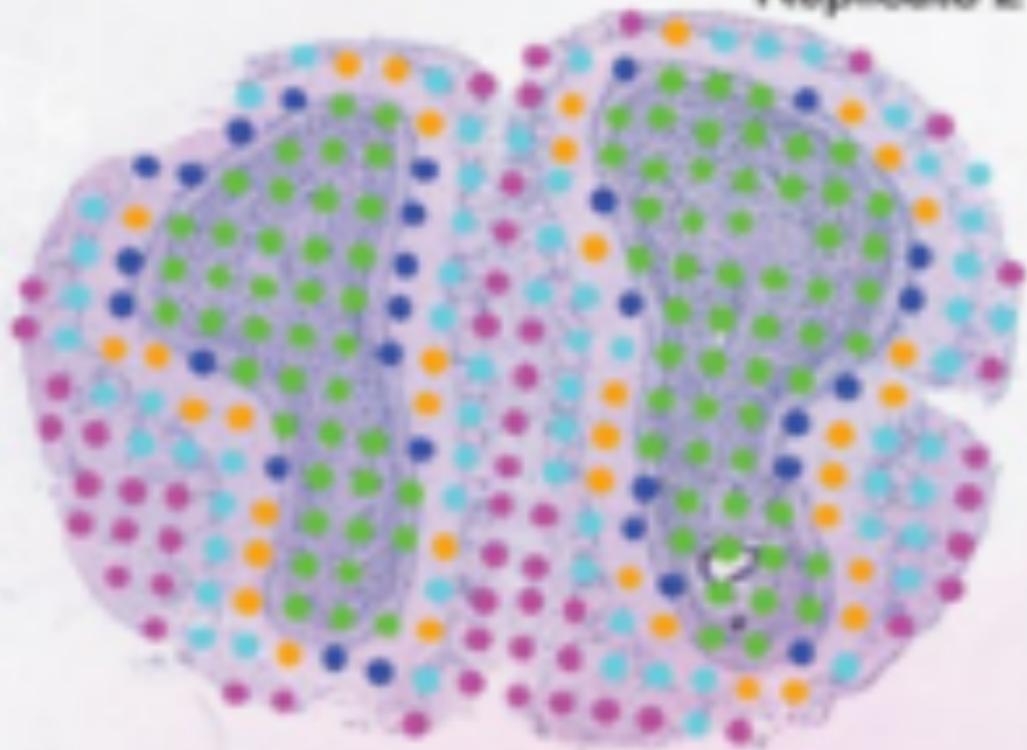
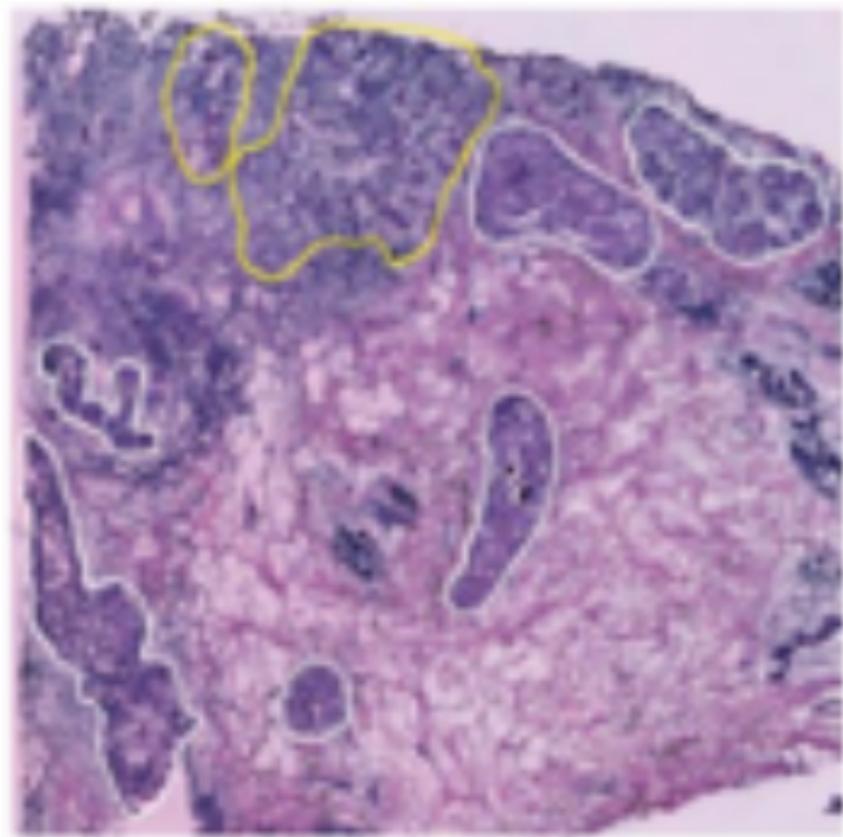
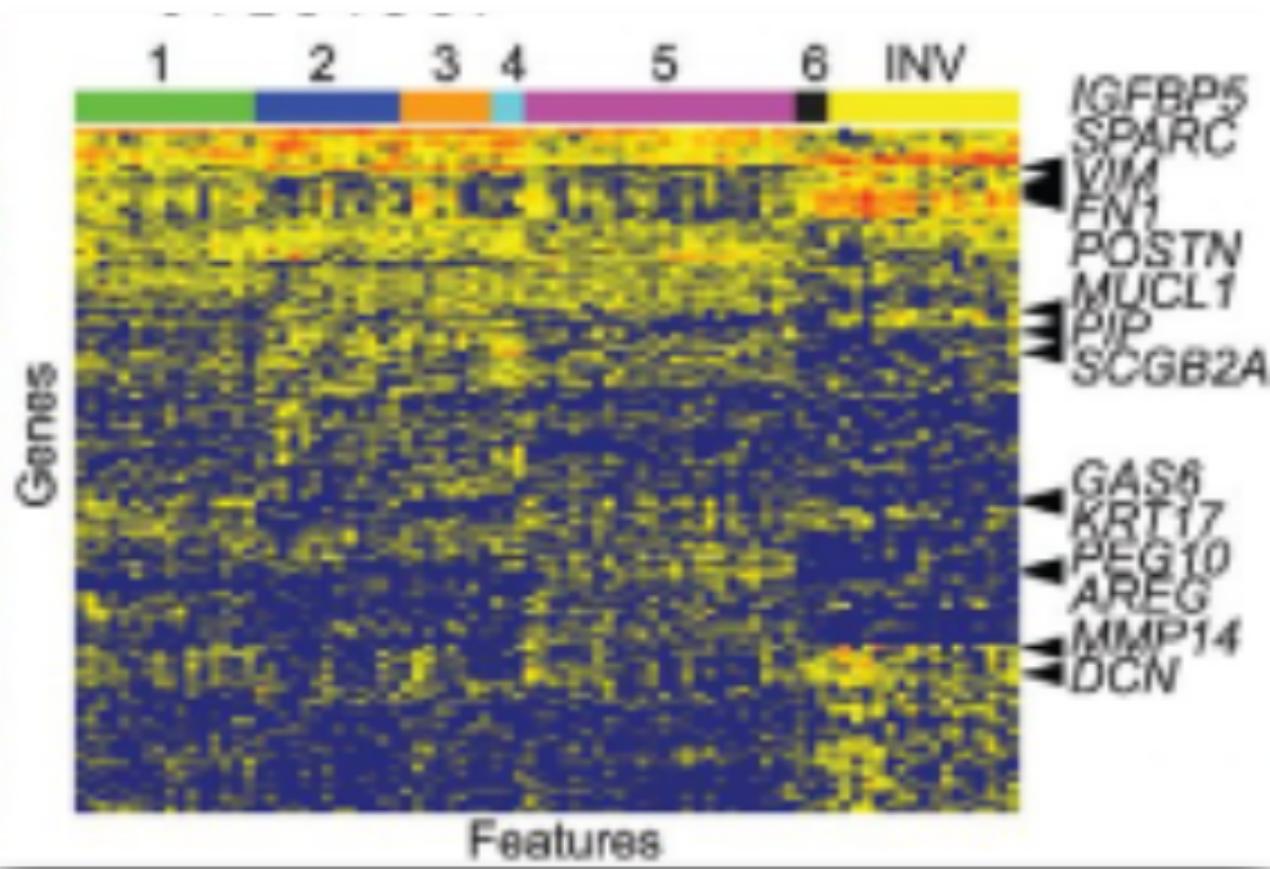


