

# Rを用いた空間解析の基礎 と 空間データベースの紹介

京都大学医生物学研究所 准教授

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空間トランスクリプトーム解析の基礎  
&  
DeepSpaceDBを含む公共データベースの  
特徴や利用方法

- 空間トランスクリプトーム・データの読み取り方や解析手法の概略を知りたい方
- 公共データベースの所在や特徴を知りたいといった方
- 公共の空間トランスクリプトームデータを比較・解析してみたい方
- Rの経験がある方が望ましいです

# 自己紹介



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バンデンボン アレクシス

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略歴 (1981年9月生まれ・ベルギー出身)

2005年

来日

2006年～2009年

東京大学 新領域創成科学研究科 博士課程

(指導教員：中井 謙太 教授)

2009年～2014年

大阪大学 免疫学フロンティア研究センター(iFReC) 特任研究員

2014年～2017年

大阪大学 免疫学フロンティア研究センター 特任助教

2017年～2022年

京都大学 医生物学研究所 講師

2022年～現在

京都大学 医生物学研究所 准教授

- Rを使った空間トランスクリプトミクスデータ解析
  - Visium example
  - Other platforms
- 既存の空間トランスクリプトミクスデータベースの紹介
- DeepSpaceDBの紹介
  - Visium interface
  - Xenium interface
- まとめ



# The R Seurat package

<https://satijalab.org/seurat/>

[https://satijalab.org/seurat/articles/get\\_started\\_v5\\_new](https://satijalab.org/seurat/articles/get_started_v5_new)

Seurat 5.2.0 Install Get started Vignettes Extensions FAQ News Reference Archive

## Getting Started with Seurat

Source: vignettes/get\_started\_v5\_new.Rmd

We provide a series of vignettes, tutorials, and analysis walkthroughs to help users get started with Seurat. You can also check out our [Reference page](#) which contains a full list of functions available to users.

Our previous Get Started page for Seurat v4 is archived [here](#).

### Introductory Vignettes

For new users of Seurat, we suggest starting with a guided walk through of a dataset of 2,700 Peripheral Blood Mononuclear Cells (PBMCs) made publicly available by 10X Genomics. This tutorial implements the major components of a standard unsupervised clustering workflow including QC and data filtration, calculation of high-variance genes, dimensional reduction, graph-based clustering, and the identification of cluster markers. We provide additional vignettes introducing visualization techniques in Seurat, the SCTransform normalization workflow, and storage/interaction with multimodal datasets. We also provide an 'essential commands cheatsheet' as a quick reference.

Contents

- Introductory Vignettes
- scRNA Data Integration
- Multi-assay data
- Flexible analysis of massively scalable datasets
- Spatial analysis
- Other
- SeuratWrappers

or

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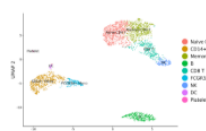
### Introductory Vignettes

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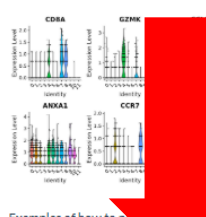
Guided tutorial — 2,700 PBMCs



A basic overview of Seurat that includes an introduction to common analytical workflows.

GO

SCTransform



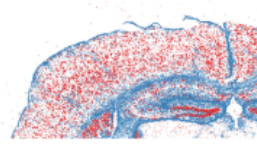
Examples of how to perform SCTransform normalization, feature selection, integration, and differential expression analysis with an updated version of SCTransform.

GO

## Spatial analysis

These vignettes will help introduce users to the analysis of spatial datasets in Seurat v5, including technologies that leverage sequencing-based readouts, as well as technologies that leverage in-situ imaging-based readouts. The vignettes introduce data from multiple platforms including 10x Visium, SLIDE-seq, Vizgen MERSCOPE, 10x Xenium, Nanostring CosMx, and Akoya CODEX.

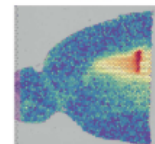
[Analysis of spatial datasets \(Imaging-based\)](#)



Learn to explore spatially-resolved data from multiplexed imaging technologies, including MERSCOPE, Xenium, CosMx SMI, and CODEX.

GO

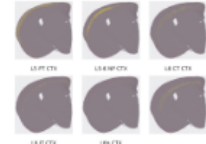
[Analysis of spatial datasets \(Sequencing-based\)](#)



Learn to explore spatially-resolved transcriptomic data with examples from 10x Visium and Slide-seq v2.

GO

[Analysis of Visium HD spatial datasets](#)



Learn to explore spatially-resolved transcriptomic data in high-definition from 10x Visium HD.

GO

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Seurat Object data access

Pseudobulk analysis

Multi-Assay features

Subsetting and merging

Visualization in Seurat

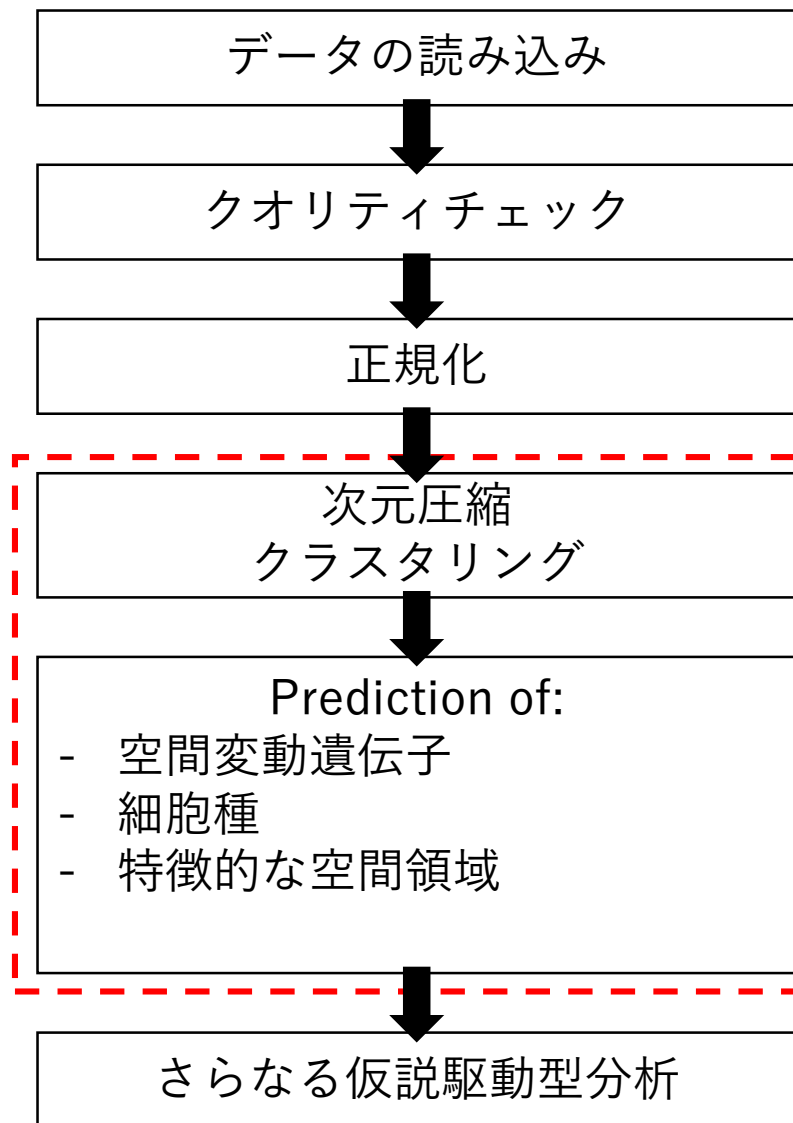
Reference list of commonly used commands to store, access, explore, and analyze datasets.

# ワークフローの概要



[https://satijalab.org/seurat/articles/spatial\\_vignette](https://satijalab.org/seurat/articles/spatial_vignette)

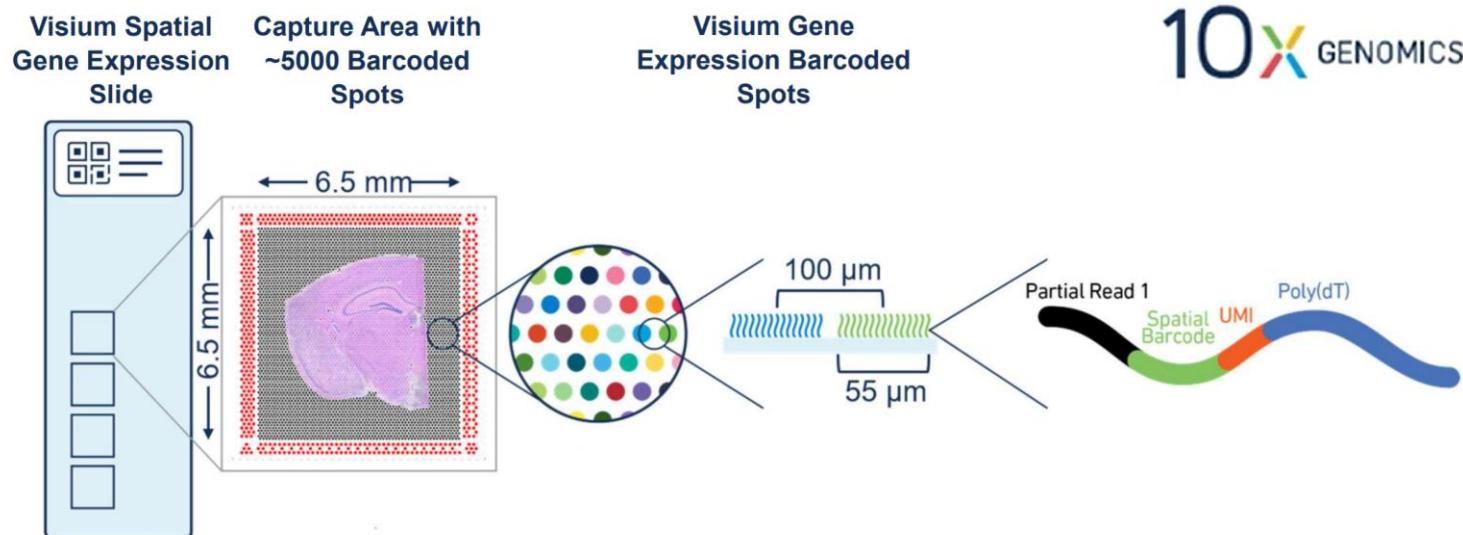
[https://github.com/alexisvdb/ajacs\\_20251218](https://github.com/alexisvdb/ajacs_20251218)



## データ探索

- 高次元データの解析で特に重要となる
- データの品質評価や異常値の特定
- データ中の主要な構造を見つける
- 仮説の生成と検証
- 単純に正解をだすような解法は無い

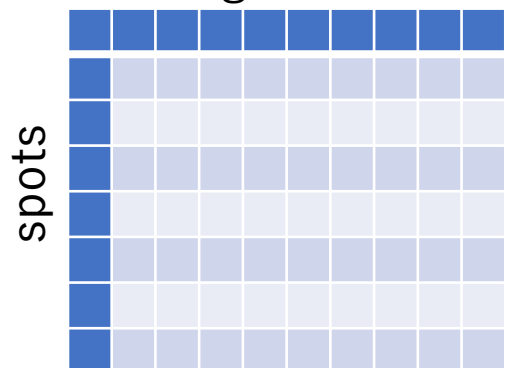
# 10X Genomics Visium platform



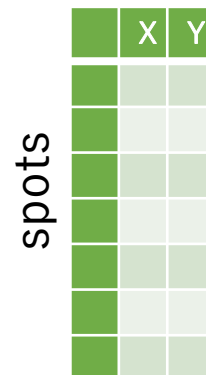
- 各スポットには約10個の細胞が含まれている (“single cell”ではない)

- Final data:

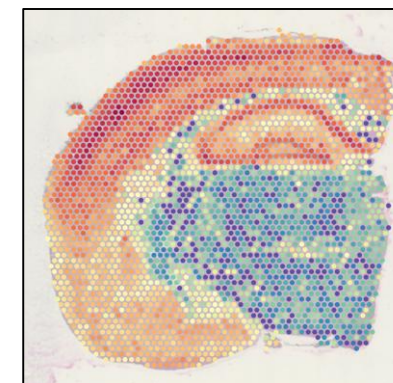
スポットあたりの遺伝子発現 + 位置情報  
genes



+



=



# Seurat tutorial – クオリティチェック (1)

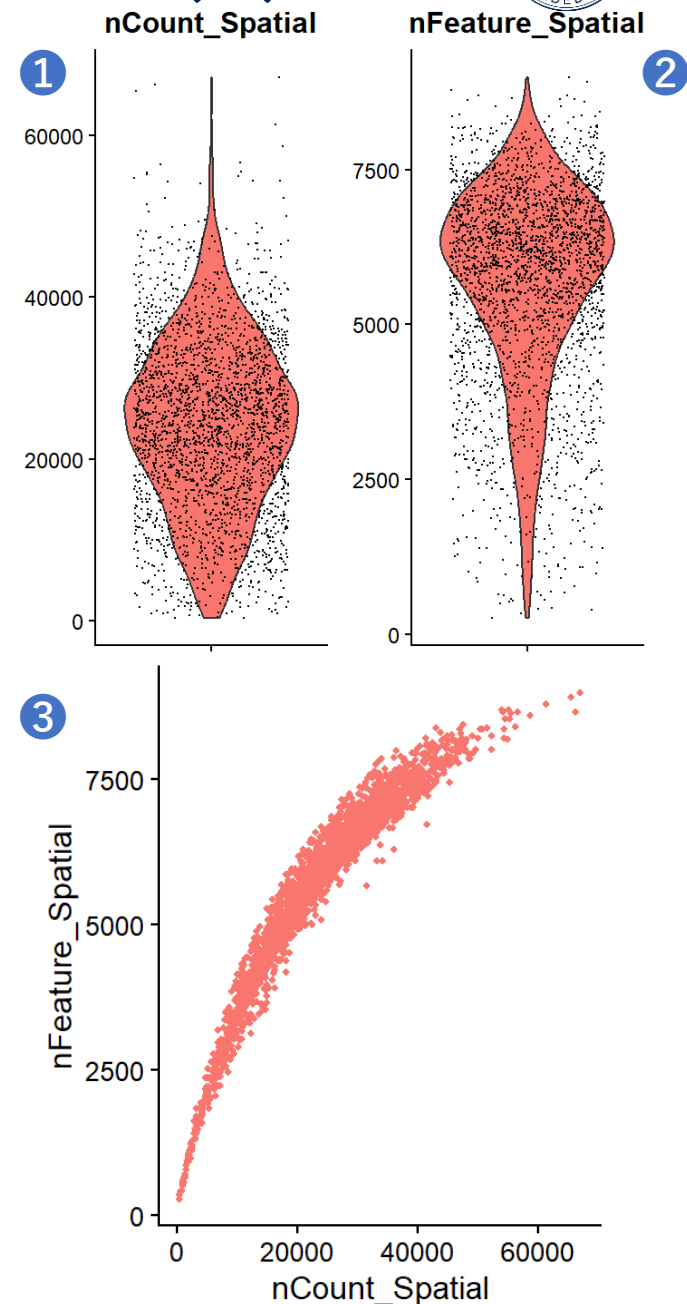


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```
#### load packages ####
library(Seurat) # version 5.3.0
library(SeuratData)

#### Install and load example Visium dataset ####
InstallData("stxBrain")
brain <- LoadData("stxBrain", type = "anterior1")

#### Quality check ####
VlnPlot(brain, features = "nCount_Spatial") ← ①
VlnPlot(brain, features = "nFeature_Spatial") ← ②
FeatureScatter(brain, feature1 = "nCount_Spatial",
               feature2 = "nFeature_Spatial") ← ③
```



クオリティの指標として使われるもの

- ① スポット当たりのリード数
- ② スポット当たりの遺伝子検出数

1 細胞データとの共通点：

- ①② スポット間にかなりのばらつきがある
- ③ リード数と遺伝子検出数に相関がある

1 細胞データとの相違点：「Doublet」という概念がない



# Seurat tutorial – クオリティチェック (2)

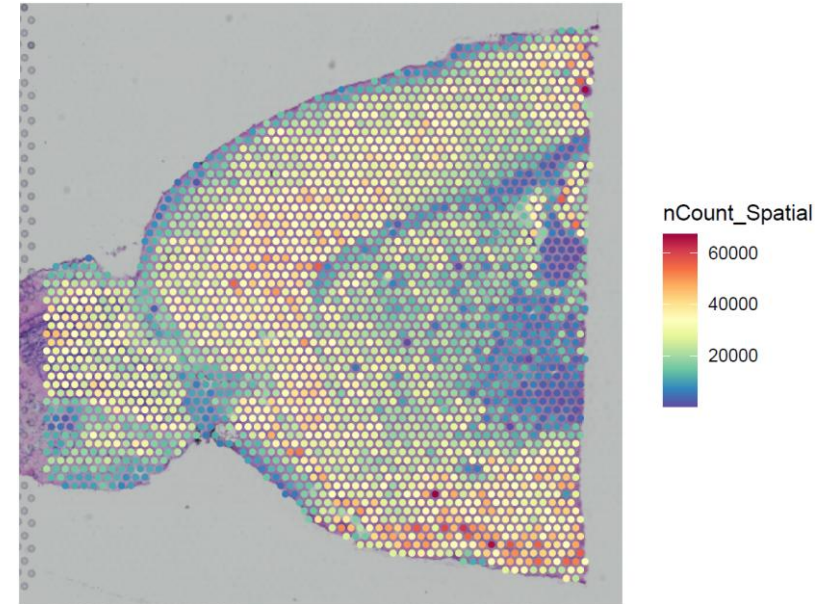
```
#### Quality within slices ####
```

