

Spatial transcriptomics database



DeepSpaceDB v.2.0
<https://deepspace-db.com>

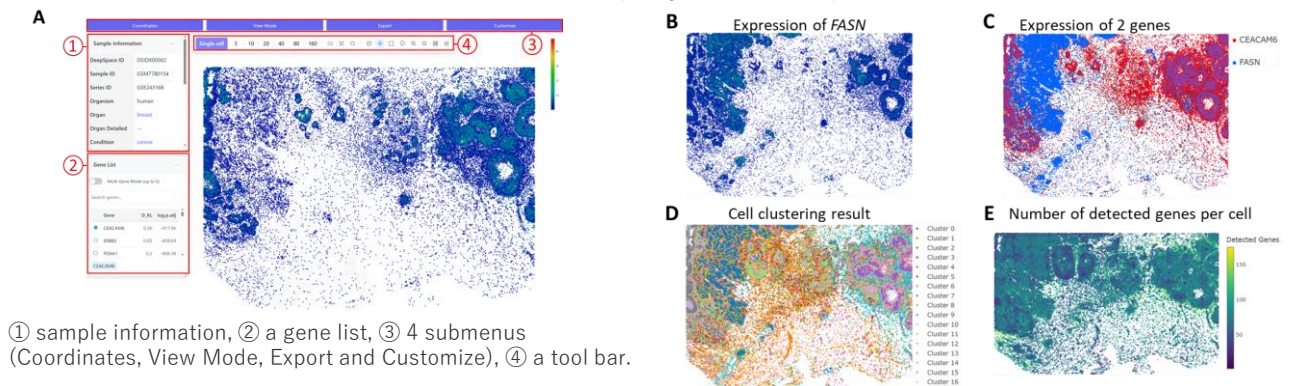


DeepSpaceDB enables easy browsing of spatial transcriptomics data from various tissues and facilitates straightforward, interactive analysis online—even for non-bioinformatics experts. It collects spatial transcriptomics data published in NCBI GEO and similar repositories, primarily focusing on data acquired using 10X Genomics' Visium and Xenium platforms. Nearly all data is included, excluding samples identified as problematic during data quality assessment.

DeepSpaceDB meticulously examines sample metadata such as tissue origin and disease state, standardizes notation and ontologies, and enables various analysis tools. These include: displaying the spatial expression distribution of any gene, visualizing pathways with spatially variable expression, showing the spatial distribution of cell types predicted from expressed genes, and comparing gene expression between arbitrarily selected areas. Additionally, users can upload their own data to undergo the same normalization processing and quality assessment metric calculations as data stored in DeepSpaceDB, obtaining results such as dimensionality reduction, clustering, and identification of Spatially Variable Genes (SVGs) or activated pathways. Uploaded data can be compared with sample data within DeepSpaceDB. For example, users can perform comparative analysis using healthy samples as a reference or compare against samples under similar conditions. Uploaded data is assigned a unique URL for sharing with collaborators but is not incorporated into DeepSpaceDB's public data and remains invisible to other users. Uploaded data is automatically deleted after a set retention period on the server, though users can delete it at any time.

By utilizing DeepSpaceDB together with other analytical tools, it becomes possible to reveal which types of neurons exist in which regions of brain tissue sections, identify which cells in the complex internal structure of kidney tissue are abnormal in kidney disease, or determine where and what types of immune cells are infiltrating in breast cancer tumor samples.

Xenium Interface (Sample: DSIDX00002)



① sample information, ② a gene list, ③ 4 submenus (Coordinates, View Mode, Export and Customize), ④ a tool bar.

< Number of Samples in DeepSpaceDB > (As of Jan 16, 2026)

Species	Visium (V1)	Visium (V2)	Xenium
Human	1,020 samples	341 samples	432 samples
Mouse	648 samples	135 samples	187 samples
Other	0 samples	0 Samples	9 Samples

DeepSpaceDB was supported from 2022 to 2025 under JST Database Integration Coordination Program (DICP), "Development of a database for spatial genomics data analysis (Principal Investigator: VANDENBON Alexis, Associate Professor, Institute for Life and Medical Sciences, Kyoto University)".