Replicate 2







Ståhl PL, Salmén F, Vickovic S, Lundmark JF, Huss M, Molibrick Å, Giacomello S, Pontén F, Sahlgren A, Codeluppi S, Borghén P, Linnarsson S, Costea PI, Westermark J, Bergmann O, Lundberg J, Frisén J (2016) Visualisation and analysis of gene expression in tissue sections by spatial transcriptomics. *Science*, 353(6294):78–82. <https://doi.org/10.1126/science.aaf2403>

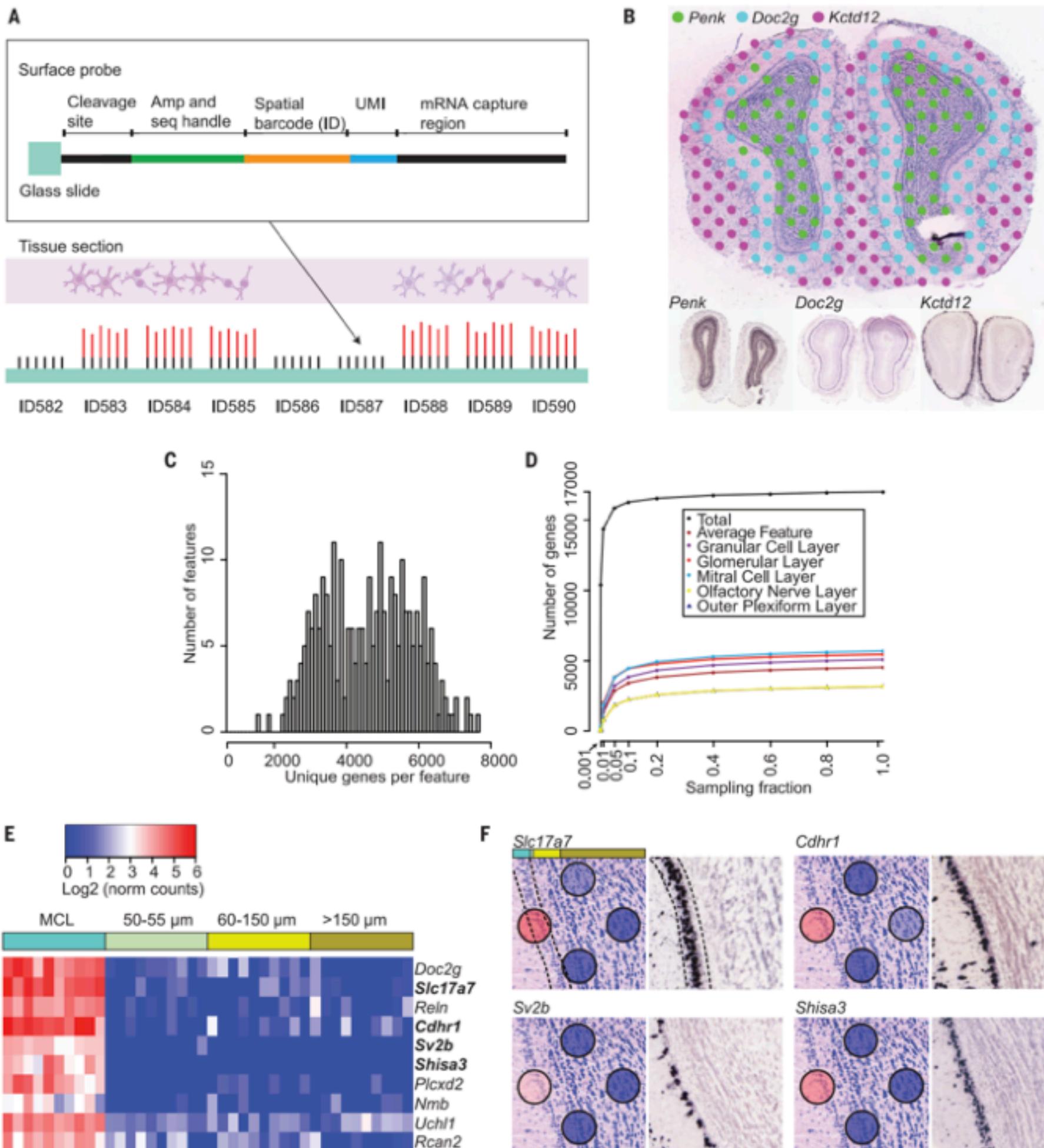


Fig. 2. Spatially resolved gene expression. (A) Each array feature contains unique DNA-barcoded probes containing a cleavage site, a T7 amplification and sequencing handle, a spatial barcode, a unique molecular identifier (UMI), and an oligo(dT) VN-capture region, where V is anything but T and where 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).