```
SpatialFeaturePlot(brain, features = "nCount_Spatial") ← ①
```

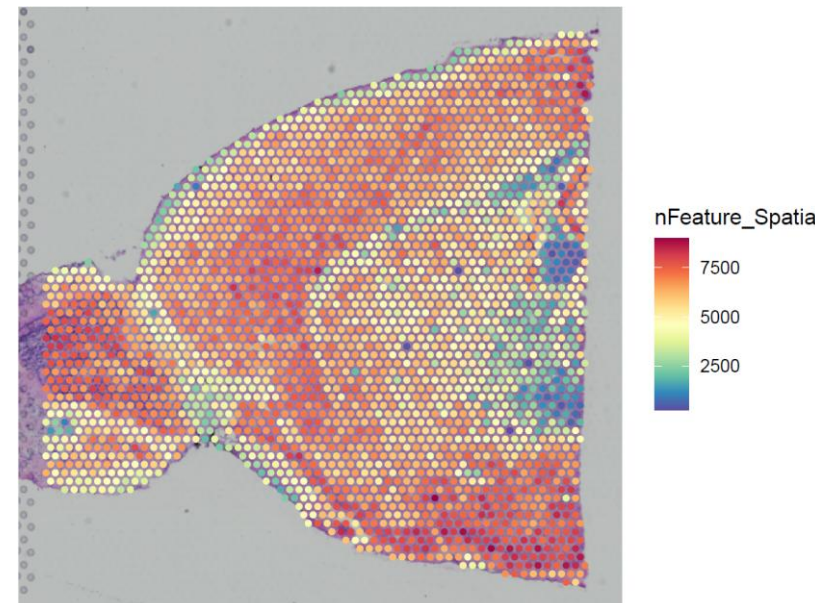
```
SpatialFeaturePlot(brain, features = "nFeature_Spatial") ← ②
```

- クオリティの指標として使われるもの
  - ① スポット当たりのリード数
  - ② スポット当たりの遺伝子検出数
- シングルセル解析以上に注意深い解釈が必要となる
  - 組織内における細胞密度のばらつき
  - 細胞種の違い
  - 組織の透過性の違い
- 脳の組織構造を反映した空間的パターンを見ることが出来る

①



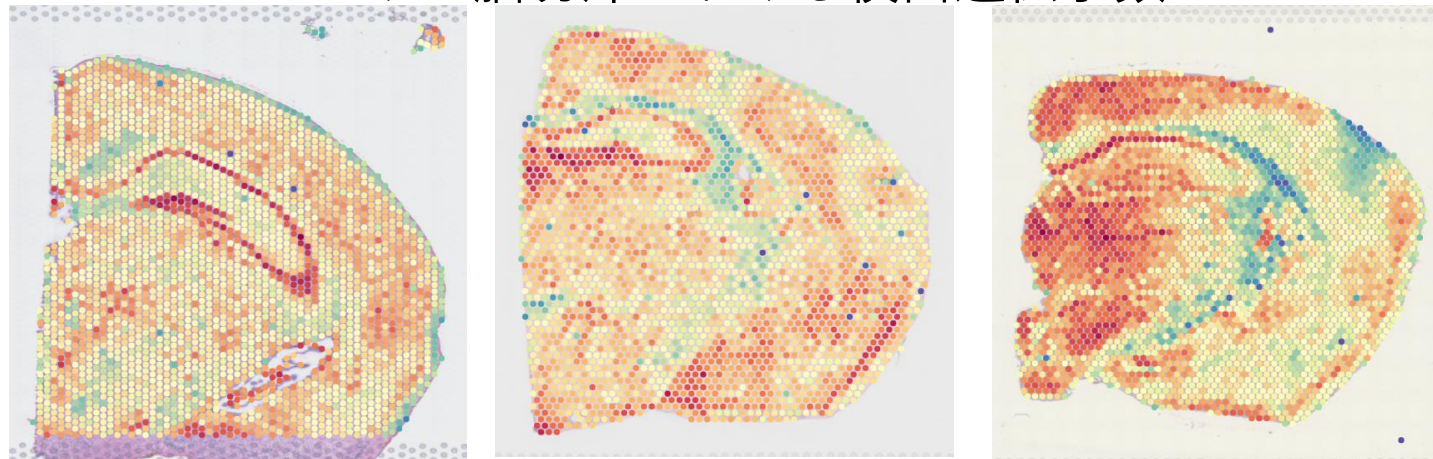
②



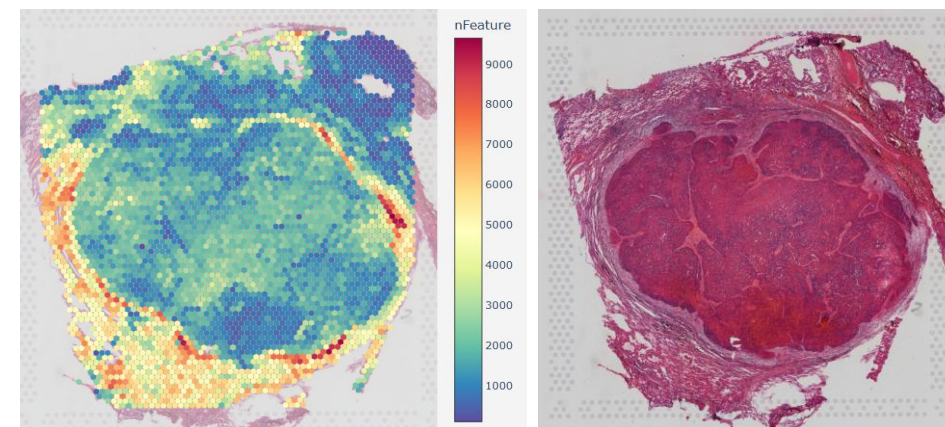
# クオリティ値の空間パターン

- DeepSpaceDBからの例
- 一部のパターンでは**生物学的な特徴**を反映している
  - 脳の神経解剖学的構造
  - ガン組織の存在

マウス脳切片における検出遺伝子数

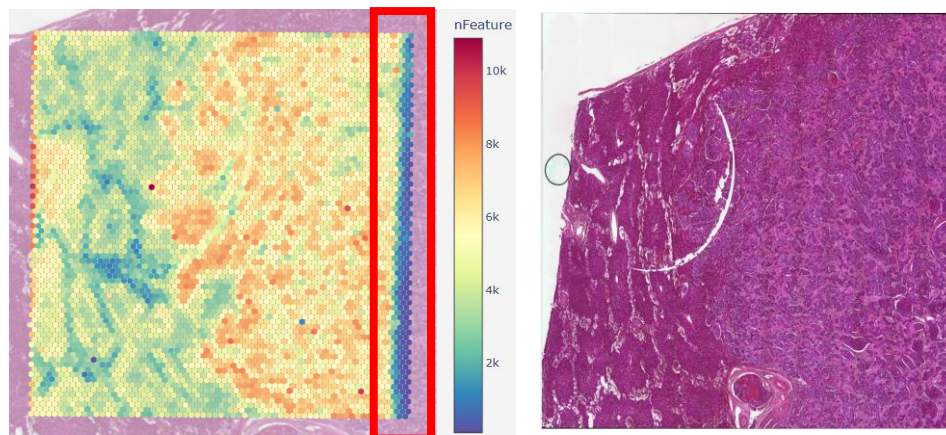


肝芽腫 (sample ID DSID001904)



**技術的な問題**でパターンが生じることもある

乳がん由来の肝臓転移  
(sample ID DSID001370)





- 生データのUMIカウントは、スポット間のシーケンシング深度の違いに左右される
- スポット間の比較を妥当とするには正規化が必要である
- オプション:

Option 2. ライブラリサイズ（シーケンシング深度）による正規化

Option 1. SCTransform 負の二項分布に基づく複雑な正規化アプローチ

```
#### Normalization ####  
# option 1: SCTransform residuals for all genes  
brain <- SCTransform(brain, assay = "Spatial")  
  
# option 2: standard log normalization for comparison  
# brain <- NormalizeData(brain, assay = "Spatial")
```

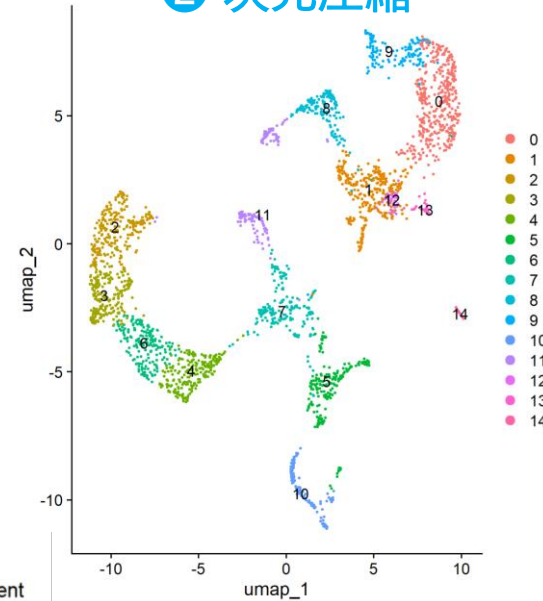
# Seurat チュートリアル – 次元圧縮

## 探索的データ解析

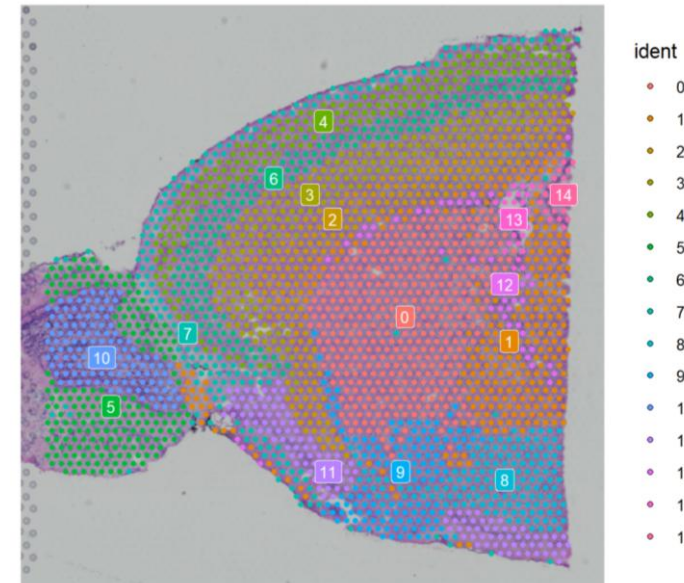
高次元データ

人間が理解しやすい  
単純化された要約

### ② 次元圧縮



### ① 類似性によるグループ分け



```
#### Dimensionality reduction & clustering ####
```

```
brain <- RunPCA(brain, assay = "SCT")
```

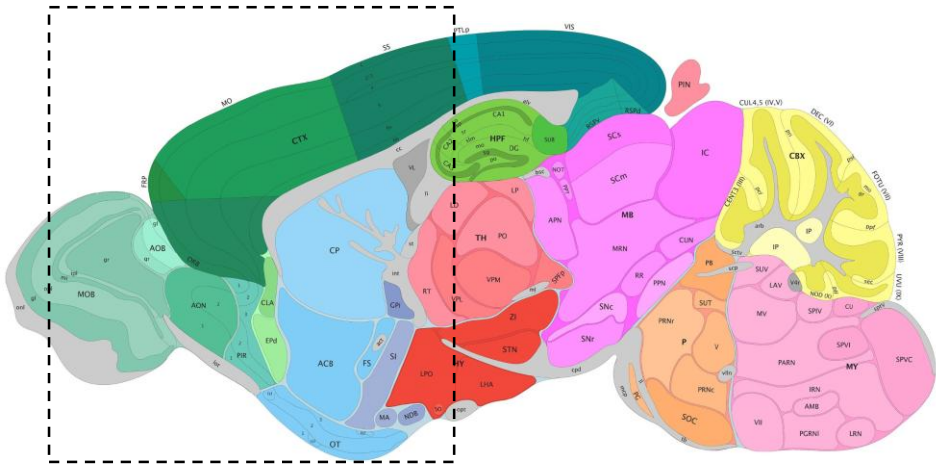
```
brain <- FindNeighbors(brain, reduction = "pca", dims = 1:30)
```

```
brain <- FindClusters(brain)
```

```
SpatialDimPlot(brain, label = TRUE, label.size = 3) ← ①
```

```
brain <- RunUMAP(brain, reduction = "pca", dims = 1:30)
```

```
DimPlot(brain, reduction = "umap", label = TRUE) ← ②
```



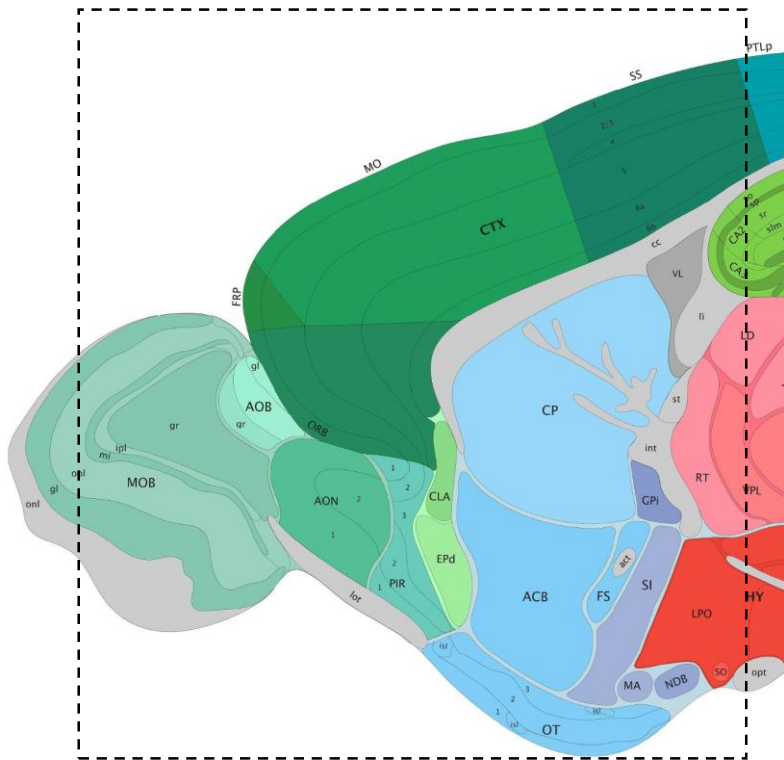
マウス脳 サジタル断面 (Image from Allen brain atlas)

# Seurat tutorial – クラスタリング結果の検証

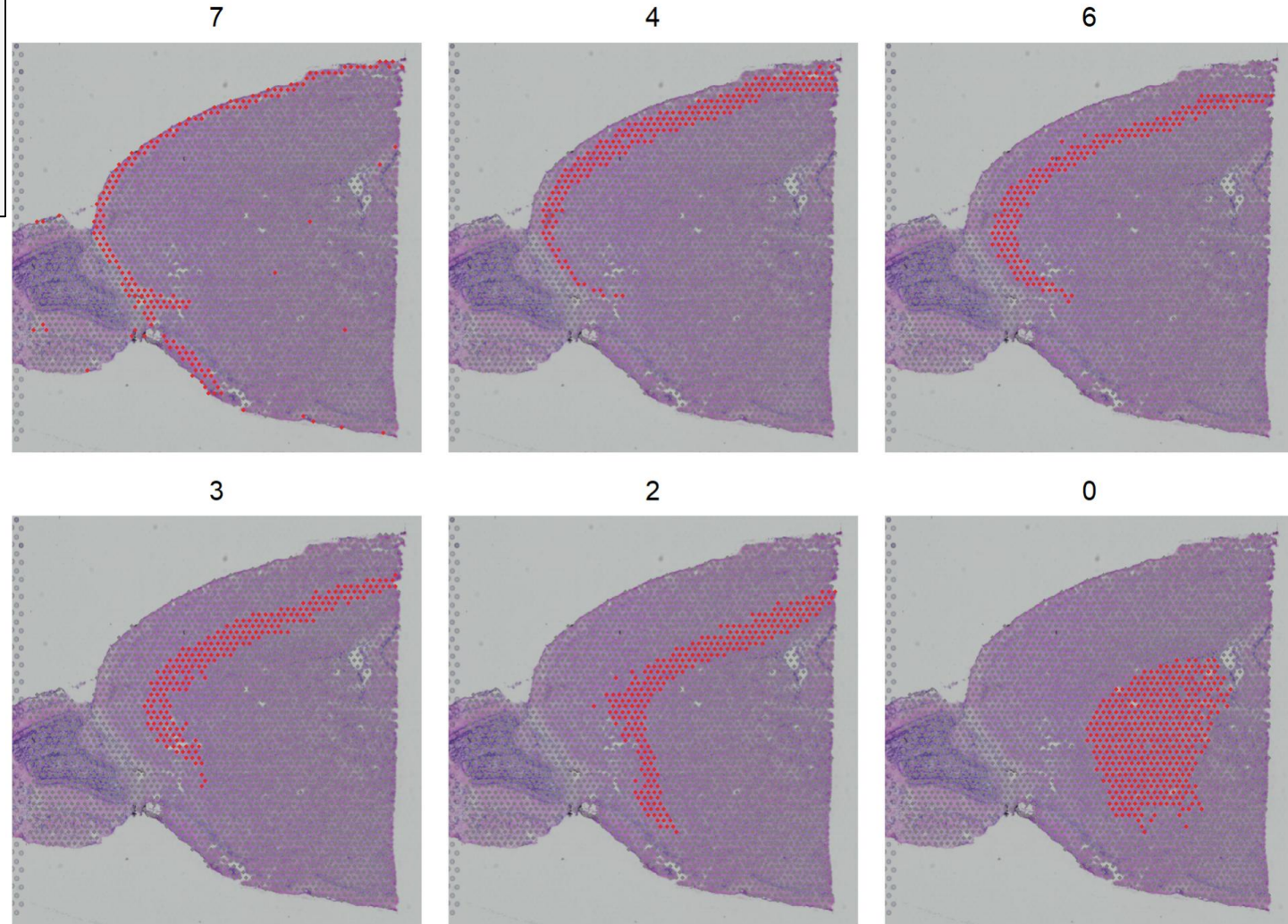


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```
# highlighting clusters
SpatialDimPlot(brain,
  cells.highlight = CellsByIdentities(object =
    brain, idents = c(7, 4, 6, 3, 2, 0)),
  facet.highlight = TRUE, ncol = 3)
```