1. Honcharuk V et al. DeepSpaceDB: a spatial transcriptomics atlas for interactive in-depth analysis of tissues and tissue microenvironments. NAR 2025. (doi: <https://doi.org/10.1093/nar/gkaf1117>)
2. Honcharuk Vet al. DeepSpaceDB 2.0: an interactive spatial transcriptomics database for large-scale Xenium data exploration. bioRxiv 2026 (doi: <https://doi.org/10.64898/2026.01.15.699623>)

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1. Selecting a Sample to View

In the “Database” tab, narrow down your search by organism name, organ, etc., then select the sample you wish to view from the list. If you know the sample number, you can also search for it directly using the search box.

2. Displaying Data Quality Evaluation Results

The “Quality of this sample tab” allows you to evaluate the data quality of the selected sample. Selecting options like detected genes, read count, or Mito from the “Select quality measure” dropdown menu lets you view each parameter for individual spots.

3. Displaying Sample Image Annotations Predicted by LLMs

In the “Image annotation” tab, check “Show LLM annotation” and hover your mouse cursor over the image to display annotations predicted by a large language model (LLM) for each grid, along with information about anatomical structures and conditions.

4. Displaying cell type clustering results

The “Spot clustering” tab displays clustering results for cell types based on detected genes, color-coded for visualization.

5. Displaying Genes with Spatially Variable Genes (SVGs)

The “Spatially Variable Genes” tab displays a list of genes predicted to exhibit spatially distinctive expression (SVGs) within samples identified by the singleCellHaystack function. Genes with high scores show clearly distinct spatial expression patterns. Clicking a gene in the list displays its expression levels at each spot in the specified sample, color-coded.

6. Display of biologically pathways showing spatially distinctive activity

The “Spatially Variable Pathways” tab displays a list of biological pathways predicted to exhibit spatially distinctive activity based on the SVG set. Clicking a pathway in the list displays the activity of the specified biological pathway at each spot in the sample, color-coded.

7. Display of predicted cell composition at each spot

The “Cell type compositions tab” displays the predicted cell composition for each spot. The image on the left, “Predicted cell type fractions,” shows clustering results based on the predicted cell composition. The image on the right, “Top predicted cell type,” displays the top cell type composition for each spot color-coded.

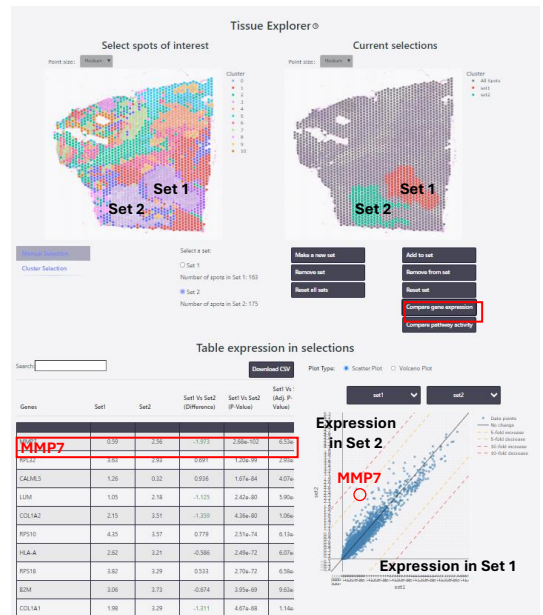
8. Displaying Genes with Different Expression Patterns or Biological Pathways with Different Activity Across Regions

The “Tissue Explorer” tab allows you to investigate genes or biological pathways with differing expression or activity levels across regions.

1) Selecting regions: Choose “Manual selection,” select Set 1 under “Select a set,” then drag your mouse to outline the region of interest in the “Select spots of interest” image on the left. Click “Add to set.” The selected region's spots will be highlighted in the “Current selections” image on the right. You can add multiple regions to Set 1 here. Next, select Set 2 under “Select a set” and similarly choose the regions you wish to compare.

2) Genes with Different Expression: Click “Compare gene expression” to display a list and scatter plot of genes with differing expression levels between the selected regions (Figure 1). In the scatter plot, hovering the mouse cursor over each spot reveals the gene name and the average expression value for each region.

3) Biological pathways with differing activity: Clicking “Compare pathway activity” displays a list and scatter plot of biological pathways with differing activity between the selected regions.



(Fig 1) Example of displaying Spatially Variable Genes (SVGs)

Analysis example using a breast cancer sample (DSID000277). Specify regions Set 1 and Set 2 in the upper-left image and execute Compare gene expression. The list and scatter plot of genes with differing expression levels between the selected regions are shown, indicating that MMP7 expression is higher in Set 2 than in Set 1.