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

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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.

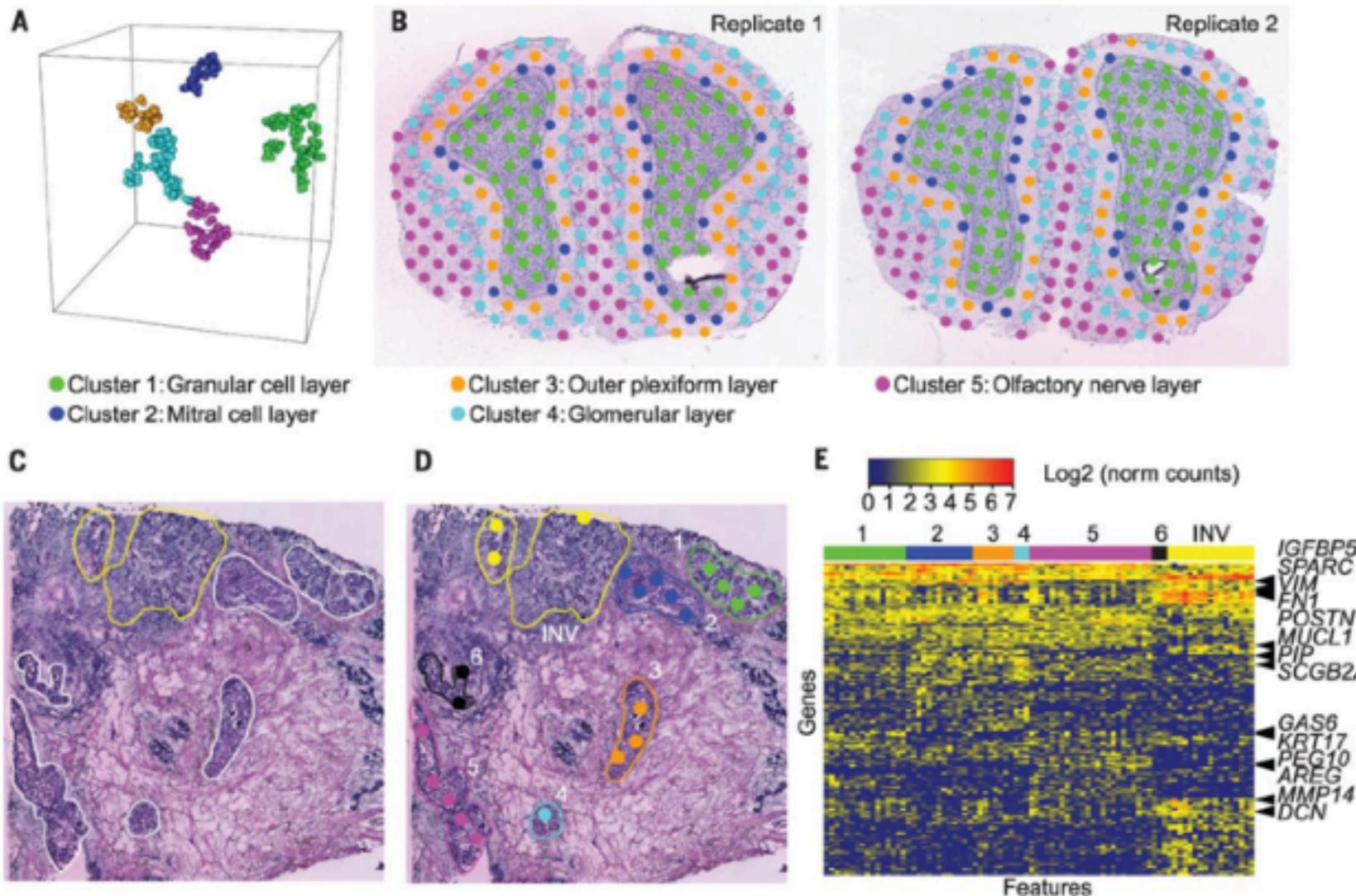


Fig. 4 Comparative analyses of tissue domains. (A) t-SNE analysis and hierarchical clustering of 551 features from two replicates creates five distinct clusters. (B) The features placed back onto the two tissue images. (C and D) Histological section of a breast cancer biopsy (C) containing invasive ductal 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