マウス脳サジタル断面  
(Image adapted from Allen brain atlas)



このクラスタリングは遺伝子発現パターンの類似性のみに基づいており、空間的情報は一切用いていない



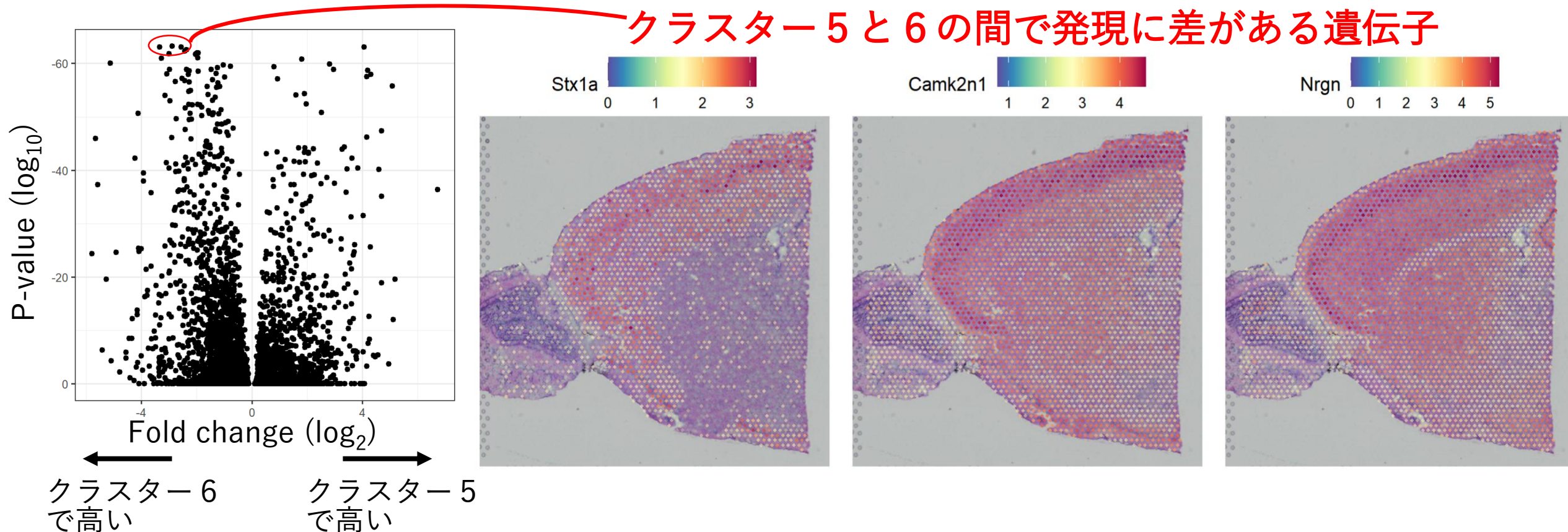
# Seurat tutorial – 空間的変動遺伝子 (SVG) (1)



14

```
#### Identifying spatially variable features ####  
# comparisons between clusters (here: between 5 and 6)  
de_markers <- FindMarkers(brain, ident.1 = 5, ident.2 = 6)  
# plot the top 3 genes with the highest expression in cluster 6 vs 5  
SpatialFeaturePlot(object = brain, features = rownames(de_markers)[1:3], alpha = c(0.1, 1), ncol = 3)
```

FindMarkersでは空間情報（位置や隣接関係など）は一切利用しない



## 空間情報を取り込んだSVG 予測法

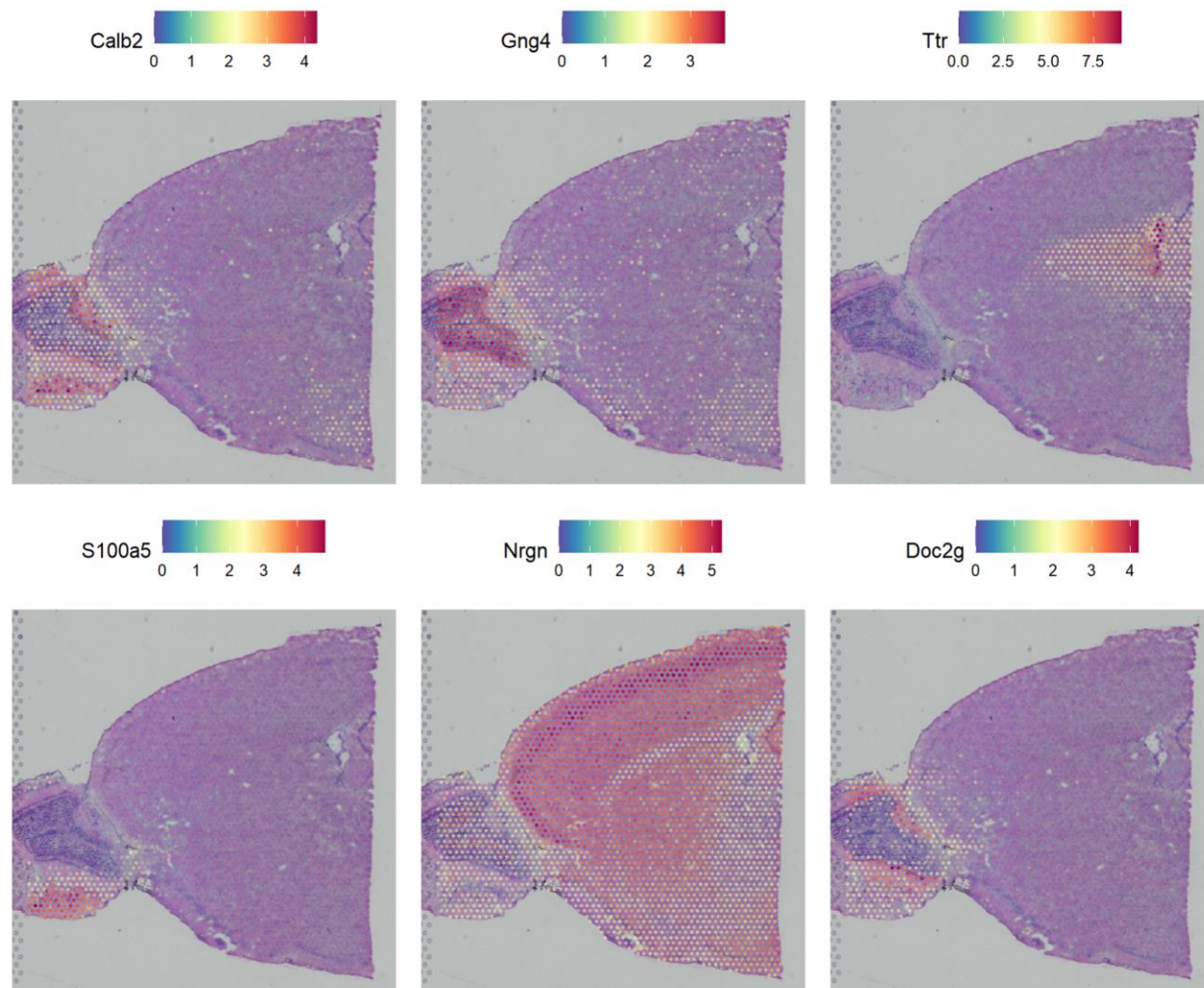
- Moran's I (used in this tutorial)
- SPARK-X (Zhu *et al.*, Genome Biol, 2021)
- binSpect (Giotto package; Dries *et al.*, Genome Biol, 2021)
- singleCellHaystack (Vandenbon and Diez, Nat Commun, 2020)

```
# Use spatial info to find SVGs (slow)
# Optional speed-up: install.packages('Rfast2')
brain <- FindSpatiallyVariableFeatures(
  brain, assay = "SCT",
  features = VariableFeatures(brain)[1:1000],
  selection.method = "moransi")

# plot the top-scoring genes
top.features <- head(SpatiallyVariableFeatures(brain,
  selection.method = "moransi"), 6)

SpatialFeaturePlot(brain, features = top.features,
  ncol = 3, alpha = c(0.1, 1))
```

## Moran's I 法によるトップ変動遺伝子



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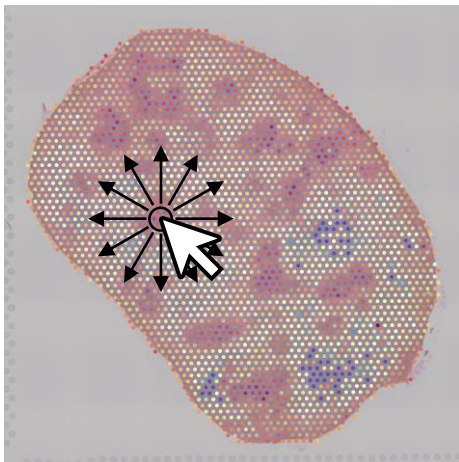
# 他のプラットフォームについて

- The Seuratのウェブサイト上のチュートリアルはシーケンスベースのプラットフォームを対象としている
  - Visium
  - Slide-seq
- しかし、イメージベースのプラットフォームも同様のワークフローで解析可能である
  - Vizgen MERSCOPE
  - Xenium
  - Nanostring CosMx Spatial Molecular Imager
  - Akoya CODEX

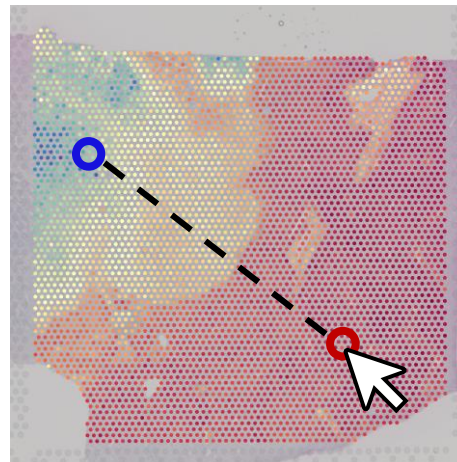
# Seurat tutorial – 結論

- Seurat は空間データ解析ツールとして大変優れている
- 解析の大部分はscRNA-seq 解析と同様の流れである
- しかし空間的な要素を完全には活用していない
- インタラクティブな探索には限界がある

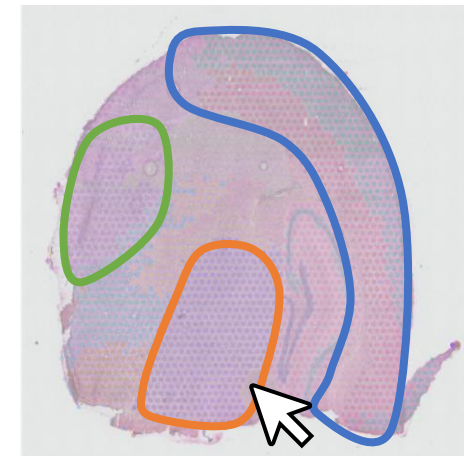
遺伝子発現は、ある点からの距離に応じてどのように変化するのか？



この軸に沿って起こっている遺伝子発現変化は何か？



マウスで選んだ領域どうしを比較したい。どの遺伝子の発現に差があるのか？



Selections

	●	●	●
Gene 1	0.26	0.98	0.99
Gene 2	0.15	0.63	0.39
Gene 3	0.70	0.05	0.41
Gene 4	0.74	1.00	0.63
Gene 5	0.79	0.84	0.56
Gene 6	0.55	0.44	0.79
Gene 7	0.67	0.74	0.93
Gene 8	0.24	0.52	0.06
Gene 9	0.28	0.92	0.53
Gene 10	0.63	0.51	0.85

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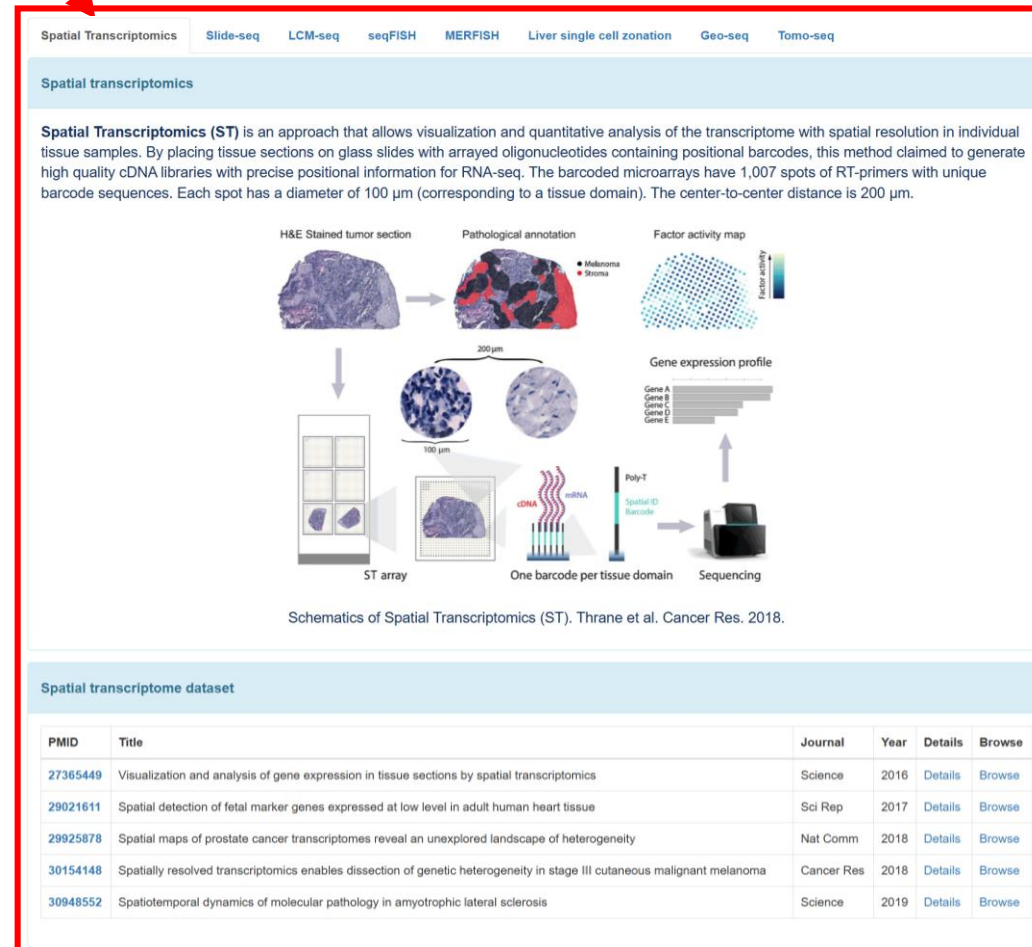
# Spatial transcriptomics databases

- 多くのデータベースが公開されている

	Database	URL	Publication	PMID	Comment
★	SpatialDB	<a href="#">link</a>	Nucleic Acids Res, 2020	<a href="#">31713629</a>	No longer maintained?
★	SODB	<a href="#">link</a>	Nat Methods, 2023	<a href="#">36797409</a>	Sometimes long load times
	SCAR	<a href="#">link</a>	Nucleic Acids Res, 2024	<a href="#">37739405</a>	Focus on cancer
	SORC	<a href="#">link</a>	Nucleic Acids Res, 2024	<a href="#">37811897</a>	Focus on cancer
★	STOmicsDB	<a href="#">link</a>	Nucleic Acids Res, 2024	<a href="#">37953328</a>	>15,000 samples
★	SOAR	<a href="#">link</a>	Sci Adv, 2025	<a href="#">40498826</a>	Sometimes long load times
★	DeepSpaceDB	<a href="#">link</a>	Nucleic Acids Res, 2025	<a href="#">41160880</a>	Our database!

★ :本日の紹介予定

異なる実験手法・技術からなるサンプル

**Spatial transcriptomics**

**Spatial Transcriptomics (ST)** is an approach that allows visualization and quantitative analysis of the transcriptome with spatial resolution in individual tissue samples. By placing tissue sections on glass slides with arrayed oligonucleotides containing positional barcodes, this method claimed to generate high quality cDNA libraries with precise positional information for RNA-seq. The barcoded microarrays have 1,007 spots of RT-primers with unique barcode sequences. Each spot has a diameter of 100  $\mu\text{m}$  (corresponding to a tissue domain). The center-to-center distance is 200  $\mu\text{m}$ .

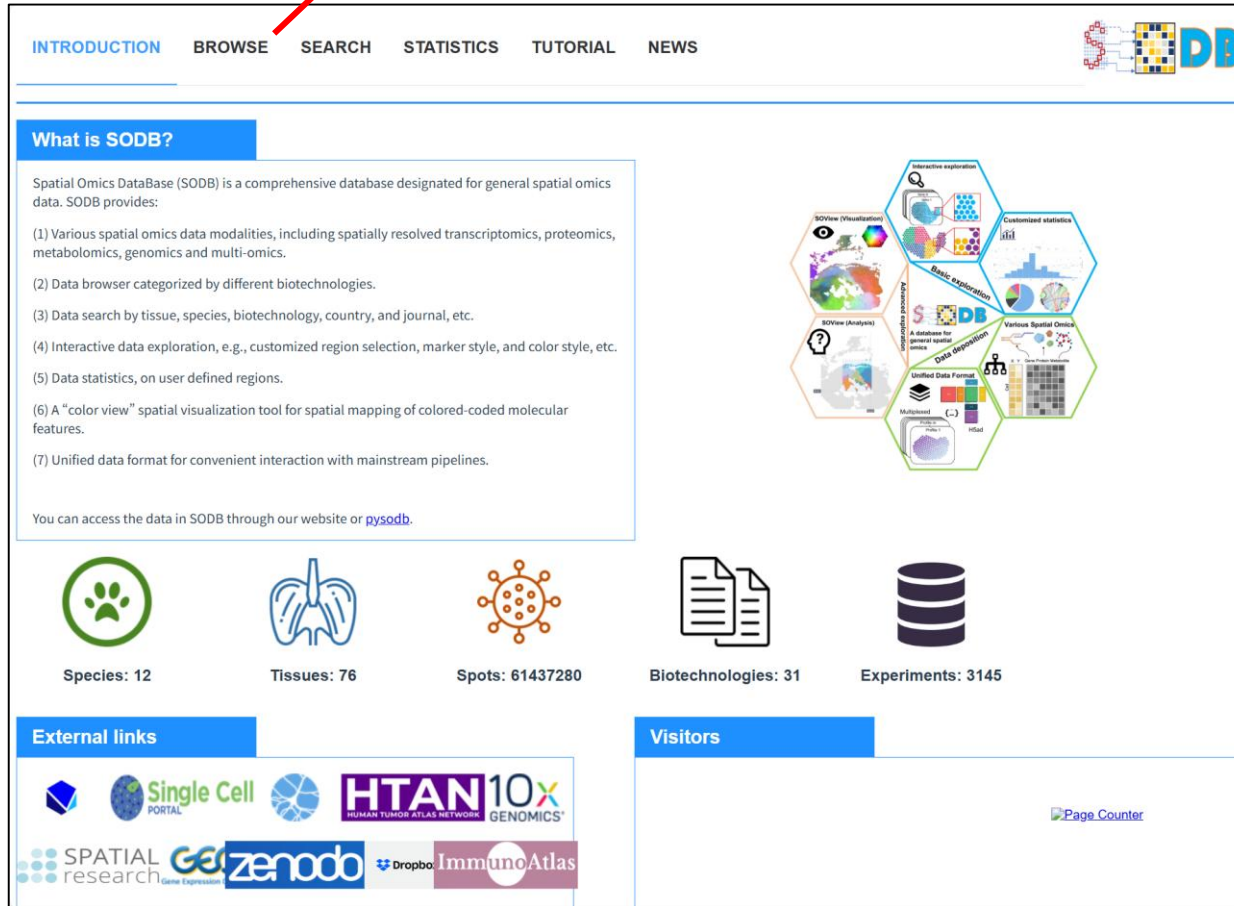
Schematics of Spatial Transcriptomics (ST). Thrane et al. Cancer Res. 2018.

PMID	Title	Journal	Year	Details	Browse
27365449	Visualization and analysis of gene expression in tissue sections by spatial transcriptomics	Science	2016	<a href="#">Details</a>	<a href="#">Browse</a>
29021611	Spatial detection of fetal marker genes expressed at low level in adult human heart tissue	Sci Rep	2017	<a href="#">Details</a>	<a href="#">Browse</a>
29925878	Spatial maps of prostate cancer transcriptomes reveal an unexplored landscape of heterogeneity	Nat Comm	2018	<a href="#">Details</a>	<a href="#">Browse</a>
30154148	Spatially resolved transcriptomics enables dissection of genetic heterogeneity in stage III cutaneous malignant melanoma	Cancer Res	2018	<a href="#">Details</a>	<a href="#">Browse</a>
30948552	Spatiotemporal dynamics of molecular pathology in amyotrophic lateral sclerosis	Science	2019	<a href="#">Details</a>	<a href="#">Browse</a>

- 24 studies
- 8 Biotechnologies
- 305 samples
- 組織切片上に発現遺伝子をプロットできるが
- 公開以来一度も更新されていない
- いくつかのツールが動かない



## 異なる実験手法・技術の数々



**INTRODUCTION** **BROWSE** **SEARCH** **STATISTICS** **TUTORIAL** **NEWS**

**What is SODB?**

Spatial Omics DataBase (SODB) is a comprehensive database designated for general spatial omics data. SODB provides:

- (1) Various spatial omics data modalities, including spatially resolved transcriptomics, proteomics, metabolomics, genomics and multi-omics.
- (2) Data browser categorized by different biotechnologies.
- (3) Data search by tissue, species, biotechnology, country, and journal, etc.
- (4) Interactive data exploration, e.g., customized region selection, marker style, and color style, etc.
- (5) Data statistics, on user defined regions.
- (6) A "color view" spatial visualization tool for spatial mapping of colored-coded molecular features.
- (7) Unified data format for convenient interaction with mainstream pipelines.

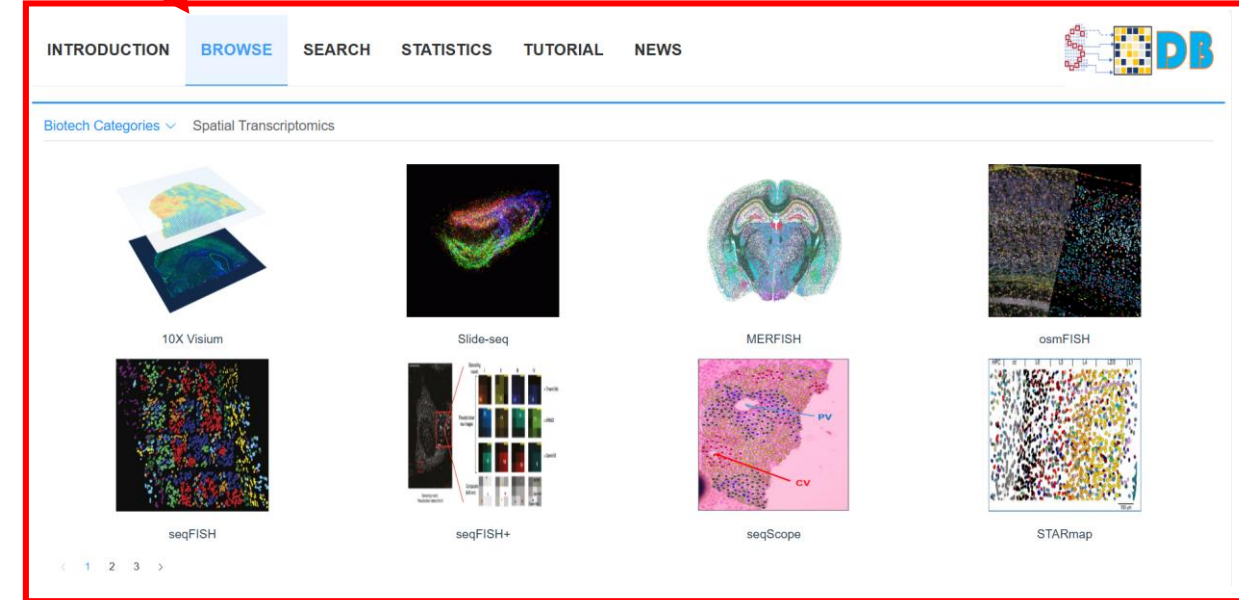
You can access the data in SODB through our website or [pysodb](#).

**Statistics:**

- Species: 12
- Tissues: 76
- Spots: 61437280
- Biotechnologies: 31
- Experiments: 3145

**External links:** [Single Cell PORTAL](#), [HTAN10x GENOMICS](#), [SPATIAL research](#), [Geozenodo](#), [Dropbo](#), [ImmunoAtlas](#)

**Visitors:** [Page Counter](#)

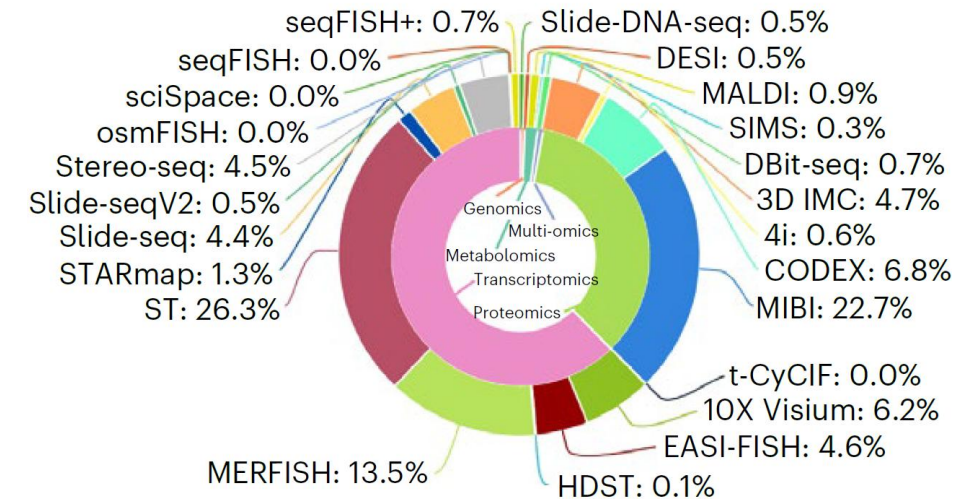


**INTRODUCTION** **BROWSE** **SEARCH** **STATISTICS** **TUTORIAL** **NEWS**

**Biotech Categories** **Spatial Transcriptomics**

10X Visium, Slide-seq, MERFISH, osmFISH, seqFISH, seqFISH+, seqScope, STARmap

## Spatial technologies



- 31 Biotechnologies
- 3145 samples
- しばしば反応が遅くなる



# SODB – browsing Visium data



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INTRODUCTION **BROWSE** SEARCH STATISTICS TUTORIAL NEWS

Biotech Categories ▾ Spatial Transcriptomics / 10X Visium

Date  To   Search

Country

Journal

Tissue

Species

Submit

Dataset Name	Date	doi	Country	Operations
The spatial transcriptomic landscape of the healing mouse intestine following wing damage	2022	10.1038/s41467-022-28497-0	USA	<a href="#">View</a>
Spatial proteogenomics reveals distinct and evolutionarily conserved hepatic macrophage niches	2022	10.1016/j.cell.2021.12.018	Belgium	<a href="#">View</a>
Transcriptome-scale spatial gene expression in the human dorsolateral prefrontal cortex	2021	10.1038/s41593-020-00787-0	USA	<a href="#">View</a>
Spatiotemporal single-cell RNA sequencing of developing chicken hearts identifies interplay between cellular differentiation and morphogenesis	2021	10.1038/s41467-021-21892-z	USA	<a href="#">View</a>
Spatially resolved transcriptomics reveals the architecture of the tumor-microenvironment interface	2021	10.1038/s41467-021-26614-z	USA	<a href="#">View</a>
Spatial Transcriptomics to define transcriptional patterns of zonation and structural components in the mouse liver	2021	10.1038/s41467-021-27354-w	Sweden	<a href="#">View</a>
Spatiotemporal analysis of human intestinal development at single-cell resolution	2021	10.1016/j.cell.2020.12.016	UK	<a href="#">View</a>
Spatial mapping reveals human adipocyte subpopulations with distinct sensitivities to insulin	2021	10.1016/j.cmet.2021.07.018	Sweden	<a href="#">View</a>

Species

Axolotl

Arabidopsis

mouse

Cell Line

Drosophila

None

cell line

Mouse

Tissue

Species

NCTC1469/Hepa1-6

colon cancer

Lymph Node

Cell Line

Spleen

Kidney Organoid

neocortex

spinal cords

Biotech Categories ▾ Spatial Transcriptomics / 10X Visium / guilliams2022spatial

**Dataset detail**

Title Spatial proteogenomics reveals distinct and evolutionarily conserved hepatic macrophage niches

Short Name guilliams2022spatial

Date 2022

doi 10.1016/j.cell.2021.12.018

Country Belgium

Journal Cell

Author Guillems, M. Bonnardel, J. Haest, B. Vanderborght, B. Wagner, C. Remmerie, A. Buijko, A. Martens, L. Thone, T. Browaeys, R. De Ponti, F. F. Vanneste, B. Zwicker, C. Svedberg, F. R. Vanhalewyn, T. Goncalves, A. Lippens, S. Devriendt, B. Cox, E. Ferrero, G. Wittamer, V. Willaert, A. Kaptein, S. J. F. Neyts, J. Dallmeier, K. Geldhof, P. Casaert, S. Deplancke, B. Ten Dijke, P. Hoorens, A. Vanlander, A. Berrevoet, F. Van Nieuwenhove, Y. Saeys, Y. Saelens, W. Van Vlierberghe, H. Devisscher, L. Scott, C. L.

Access GSE192742

Biotech 10X Visium

Species Mouse(15)

Tissue Liver(15)

N\_Unit 24179

**Data exploration**

select a experiment  Download

Expression View SOView Annotation View Comparison View

**Exploration**

Genes/Features  MIR1302-10

Spatially Variable Genes  MIR1302-10

☐ Log

**Style**

Marker Size  2

Custom Color Range

Min  0 Max  0

☐ Reverse Colors

**Expression View**

# SODB – Expression View



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select a experiment

GSM5764422\_10x\_Visium

Download

1. サンプルを選ぶ GSM5764422

2. 遺伝子を選ぶ

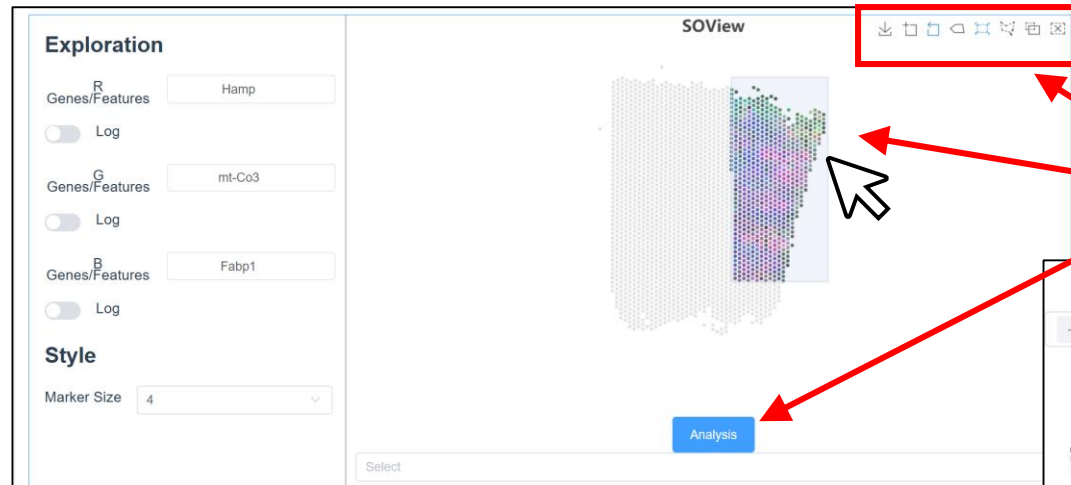
3. (optional)  
マーカーサイズ  
を変更する



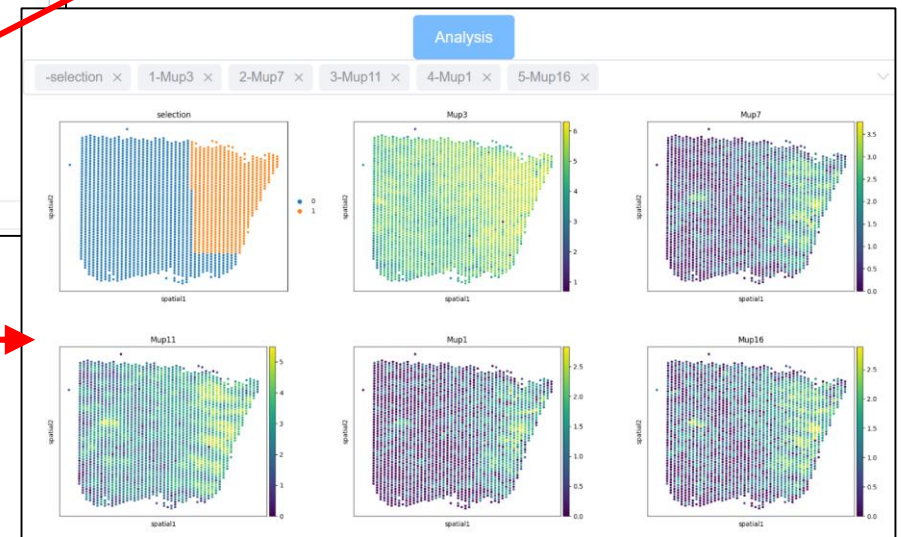
- value数値が全て整数なので、正規化していない生データのままだ可能性がある
- 切片画像データが付いていない

# SODB – SOView

遺伝子発現分布を  
3つまで表示する  
ことができる(赤青  
緑)