Spatial Transcriptomics

Data Collection

- Data**
- chr3_3DGNAME
 - 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

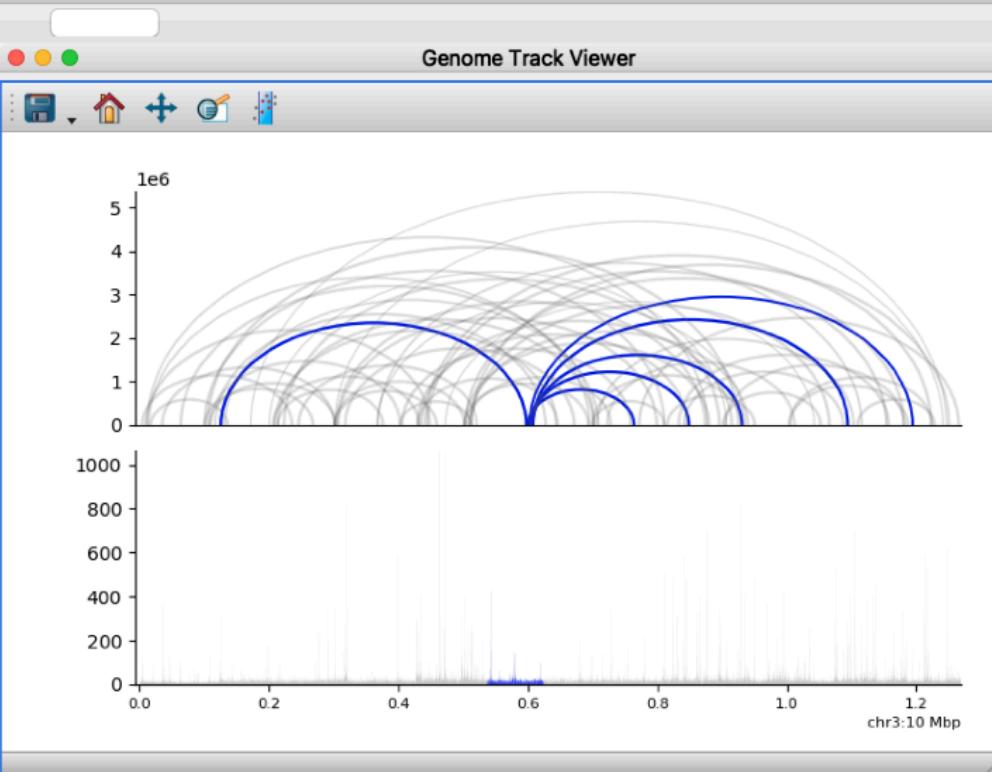
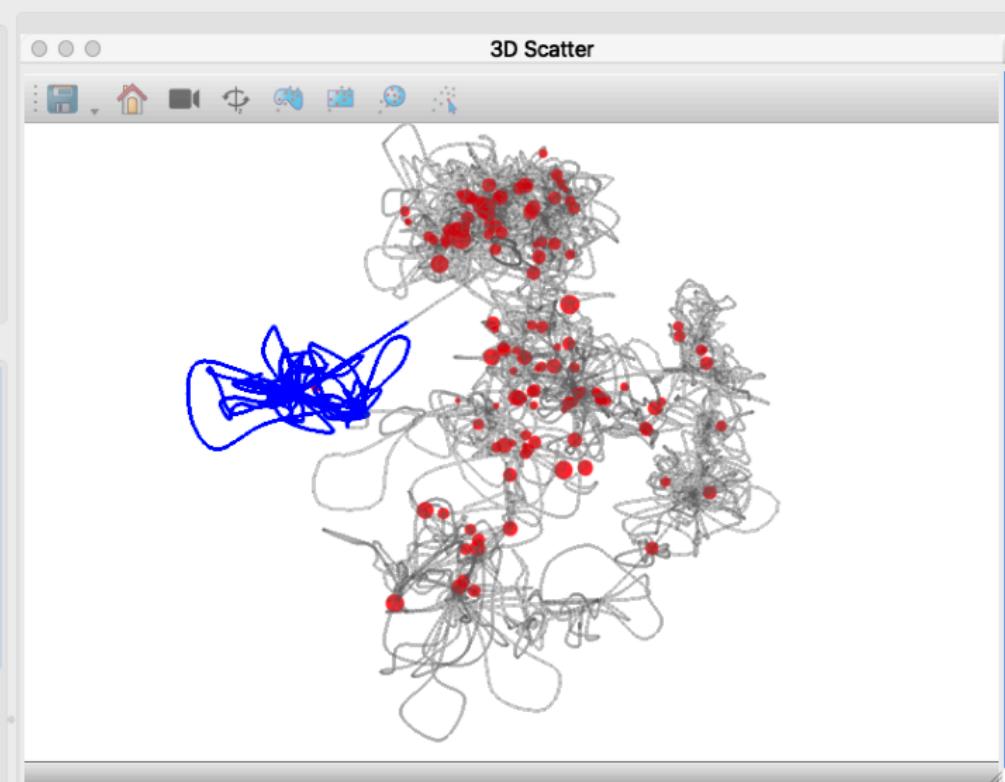