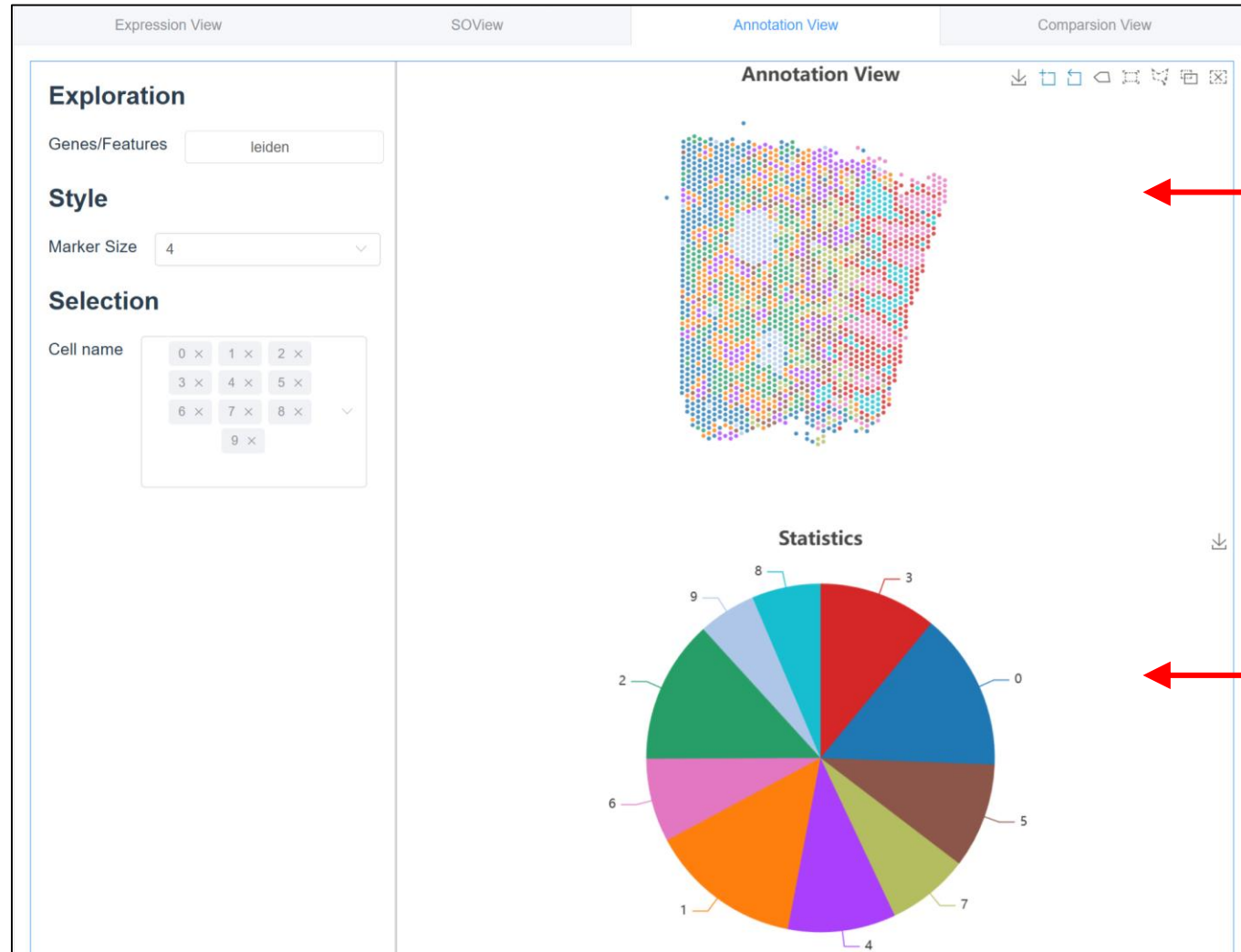


興味ある領域を選んで“Analysis”  
をクリックすると



選択した領域内で発現が高い遺伝子が  
表示される。

# SODB – Annotation View

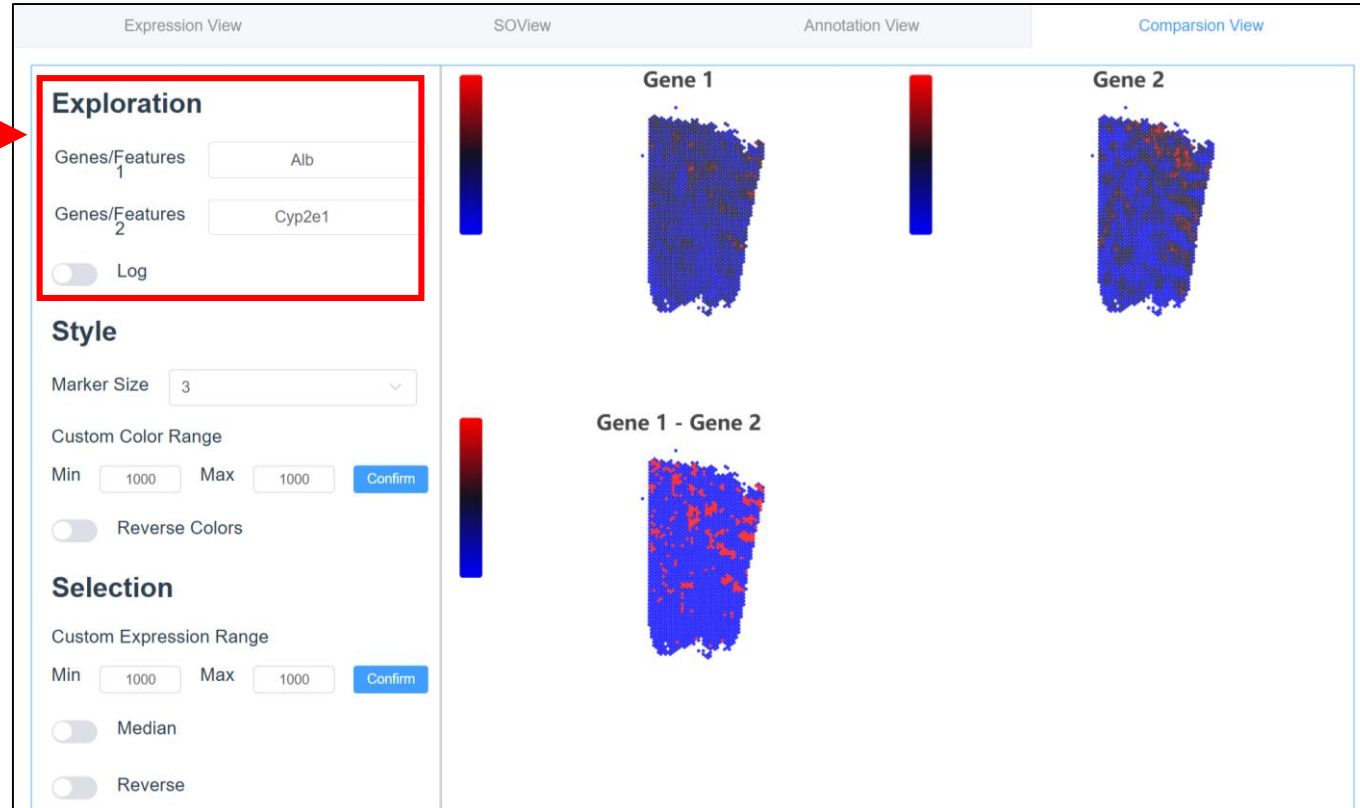


← クラスタリング結果

← クラスタあたりのスポット数

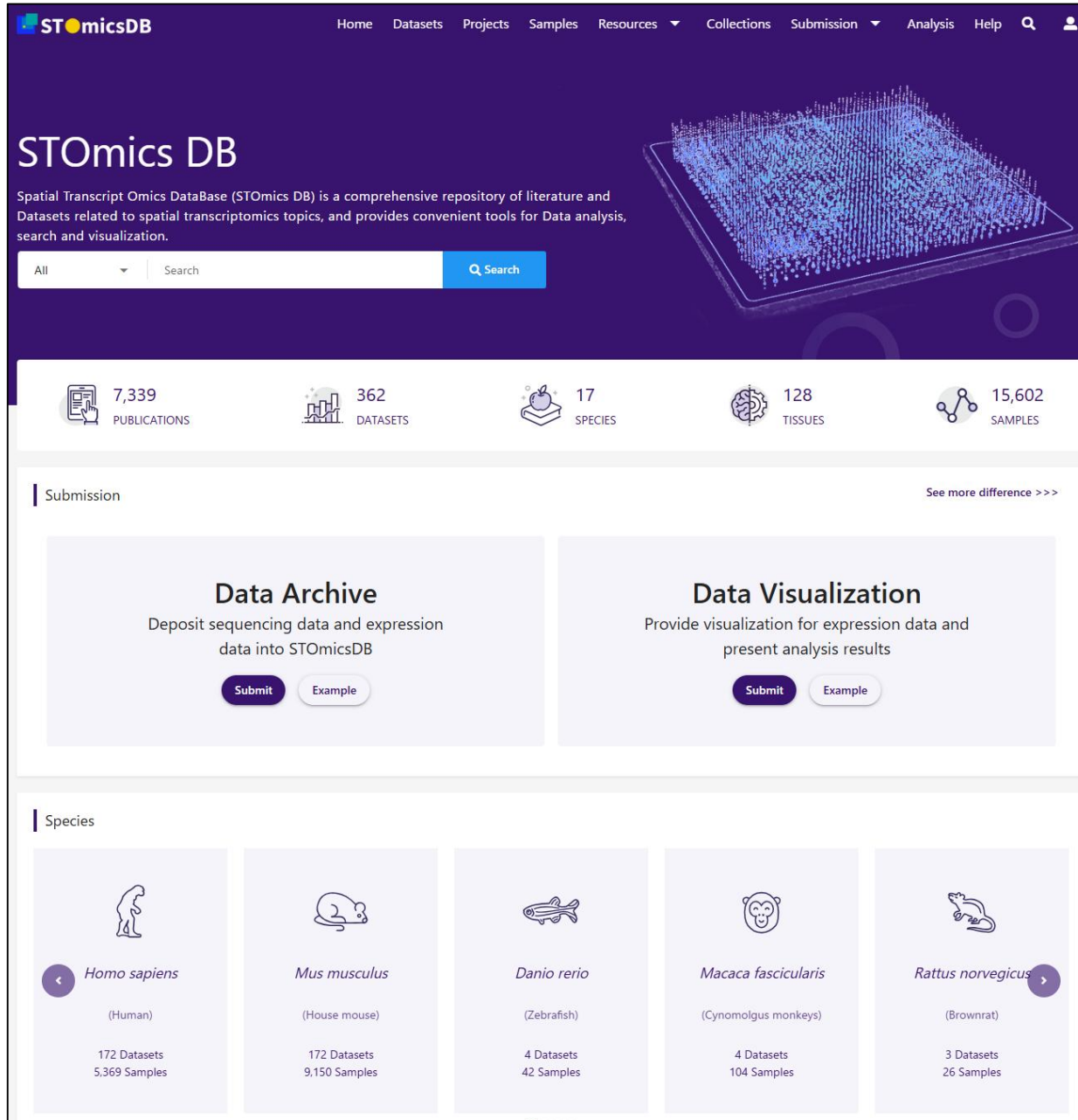
# SODB – Comparison View

遺伝子を 2 つ選択 →



- 遺伝子 1 の発現分布
- 遺伝子 2 の発現分布
- 両者間の差





STOmicsDB

Spatial Transcript Omics DataBase (STOmics DB) is a comprehensive repository of literature and Datasets related to spatial transcriptomics topics, and provides convenient tools for Data analysis, search and visualization.

Home Datasets Projects Samples Resources Collections Submission Analysis Help

STOmics DB

Spatial Transcript Omics DataBase (STOmics DB) is a comprehensive repository of literature and Datasets related to spatial transcriptomics topics, and provides convenient tools for Data analysis, search and visualization.

All Search

7,339 PUBLICATIONS 362 DATASETS 17 SPECIES 128 TISSUES 15,602 SAMPLES

Submission

Data Archive  
Deposit sequencing data and expression data into STOmicsDB  
Submit Example

Data Visualization  
Provide visualization for expression data and present analysis results  
Submit Example

Species

Human (Homo sapiens)  
172 Datasets  
5,369 Samples

House mouse (Mus musculus)  
172 Datasets  
9,150 Samples

Zebrafish (Danio rerio)  
4 Datasets  
42 Samples

Cynomolgus monkeys (Macaca fascicularis)  
4 Datasets  
104 Samples

Brownrat (Rattus norvegicus)  
3 Datasets  
26 Samples

- 362 studies
- 8 technologies
- 15,602 samples (!) 但し品質の良いサンプルは少ない

Sample quality ?		
<input type="checkbox"/>	★★★★★	1,398
<input type="checkbox"/>	★★★★	1,030
<input type="checkbox"/>	★★★	192
<input type="checkbox"/>	★★	8,513
<input type="checkbox"/>	★	4,470

5★: spatial coordinates & images

4★: spatial coordinates only

3★: images only

2★: lacks coordinates & images

1★: not processed



# STOmicsDB – “Samples” page



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STOmicsDB

Home Datasets Projects Samples Resources Collections Submission Analysis Help

Date range

Species

- ☐ Mus musculus 9,150
- ☐ Homo sapiens 5,369
- ☐ Homo sapiens / Severe acute respira... 373
- ☐ Macaca fascicularis 104
- ☐ Mesocricetus auratus 81

More >

Tissues

- ☐ Brain 3,589
- ☐ Embryo 2,435
- ☐ dMGE 957
- ☐ Pancreas 909
- ☐ CGE 856

More >

Development stage

- ☐ E12.5 1,402
- ☐ E14.5 1,291
- ☐ E14 750
- ☐ E7.0 154
- ☐ adult 414

More >

Technology

- ☐ ST 7,670
- ☐ GeoMx DSP 1,700
- ☐ Geo-seq 1,348
- ☐ Stereo-Seq 1,015
- ☐ sci-Space 960

More >

Disease

- ☐ Pancreatic ductal adenocarcinoma 608
- ☐ Amyotrophic lateral sclerosis 331
- ☐ Triple-receptor negative breast cancer 252
- ☐ Non-small cell lung cancer 120
- ☐ Hepatocellular carcinoma 108

More >

Sample quality

- ☐ ★★★★★ 1,398

More >

Statistics

Species

Tissues

Technology

Disease

List

Show 10 results

Sample ID	Sample title	Species	Tissues	Disease	Sex	Technology	Source	Sample quality	Action
STSA0001067	Zebrafinch_tectum	Taeniopygia guttata	brain	--	female	Stereo-Seq	Submission	★★★★★	⋮
STSA0000869	NKTL14_Homo sapiens	Homo sapiens	Tumor	--	male	Stereo-Seq	Submission	★★★★★	⋮
STSA0000870	NKTL15_Homo sapiens	Homo sapiens	Tumor	--	male	Stereo-Seq	Submission	★★★★★	⋮
STSA0000871	NKTL16_Homo sapiens	Homo sapiens	Tumor	--	female	Stereo-Seq	Submission	★★★★★	⋮
STSA0000731	postnatal day 0	Mus musculus	heart	--	male	Stereo-Seq	Submission	★★★★★	⋮
STSA0000732	postnatal day 7	Mus musculus	heart	--	male	Stereo-Seq	Submission	★★★★★	⋮
STSA0000733	postnatal day 56	Mus musculus	heart	--	male	Stereo-Seq	Submission	★★★★★	⋮
STSA0000004	tong-sts006test002-title	Homo sapiens	c1	u1	male	10x Visium	Submission	★★★★★	⋮
STSA0000005	tong-sts006test003-title	Pseudomonas chlororaphis subsp. chlororaphis	c2	not applicable	not applicable	10x Visium	Submission	★★★★★	⋮
STSA0000006	tong-sts006test004-title	Ancyllobacter aquaticus	c3	--	pooled male and female	10x Visium	Submission	★★★★★	⋮

Showing 1 to 10 of 15,602 result(s).

< 1 2 3 4

User notice | Data sharing policy | Privacy and security policy

Technology

Search technology

<input type="checkbox"/> ST	7,670	<input type="checkbox"/> GeoMx DSP	1,700
<input type="checkbox"/> Geo-seq	1,348	<input type="checkbox"/> Stereo-Seq	1,015
<input type="checkbox"/> sci-Space	960	<input type="checkbox"/> 10x Visium	930
<input type="checkbox"/> Spatial Transcriptomics	664	<input type="checkbox"/> scRNA	282
<input type="checkbox"/> RNA-seq	192	<input type="checkbox"/> Slide-seqV2	172
<input type="checkbox"/> APEX-seq	134	<input type="checkbox"/> LCM-seq	109
<input type="checkbox"/> EASI-FISH	101	<input type="checkbox"/> Tomo-seq	83
<input type="checkbox"/> ClumpSeq	45	<input type="checkbox"/> PIC-seq	45
<input type="checkbox"/> snRNA	31	<input type="checkbox"/> CUT&Tag	22
<input type="checkbox"/> seqFish	21	<input type="checkbox"/> DBiT-seq	20

< 1 2 >

Clear Confirm

## 様々な技術

	Technology	Count	Comment
1	ST	7,670	≈ predecessor of Visium
2	GeoMX DSP	1,700	By Nanostring
3	Geo-seq	1,348	
4	Stereo-seq	1,015	By BGI
5	Sci-Space	960	
6	10x Visium	930	By 10X Genomics

異なる技術由来のサンプルを満遍なく集めているが、利用できる解析ツールはサンプルごとに限定されている。

# STOmicsDB – “Datasets” page



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フィルターをセットする: Species = “mouse”,  
Tissues = “Brain”, Technology = “Stereo-seq”

左のリストから一つ選んだ結果

The screenshot shows the STOmicsDB Datasets page. On the left, there are filters for Date range, Species, Tissues, Technology, and Dataset quality. The Species filter is set to "Mus musculus (house mouse)". The Tissues filter is set to "Brain". The Technology filter is set to "Stereo-Seq". The main content area shows a list of datasets. The first dataset is "1 SAW: An efficient and accurate data analysis workflow for Stereo-seq spatial transcriptomics" (ID: STDS0000234). The second dataset is "2 ABSTA : Amniotes Brain Spatiotemporal Transcriptomic Atlas" (ID: STDS0000241). The third dataset is "3 A cellular resolution spatial transcriptomic landscape of the postnatal mouse brain" (ID: STDS0000139). A red arrow points from the third dataset to the right-hand screenshot.

The screenshot shows the detail page for the dataset "A cellular resolution spatial transcriptomic landscape of the postnatal mouse brain" (Dataset ID: STDS0000139). The page includes a summary, visualization, data, related, and sample sections. The summary section contains the following information:

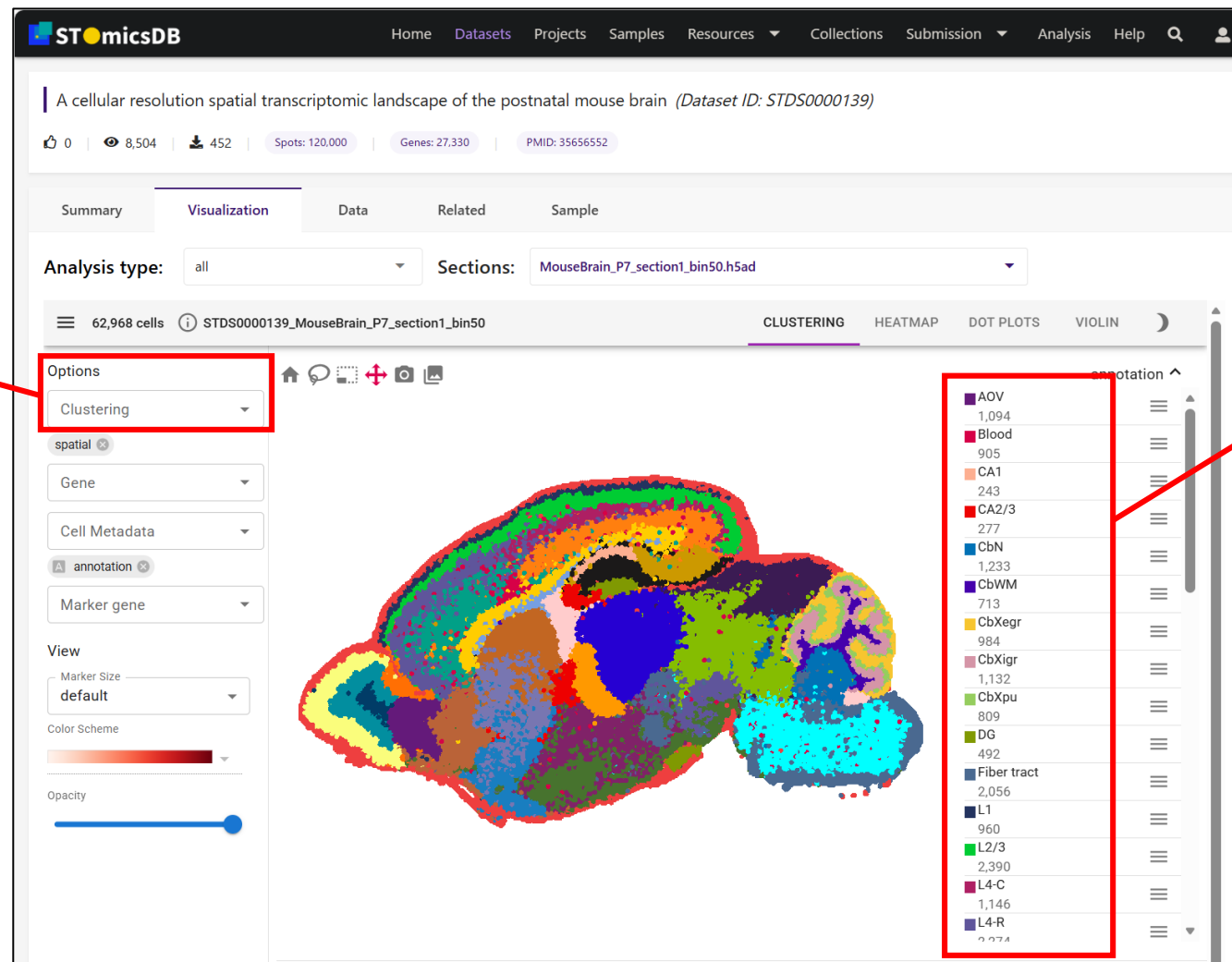
- Dataset information**
- Summary:** Here we apply Stereo-seq to generate a spatially-resolved transcriptomic description of the postnatal day 7 (P7) murine whole brain sagittal section near the middle line. Our study comprehensively dissected the anatomical regions, gene expression and gene regulatory network patterns and cell type localization at whole brain scale.
- Overall design:** The experiment were performed according to the standard protocol of Stereo-seq
- Technology:** Stereo-Seq
- Platform:** DNBSEQ-T10
- Species:** Mus musculus (mm10)
- Tissues:** Brain
- Cell types:** Fiber tract, Medulla and pons, Blood, LPO, CbXegr, CbXpu, Zona incerta, CbXigr, Meninge, CbWM, Ventricle, CbN, M
- Development stage:** P7
- Submission date:** 2022-02-16
- Update date:** 2022-02-16
- Sample number:** 1
- Section number:** 2
- DOI:** 10.26036/STDS0000139
- Contributors:** Mengnan cheng, Liang Wu, Chuanyu Liu, Longqi Liu  
Contact: chengmengnan@genomics.cn
- Accessions:** CNBP0002646  
Publication: A Cellular Resolution Spatial Transcriptomic Landscape of the Medial Structures in Postnatal Mouse Brain
- How to cite:** Cite database of STOmicsDB.

# STOmicsDB – Visualization (1)



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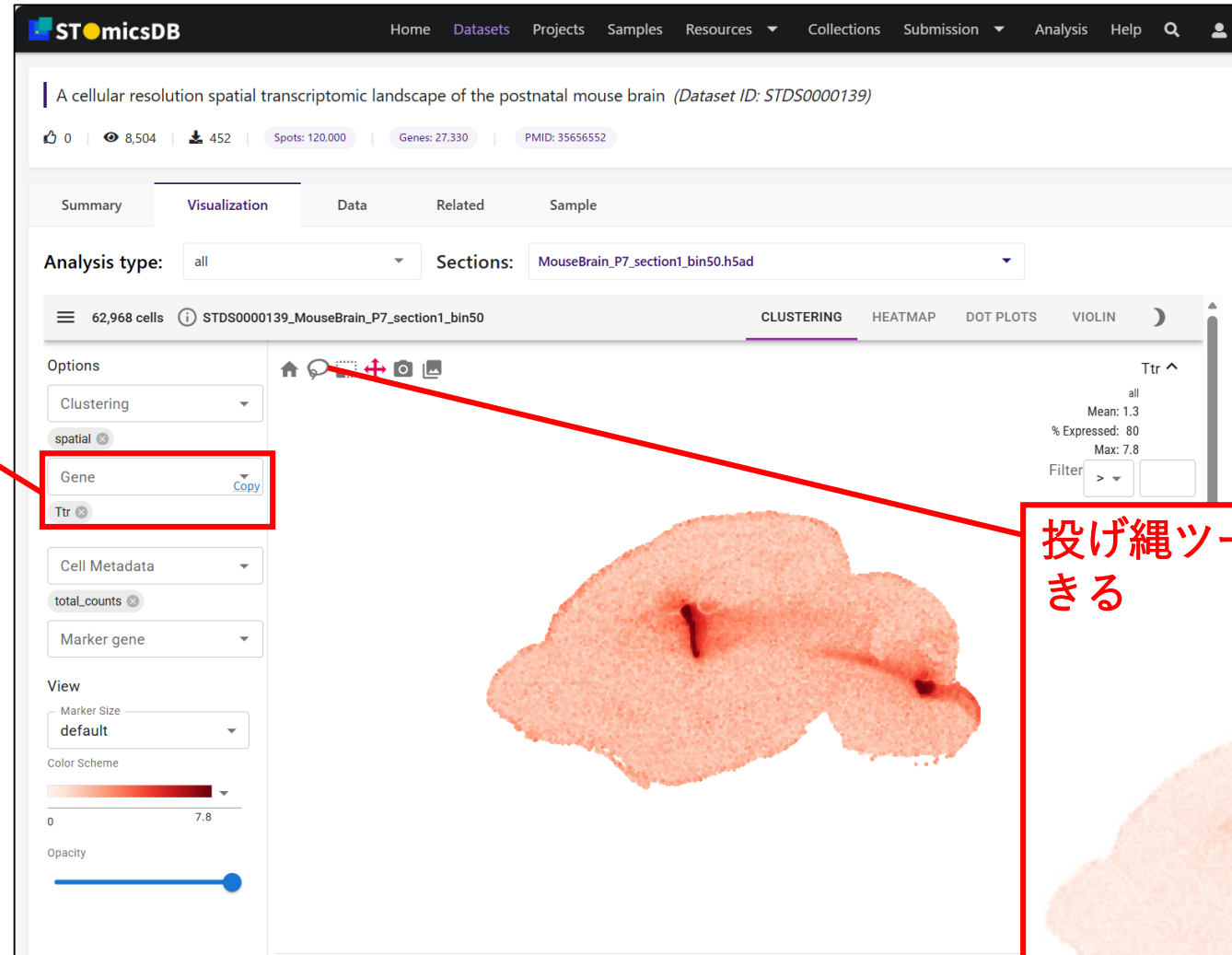
右パネルの画像表示  
種類を選択できるよ  
うに見えるが、  
Stereo-seqサンプル  
の場合は1種類しか  
ない



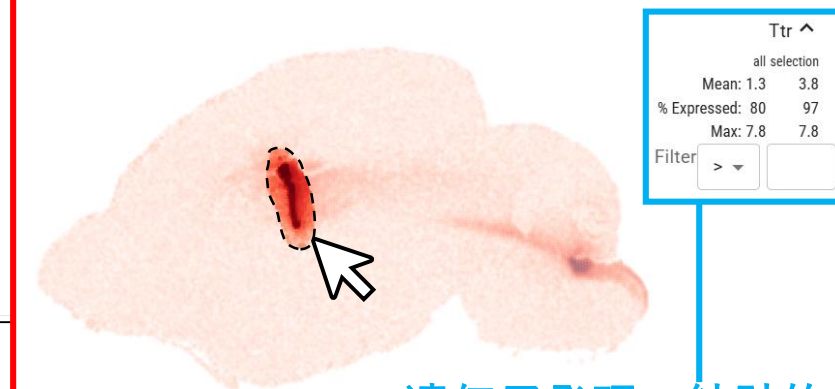
Here:  
細胞種や組織のアノ  
テーション

# STOmicsDB – Visualization (2)

遺伝子発現パターン  
を見る



投げ縄ツールで好きな領域を選択できる



遺伝子発現の統計的  
サマリー



# STOmicsDB – Data



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**STOmicsDB** Home Datasets Projects Samples Resources Collections Submission Analysis Help

A cellular resolution spatial transcriptomic landscape of the postnatal mouse brain (Dataset ID: STDS0000139)

0 8,507 452 Spots: 120,000 Genes: 27,330 PMID: 35656552

Summary Visualization **Data** Related Sample

Data type  
stomics

Show 10 results Analysis type Download table (0)

	File name	File type	Analysis type	Sample name	Size	Identifiers
<input type="checkbox"/>	MouseBrain_P7_section1_bin50.h5ad	h5ad	processed	P7_section1_Bin50	3.0G	
<input type="checkbox"/>	MouseBrain_P7_section1_singlecell.h5ad	h5ad	processed	P7_section1_singlecell	1.5G	

Showing 1 to 2 of 2 result(s).

\*h5ad: AnnData format of original data, without any additional modifications by STOmicsDB.  
\*processde.h5ad: AnnData format, with analysis results generated by STOmicsDB.

h5ad 形式でダウンロード可能

Summary Visualization Data **Related** Sample

Related type	Related ID	Related link	Related title
CNSA project	CNP0002646	<a href="https://db.cngb.org/search/project/CNP0002646/">https://db.cngb.org/search/project/CNP0002646/</a>	--

Summary Visualization Data Related **Sample**

Show 10 results

Sample ID	Sample title	Species	Tissues	Disease	Sex	Technology	Source	Sample quality	action
STSP0005129	P7_section1_singlecell	Mus musculus	Brain	--	--	Stereo-Seq	CNGB	★★★★★	
STSP0005187	P7_section1_Bin50	Mus musculus	Brain	--	--	Stereo-Seq	CNGB	★★★★★	

Showing 1 to 2 of 2 result(s).

生データへのリンク

**CNGBdb** GENOS Scientific databases Submission Analysis Download About Login

Home / Data resources / Project / CNP0002646

Spatial transcriptomics of brain for the postnatal day 7 mouse  
Source: CNGBdb Project (ID CNP0002646)

474 270

Description: Brain develops in an intricately orchestrated sequence of stages, which starts with neurulation from the ectoderm of the embryo and takes a long time to postnatal to mature. A complete understanding of this process requires a systematic characterization of cell states over the entire spatiotemporal range of brain development. Recently technology of spatial transcriptome has brought new insight to the field of brain science. This new era capitalizes on high-resolution molecular tools that enable large-scale mapping of markers, which, in an unbiased and unsupervised fashion, capture the complexity of the nervous system. Here we use stereo-seq performed the spatial characteristic of the whole brain of the developing mouse at a key timepoint: postnatal day 7 (P7).

Data type: Raw sequence reads

Sample scope: Monoisolate

Submitter: 成梦南(Grace Cheng); 深圳华大生命科学研究院

Release date: 2022-04-29

Last updated: 2022-01-27

DOI: 10.26036/CNP0002646

Statistics: 2 samples; 2 experiments; 12 runs

Data size: 2.2TB

Download data Download metadata Get FTP links of all files

Runs

Run ID	Platform	Library layout	Organism	Experiment ID	Sample ID	Operation
CNR0495629	DNBSEQ-T7	paired	Mus musculus	CNX0412126	CNS0513001	<a href="#">Download data (183.0GB)</a>
CNR0495630	DNBSEQ-T7	paired	Mus musculus	CNX0412126	CNS0513001	<a href="#">Download data (192.8GB)</a>
CNR0495631	DNBSEQ-T7	paired	Mus musculus	CNX0412126	CNS0513001	<a href="#">Download data (185.66GB)</a>
CNR0495632	DNBSEQ-T7	paired	Mus musculus	CNX0412126	CNS0513001	<a href="#">Download data (220.12GB)</a>
CNR0495633	DNBSEQ-T7	paired	Mus musculus	CNX0412126	CNS0513001	<a href="#">Download data (189.58GB)</a>

# STOmicsDB – Visium example



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フィルターをセットする: Species = “human”,  
Tissues = “Breast”, Technology = “10x Visium”

左のリストから一つ選ぶ

STOmicsDB

Home Datasets Projects Samples Resources Collections Submission Analysis Help

« Datasets

Search Advanced

Date range

Species

- ☒ Homo sapiens (human) 8
- ☐ Ambystoma mexicanum (axolotl) 0
- ☐ Arabidopsis thaliana (thale-cress) 0
- ☐ Bos taurus (cattle) 0
- ☐ Caenorhabditis elegans (roundworm) 0

More >

Tissues

- ☒ Breast 8
- ☐ ACA 0
- ☐ ACP close to the hypothalamus 0
- ☐ ACP distant from the hypothalamus 0
- ☐ AI-CLA 0

More >

Technology

- ☒ 10x Visium 8
- ☐ 10x Visium, MERFISH 0
- ☐ 10x Visium, Spatial Transcriptomic... 0
- ☐ 10x Visium, scATAC, scRNA 0
- ☐ 10x Visium, scRNA 0

List (8) Table

Relevance (0)

1 Human Breast Cancer: Ductal Carcinoma In Situ, Invasive Carcinoma (FFPE) (ID: STDS0000049)

5 µm section from Invasive Ductal Carcinoma of Homo sapiens Breast. FFPE tissue purchased from BioIVT Asterand Homo sapiens Tissue Specimens (BioIVT):

2021-06-09 0 3,944 851 Homo sapiens Spots: 2,518 10x Visium

2 Invasive Ductal Carcinoma Stained With Fluorescent CD3 Antibody (ID: STDS0000028)

Visium Spatial Gene Expression Dataset processed with Spaceranger 1.2. Invasive ductal carcinoma was obtained from BioIVT: ASTERAND (Westbury, NY). Raw sequencing data (FASTQ and BAM files) are not include...

2021-05-11 0 1,090 336 Homo sapiens Spots: 4,727 10x Visium

3 Human Cerebellum: Targeted, Neuroscience Panel (ID: STDS0000045)

10x Genomics obtained fresh frozen Homo sapiens cerebellum tissue from BioIVT Asterand. The tissue was embedded and cryosectioned as described in Visium Spatial Protocols – Tissue Preparation Guide...

2020-10-27 0 553 240 Homo sapiens Spots: 4,992 10x Visium

4 Human Cerebellum: Whole Transcriptome Analysis (ID: STDS0000044)

10x Genomics obtained fresh frozen Homo sapiens cerebellum tissue from BioIVT Asterand. The tissue was embedded and cryosectioned as described in Visium Spatial Protocols – Tissue Preparation Guide...