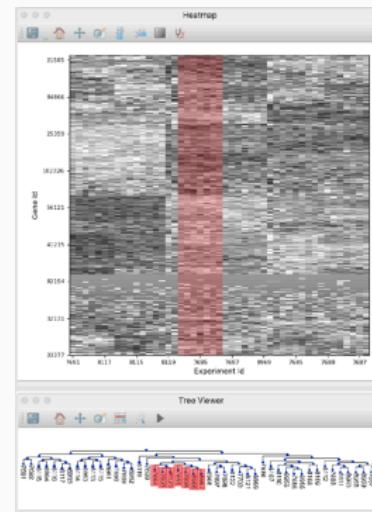
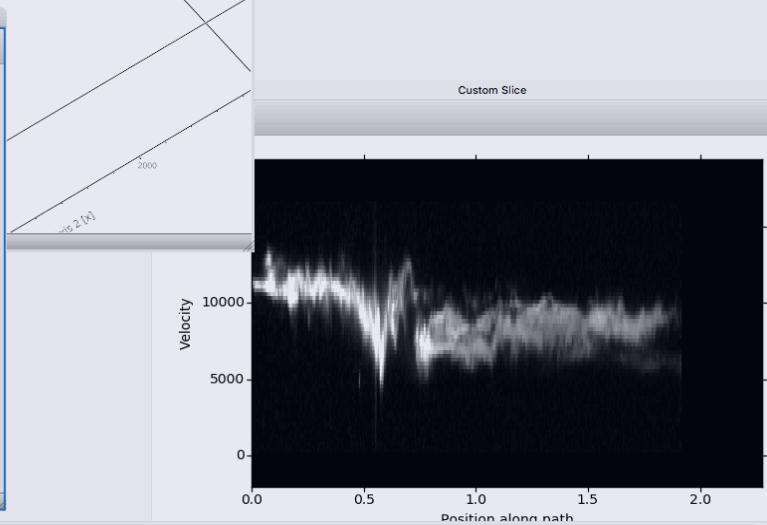
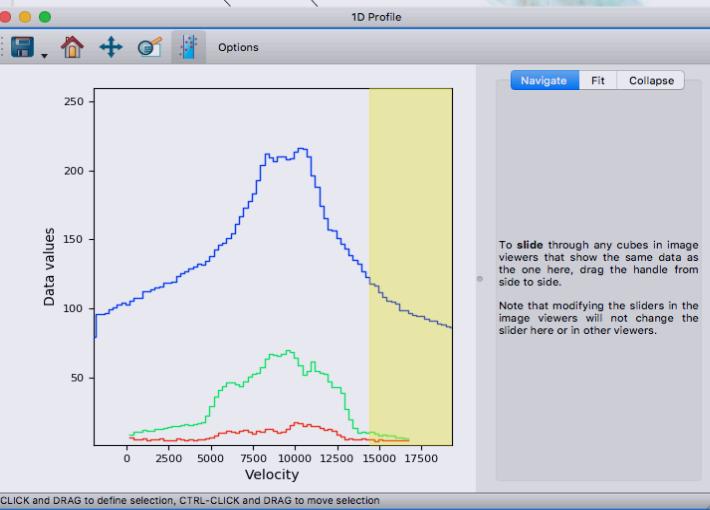
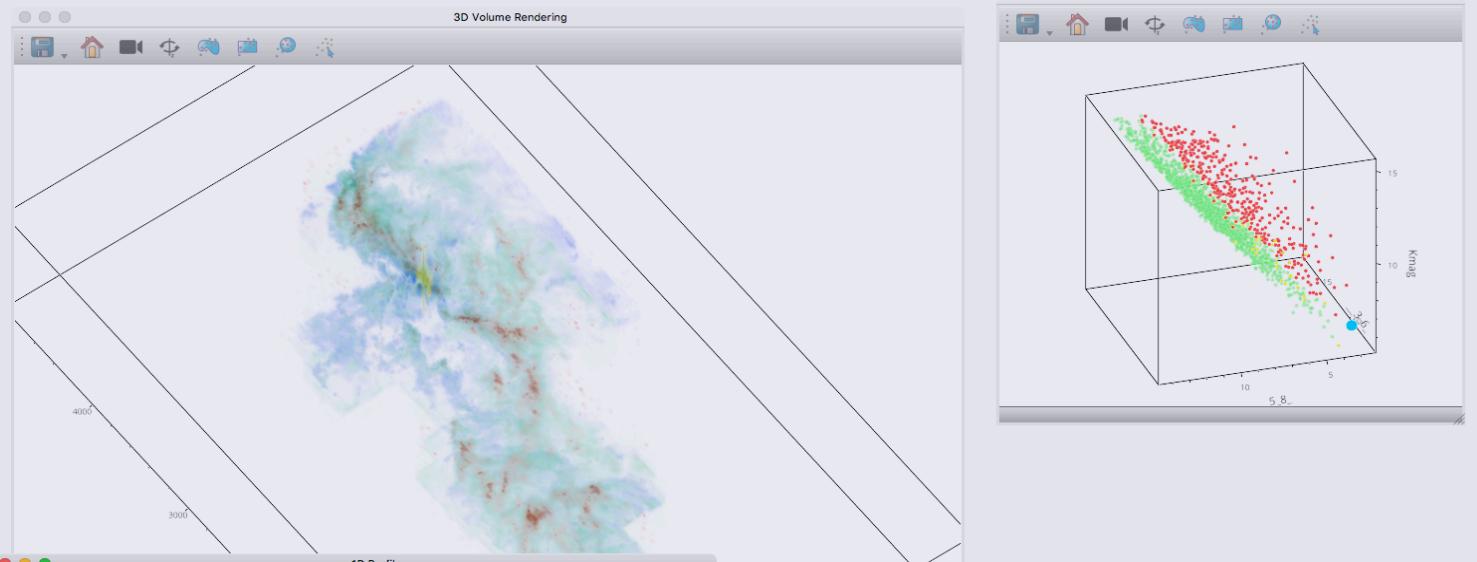
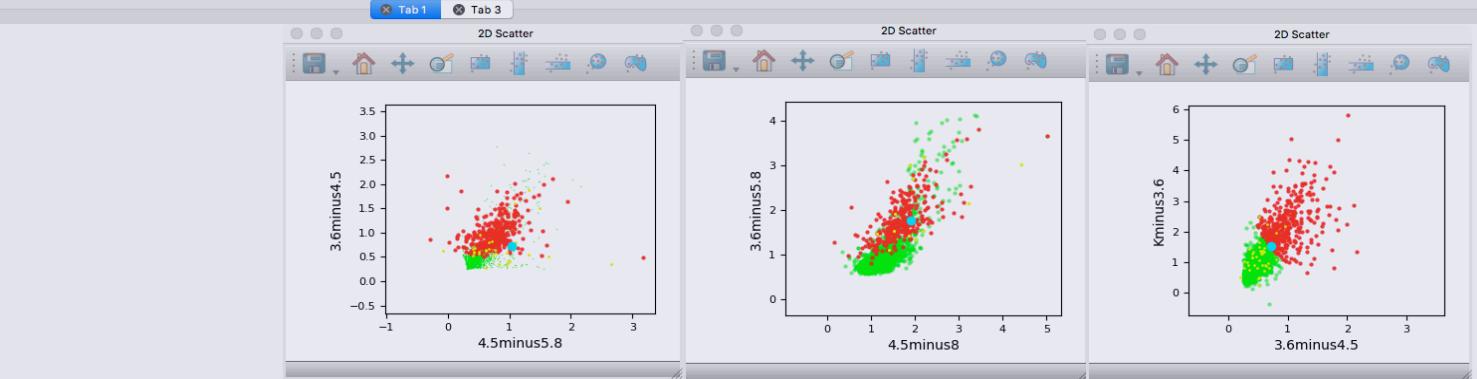