2020-10-27 0 658 300 Homo sapiens Spots: 4,992 10x Visium

5 Human Breast Cancer: Targeted, Immunology Panel (ID: STDS0000039)

STOmicsDB

Home Datasets Projects Samples Resources Collections Submission Analysis Help

Human Breast Cancer: Ductal Carcinoma In Situ, Invasive Carcinoma (FFPE) (Dataset ID: STDS0000049)

0 3,945 851 Spots: 2,518 Genes: 17,943

Summary Visualization Data Analysis results Related Sample

Catalog

Dataset information

Summary: 5 µm section from Invasive Ductal Carcinoma of Homo sapiens Breast. FFPE tissue purchased from BioIVT Asterand Homo sapiens Tissue Specimens (BioIVT):

Technology: 10x Visium

Species: Homo sapiens (hg38)

Tissues: Breast

Sex: Female

Disease: Breast Cancer

Submission date: 2021-06-09 Update date: 2021-06-09

Sample number: 1 Section number: 1

DOI: 10.26036/STDS0000049

Contributors

No results.

Accessions

10x visium data: 10x GENOMICS

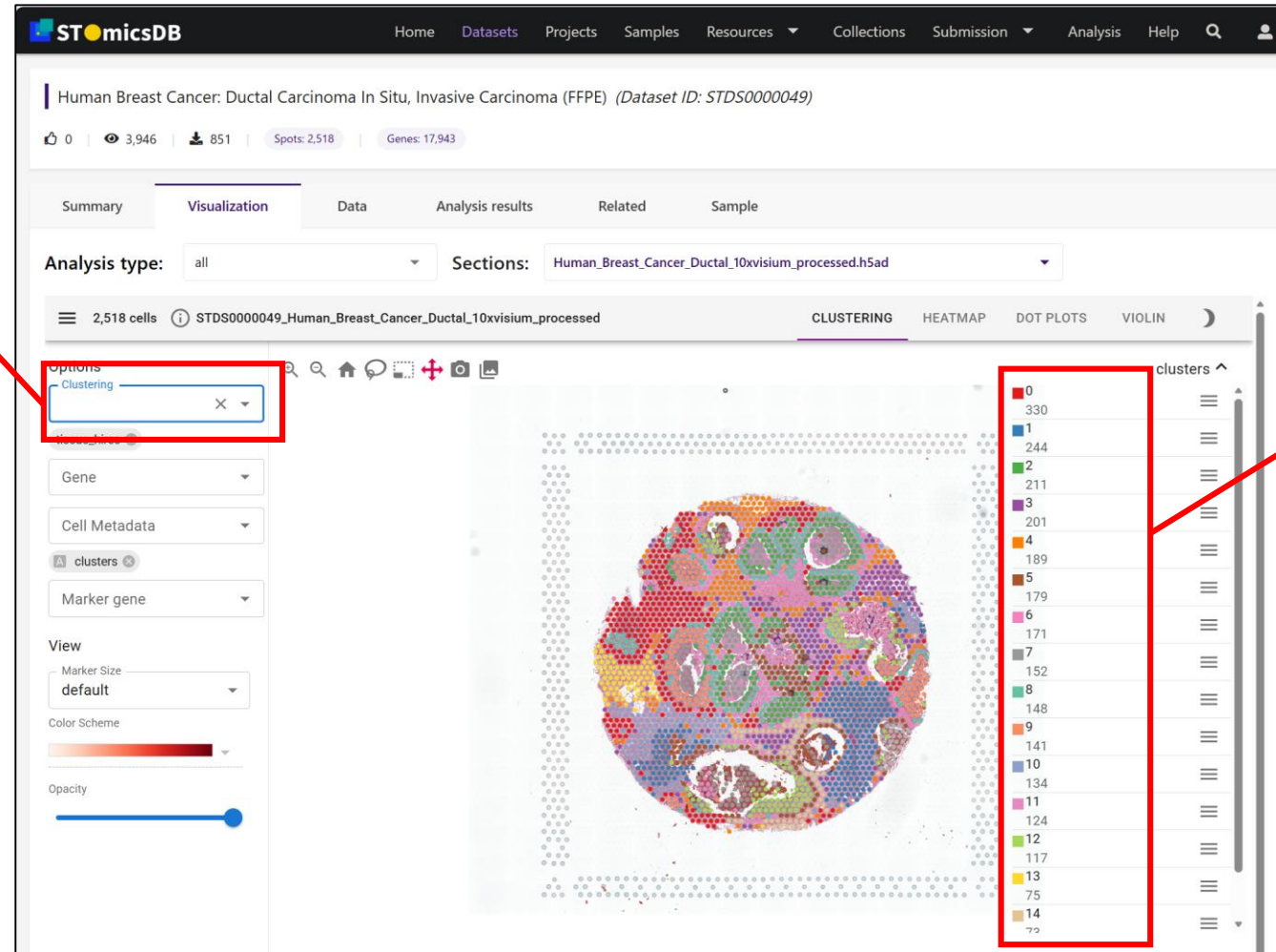
How to cite

- Cite database of STOmicsDB:  
[1] Xu, Zhicheng et al. "STOmicsDB: a comprehensive database for spatial transcriptomics data sharing, analysis and visualization." Nucleic acids research vol. 52,D1 (2024): D1053-D1061. doi: 10.1093/nar/gkad933
- Cite visualization dataset:  
[2] xxxxxx: Human Breast Cancer: Ductal Carcinoma In Situ, Invasive Carcinoma (FFPE)[DS/OL]. STOmicsDB, 2021[2021-06-09].  
<https://db.cngb.org/stomics/datasets/STDS0000049/>. doi: 10.26036/STDS0000049

# STOmicsDB – Visualization (Visium) (1)

右側の画像の表示方法  
の選択

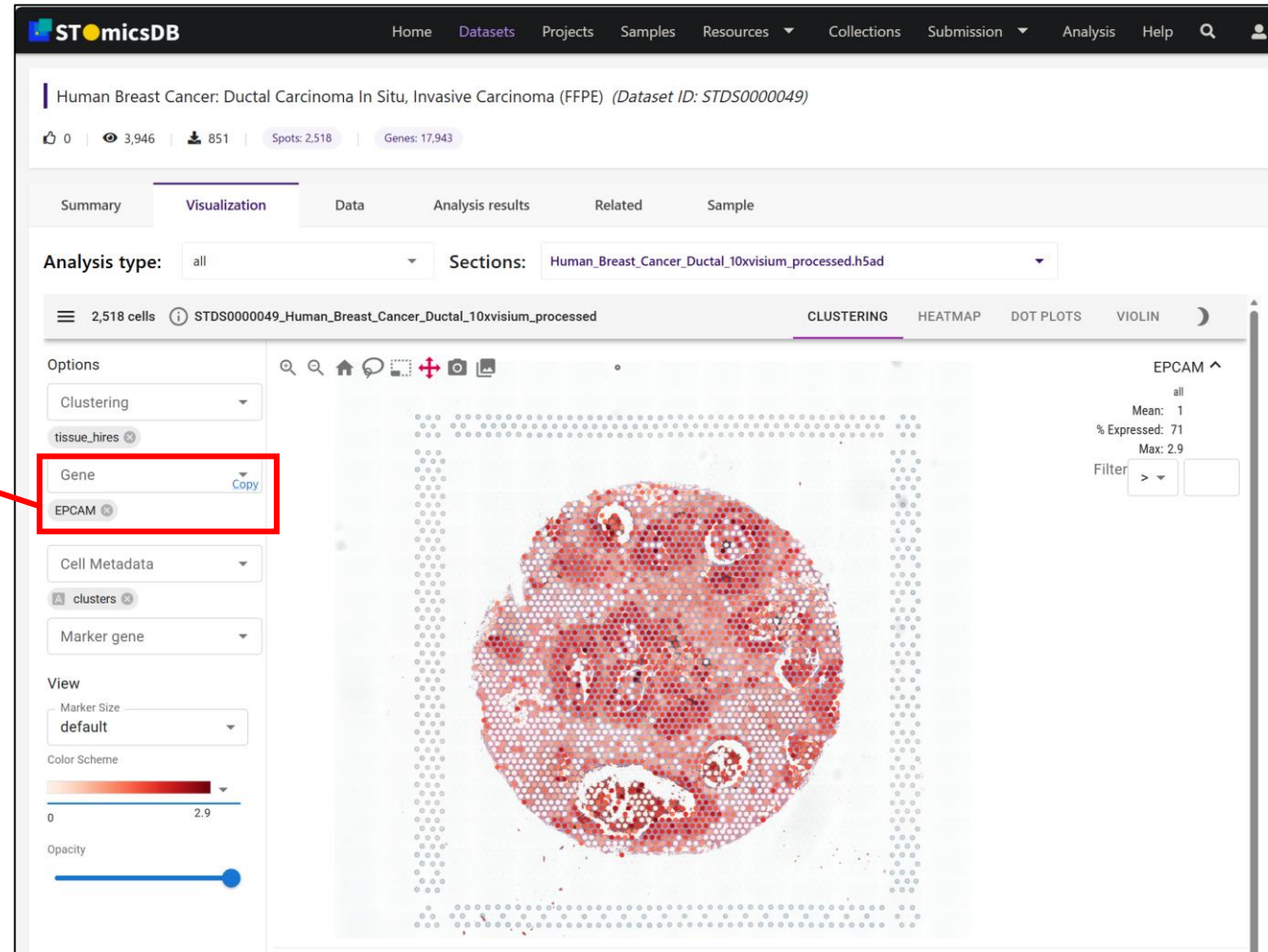
spatial  
tissue-hires  
umap



クラスター

# STOmicsDB – Visualization (Visium) (2)

遺伝子を選び、遺伝子発現パターンを表示させる



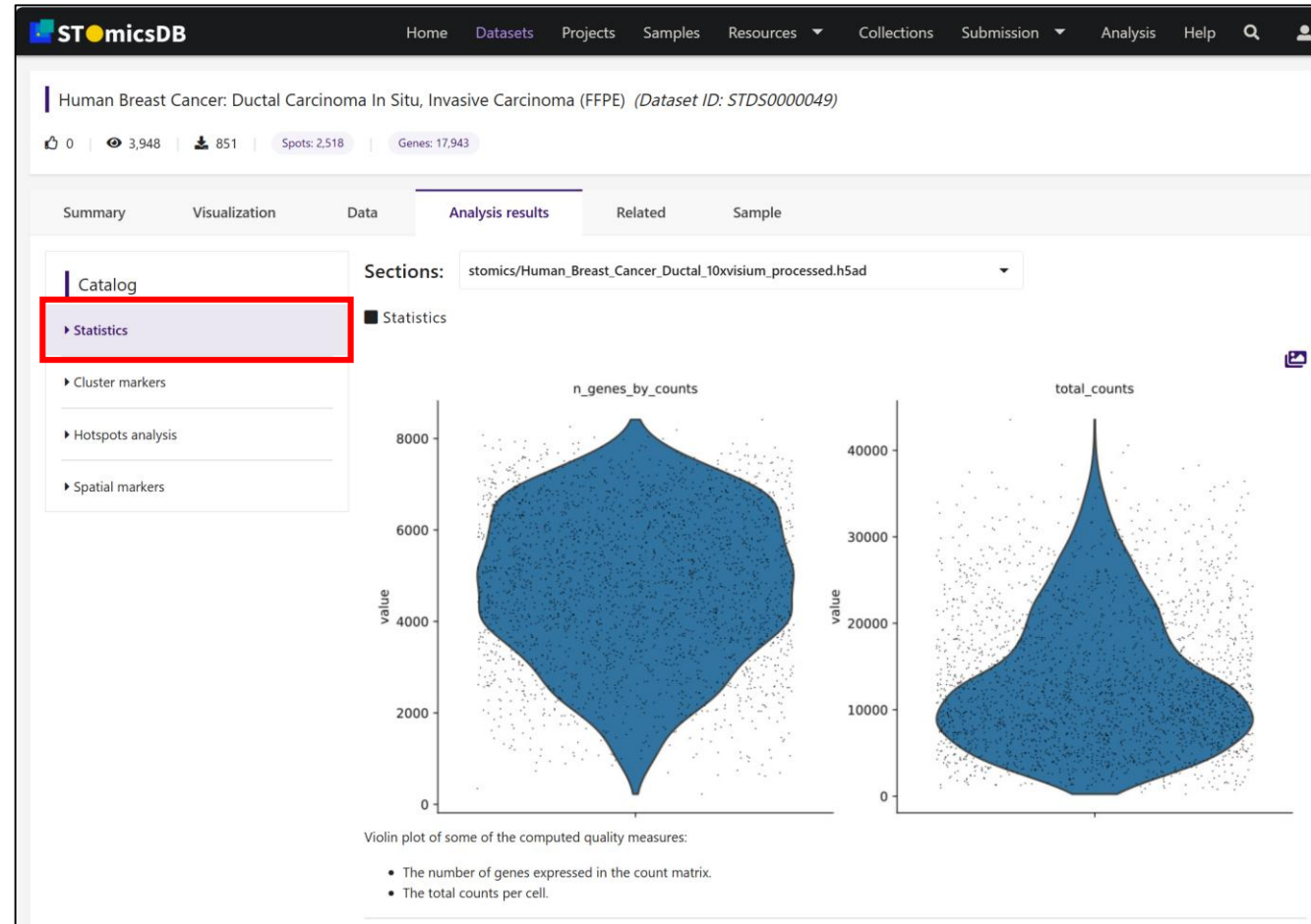


# STOmicsDB – Analysis results (Visium) (1)



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Note: プラットフォームによって利用できるツールが異なる