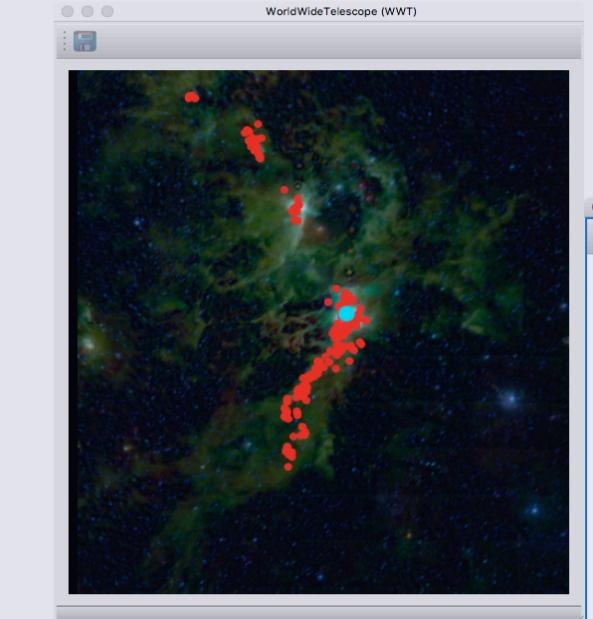
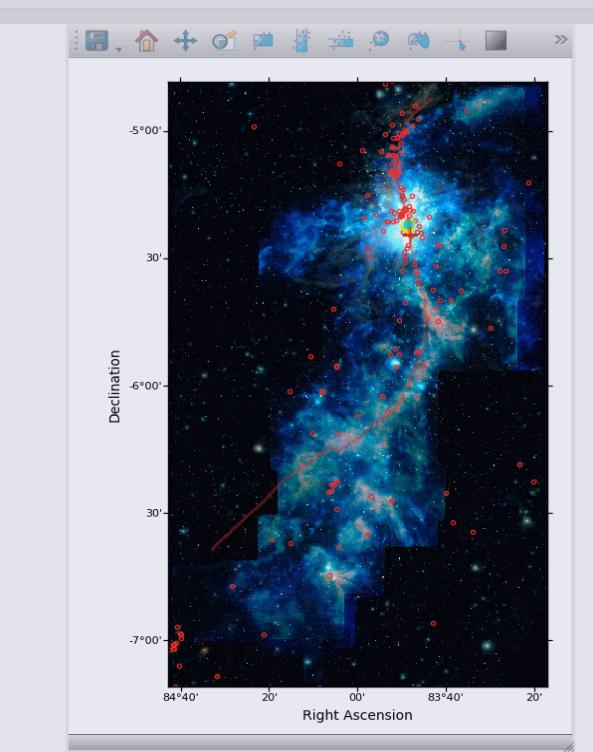
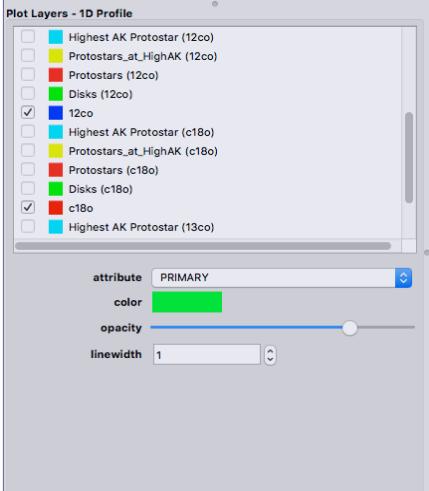
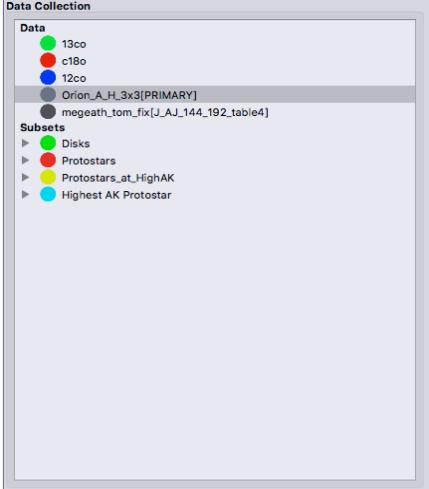
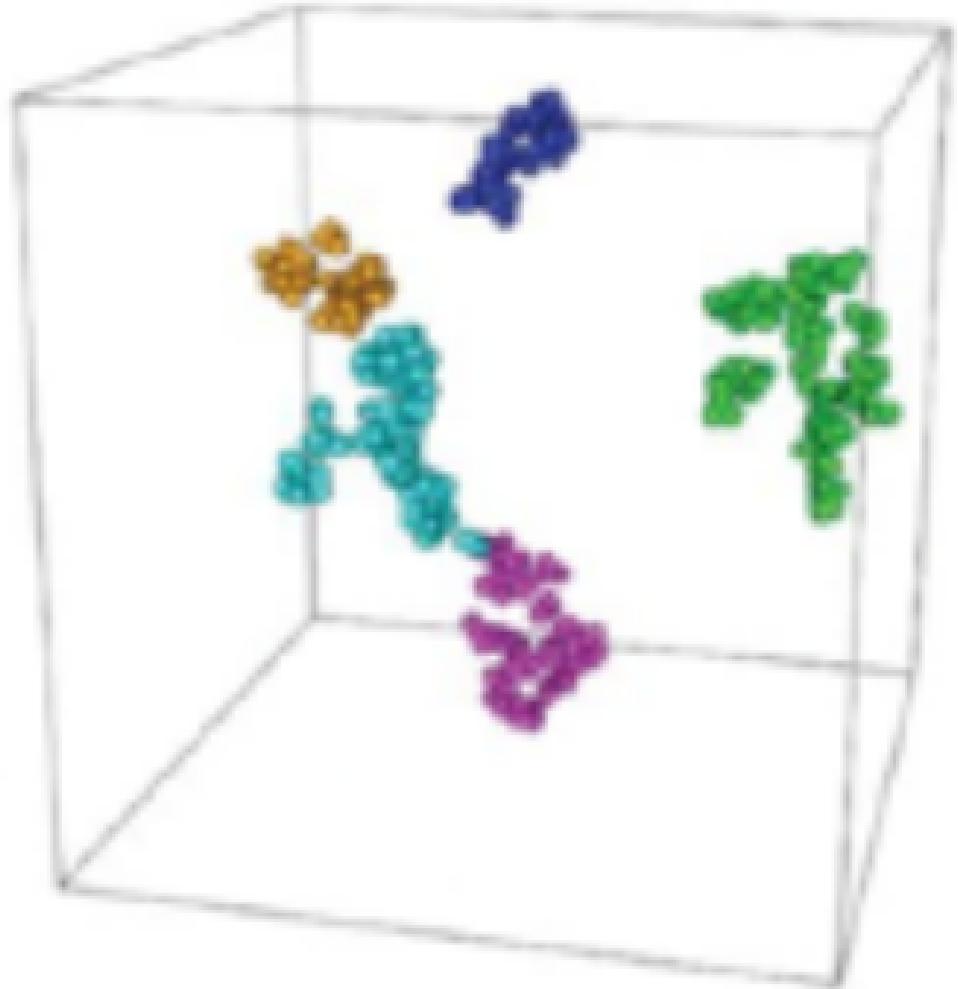


Table: ChIA-PET_Rep1_peaks_ENCFF578RML.chr3

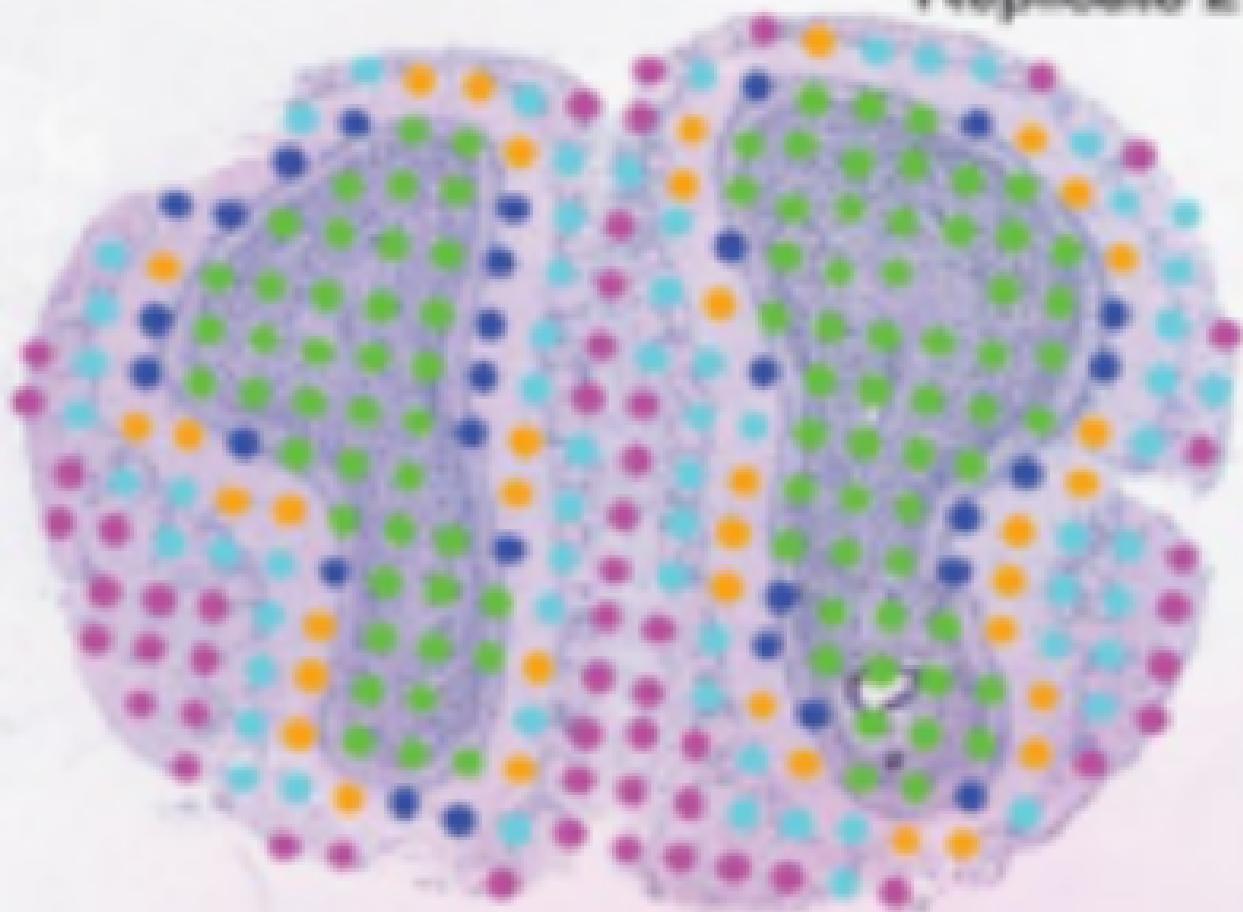
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27	chr3	5027804	5027264	4.79005547...	-15.96221...	-20.38275...
28	chr3	5058836	5057743	4.06550913...	-29.73126...	-18.92818...
29	chr3	5121954	5121471	3.4065460...	-12.510781...	-14.179771...
30	chr3	5122810	5122272	4.781716172...	-12.42688...	-10.85097...
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...

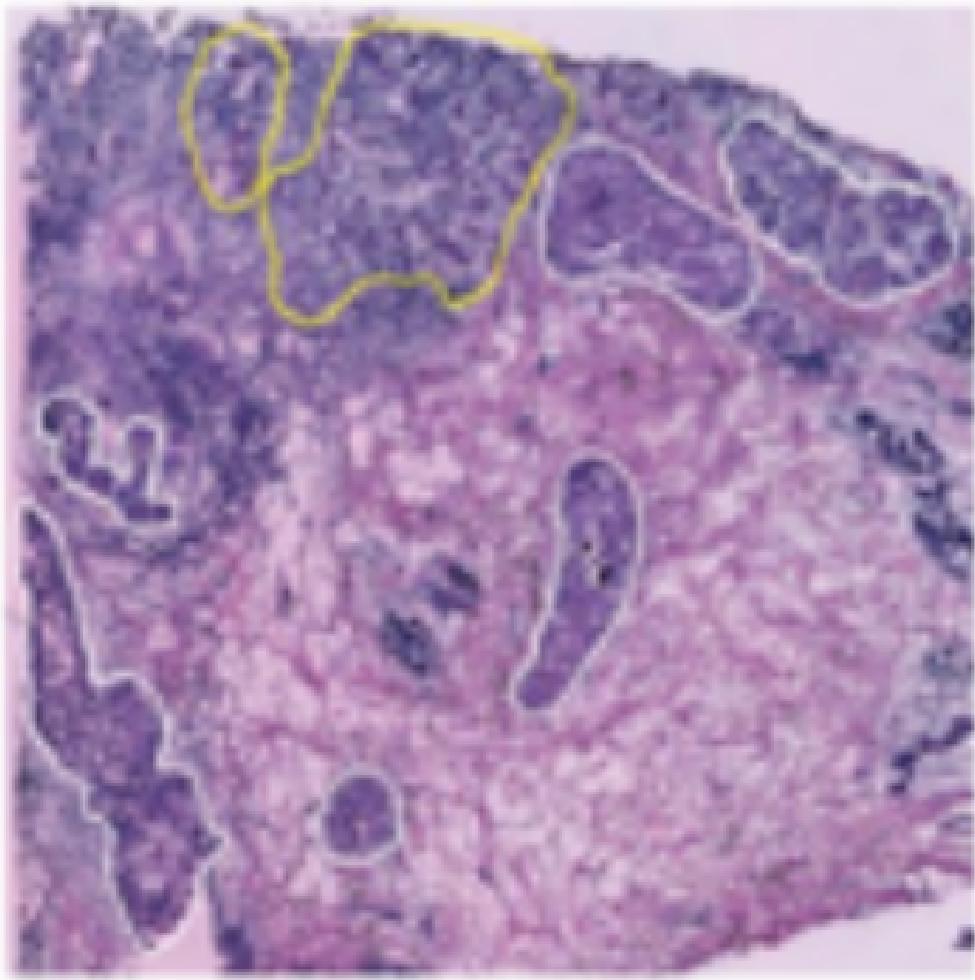




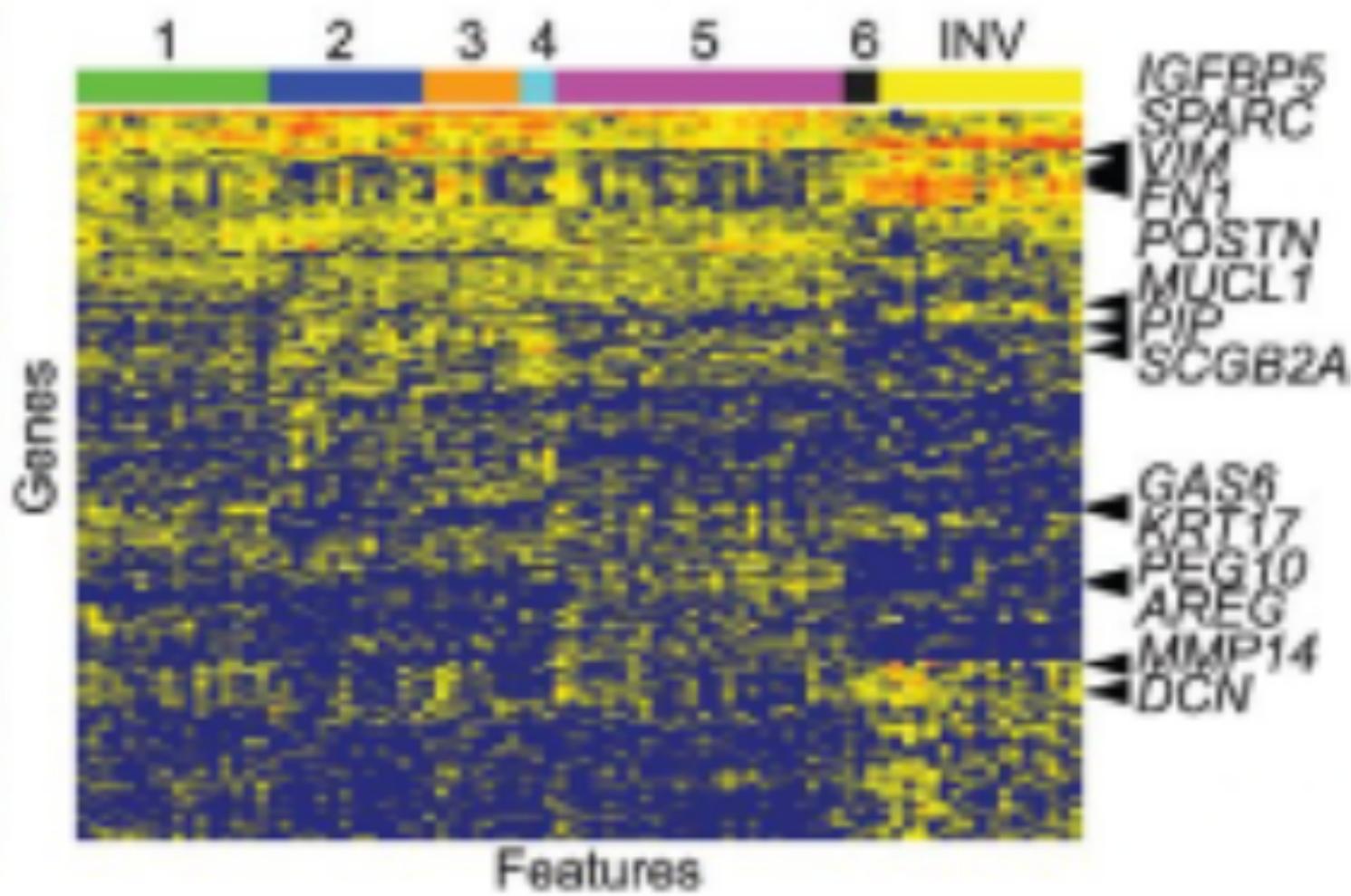


Replicate 2









<https://doi.org/10.1126/science.1253629> (2016) **353**(6294):78–82. *Sectional analysis of spatial transcriptomics reveals gene expression gradients in the developing mouse brain*

spatial

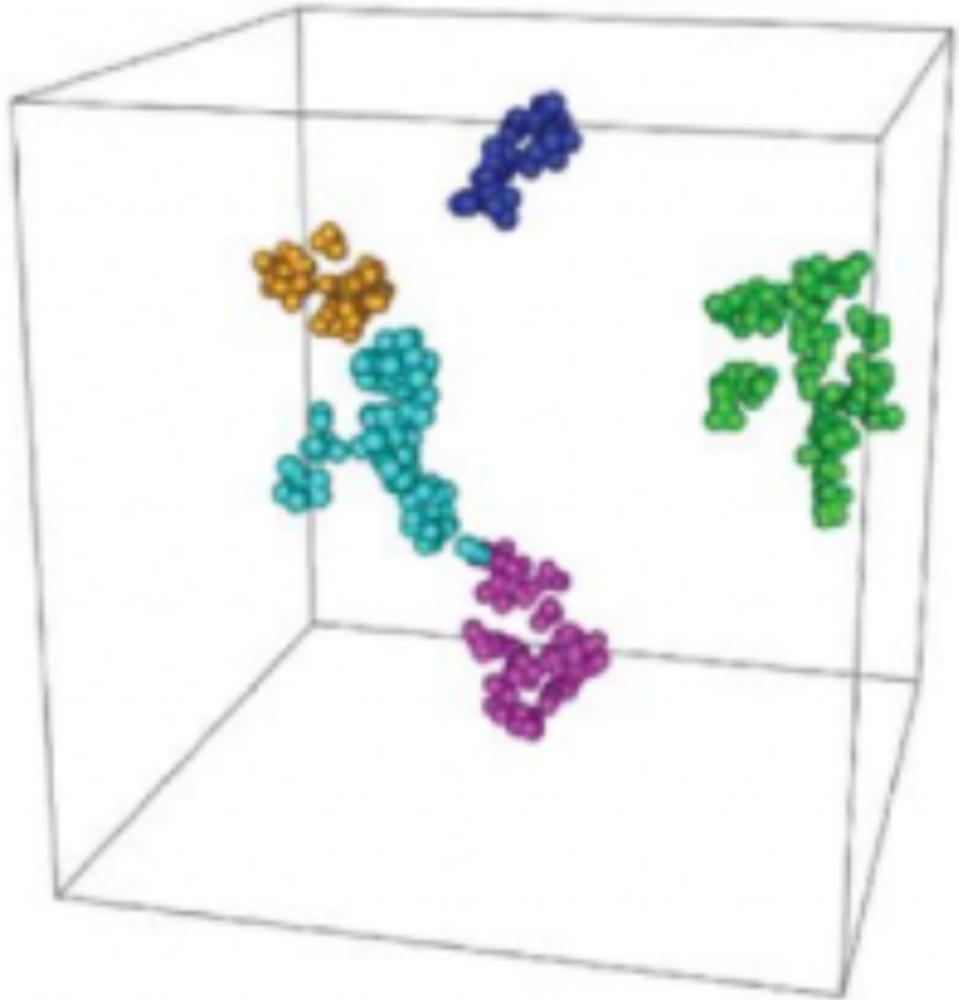
Transcripción













Replicate 2