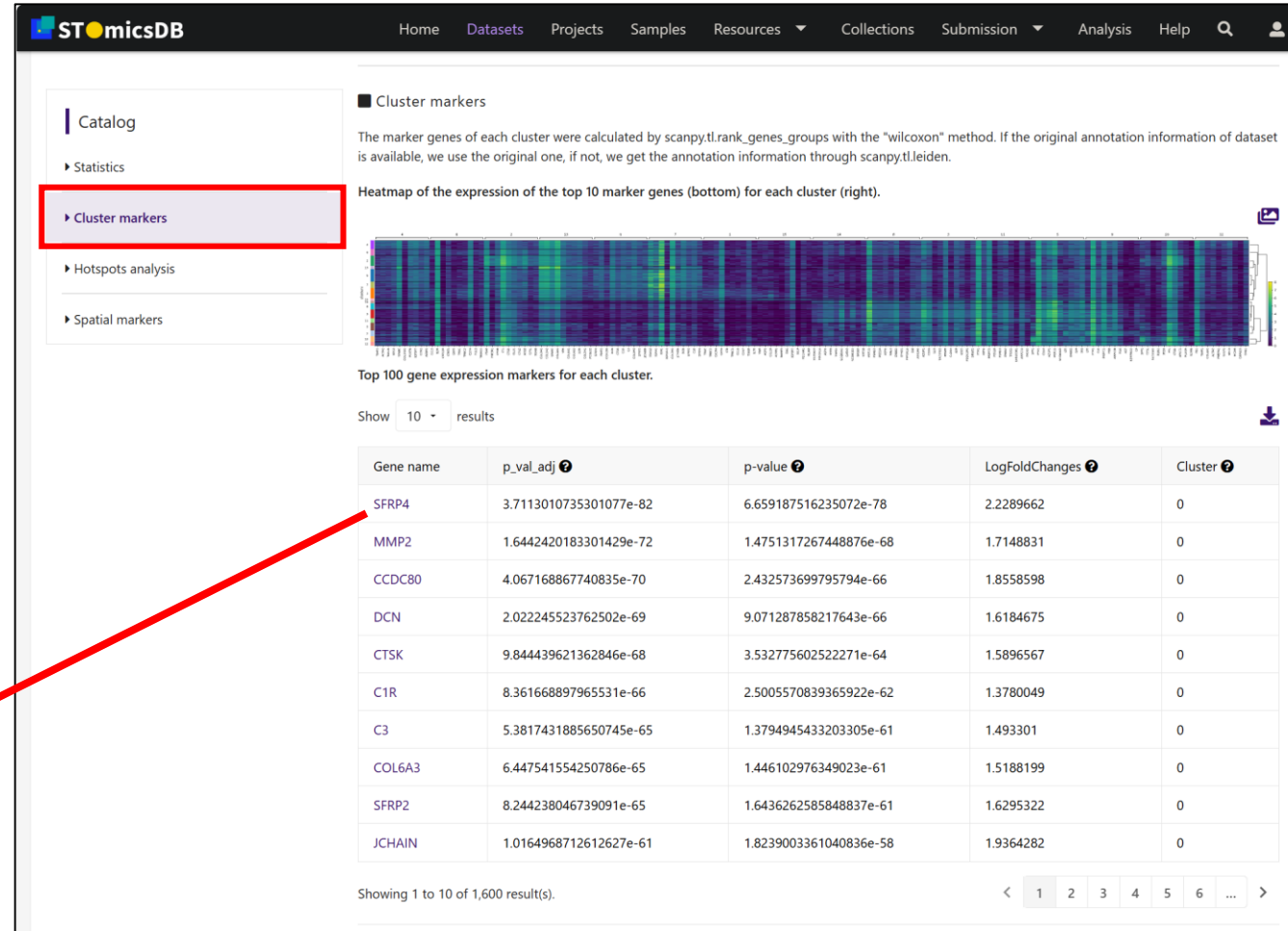


# STOmicsDB – Analysis results (Visium) (2)

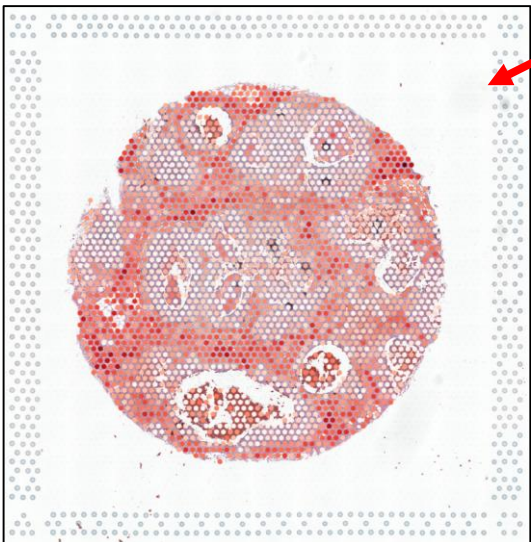


38

Note: プラットフォームによって利用できるツールが異なる

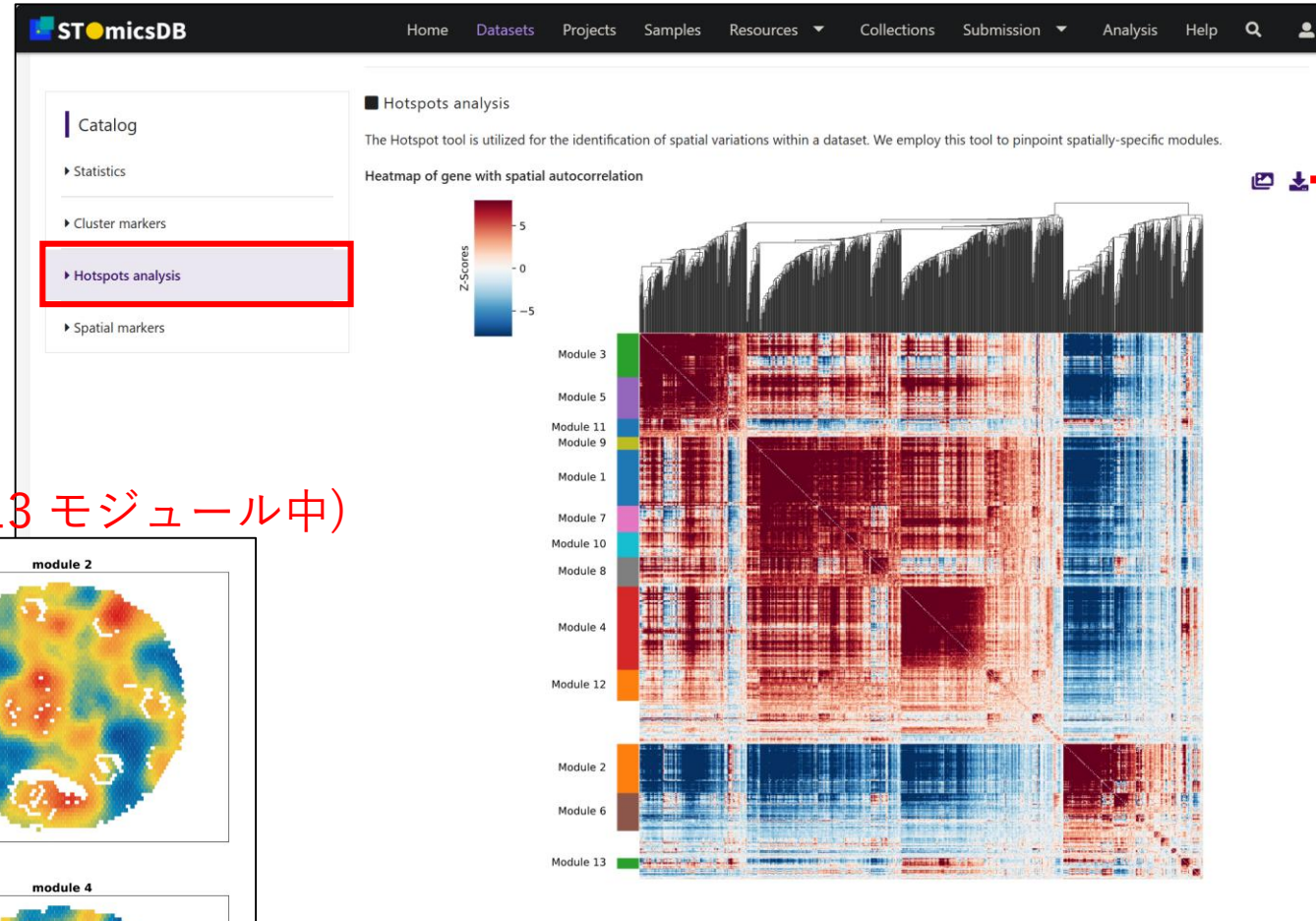


Geneをクリックすると、  
発現パターンのページに  
リンクする。



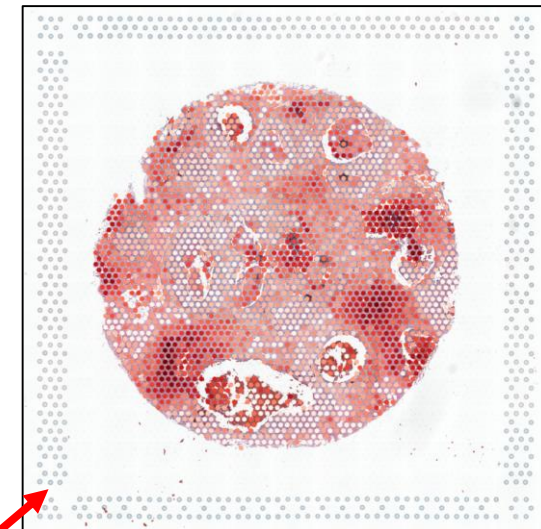
# STOmicsDB – Analysis results (Visium) (3)

Note: プラットフォームによって利用できるツールが異なる

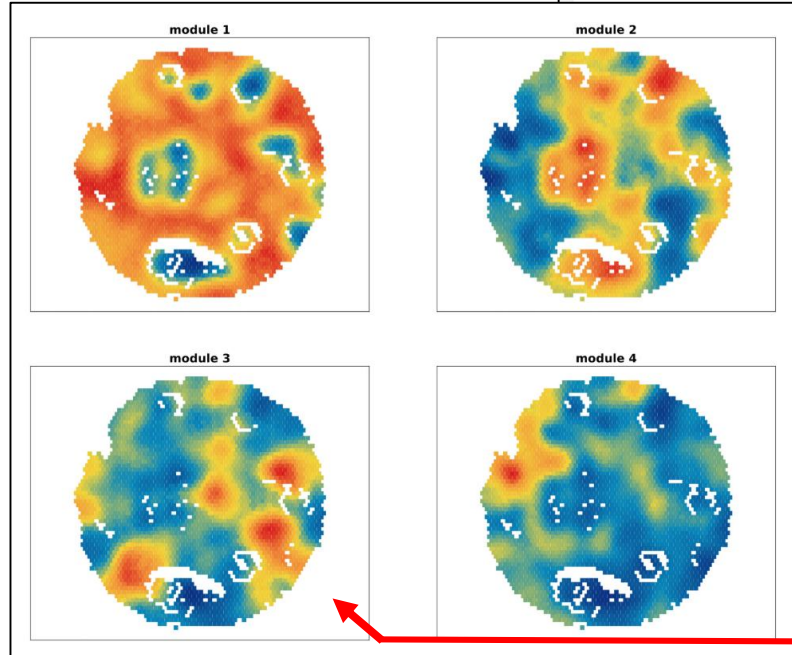


ダウンロード (約1000  
個の遺伝子リスト)  
例としてmodule3に属  
するAPOC1を見てみる  
と

APOC1発現パターン



例: モジュール1 ~ 4 (全13 モジュール中)



発現パターンはモジュール3と似ている事がわかる



# STOmicsDB – Analysis results (Visium) (4)



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Note: プラットフォームによって利用できるツールが異なる

STOmicsDB

Home Datasets Projects Samples Resources Collections Submission Analysis Help

**Spatial markers**

Spatially specific genes were identified by SpatialDE (<https://github.com/Teichlab/SpatialDE>) with default options. SpatialDE identifies genes using spatial coordinates. It can be used to spatially resolve RNA-sequencing (e.g. Spatial Transcriptomics), or in situ gene expression measurements (e.g. SeqFISH or MERFISH).

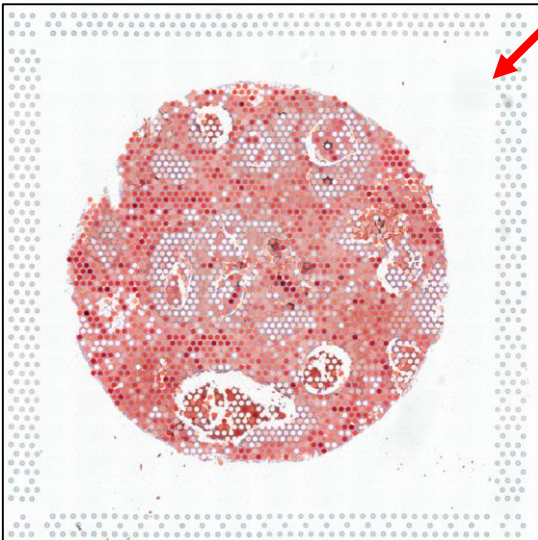
Show 10 results

Gene name	p-value	q-value	I	Max_delta	Max_ll	Max_mu_hat	Max_s2_t
A2M	0.0	0.0	482.88131414...	1.9383192508...	-2651.484957...	1.1800456542...	0.2713584
AAMP	0.0	0.0	482.88131414...	4.3509832352...	-2186.378124...	0.7667497270...	0.0938177
AARD	0.0	0.0	881.20428215...	8.0508302370...	-583.0216138...	0.1407644310...	0.0112068
ABCA1	0.0	0.0	881.20428215...	4.1787033783...	-2008.452465...	0.5381946489...	0.0683962
ABCA12	0.0	0.0	881.20428215...	2.4597702792...	-236.9229188...	0.0972780890...	0.0257953
ABCA8	0.0	0.0	881.20428215...	4.8508763297...	-1080.016141...	0.1744085227...	0.0267909
ABCC11	0.0	0.0	881.20428215...	3.1777790534...	-165.7055302...	0.1147443827...	0.0192396
ABCC3	0.0	0.0	881.20428215...	8.1848578593...	-1338.972755...	0.2353981223...	0.0204270
ABCC4	0.0	0.0	482.88131414...	3.2110560076...	-1958.676212...	0.5352351780...	0.0872909
ABCD3	0.0	0.0	482.88131414...	4.1206465969...	-1836.418633...	0.5180715840...	0.0656308

Showing 1 to 10 of 17,651 result(s).

ダウンロード (17651個の遺伝子リスト)

遺伝子をクリックすると  
発現パターンページに  
ジャンプする







- 3,461 サンプル
- 13 種
- 19 テクノロジー

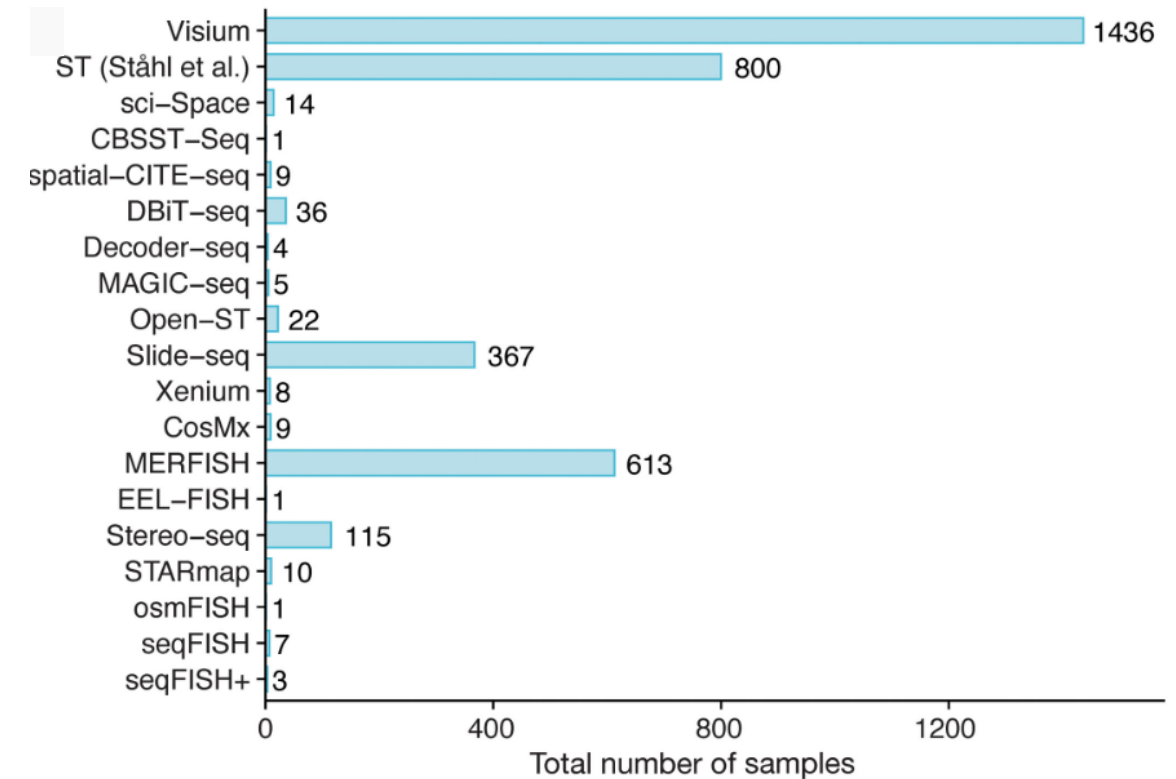


Figure from Li *et al.*, Scientific Advances, 2025

# SOAR – Data Browser (Visium) (1)



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**Data Browser**

- Click on a **Sample number** to visualize spatial gene expression and view its spatial variability analysis results
- The datasets are categorized into different research topics (the **Topic** column), and sample-wise conditions are recorded in the **Condition** column

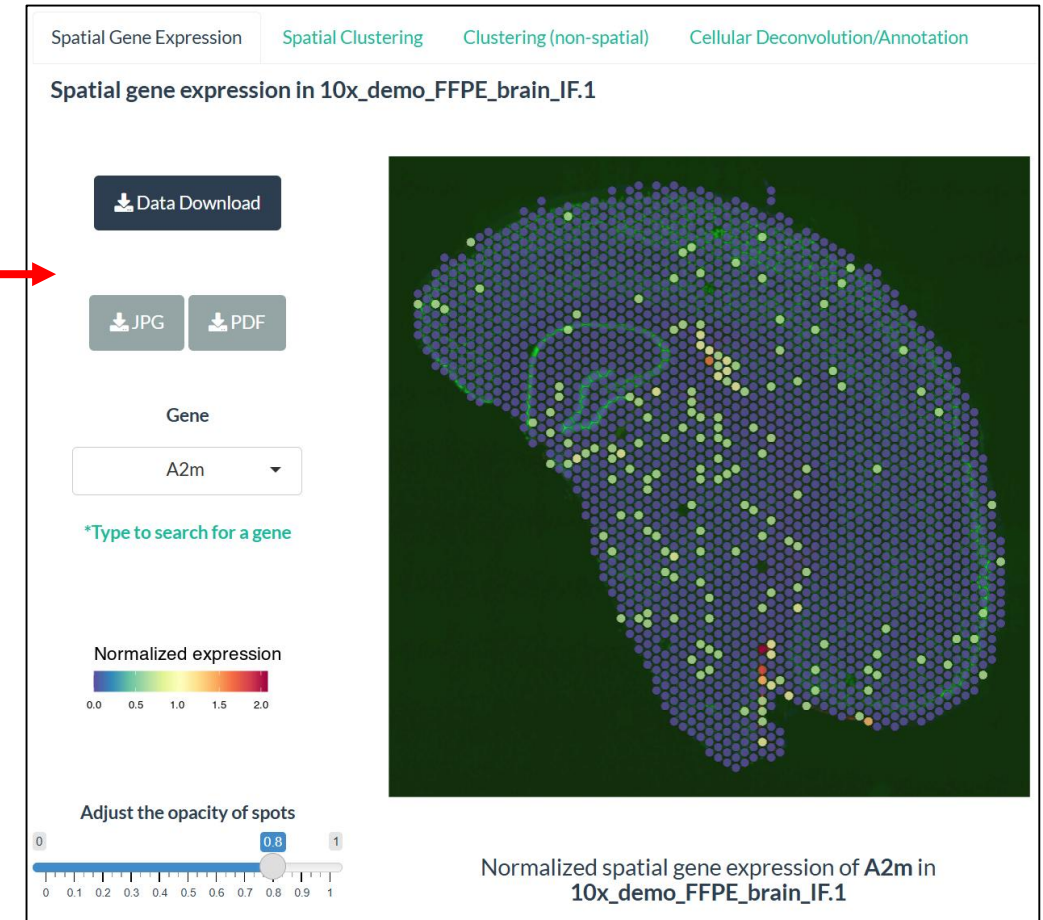
Show  entries

Search:

Dataset	Sample	Technology	Species	Organ	Tissue	Condition	Topic	#Spots	#Genes	Publication year	Source
10x_demo_GE_breast_cancer_sec1	<a href="#">1</a>	Visium	Human	Breast	Breast Cancer	Malignant	Pathological	3797	21129	2020	<a href="#">10x website</a>
10x_demo_FFPE_brain_IF	<a href="#">1</a>	Visium	Mouse	Brain		Normal	Normal	2407	15180	2020	<a href="#">10x website</a>
10x_demo_FFPE_brain	<a href="#">1</a>	Visium	Mouse	Brain		Normal	Normal	2258	15202	2020	<a href="#">10x website</a>
10x_demo_FFPE_breast_cancer	<a href="#">1</a>	Visium	Human	Breast	Breast Cancer	Malignant	Pathological	2516	15946	2020	<a href="#">10x website</a>
10x_demo_FFPE_kidney	<a href="#">1</a>	Visium	Mouse	Kidney		Normal	Normal	3106	15588	2020	<a href="#">10x website</a>
10x_demo_FFPE_prostate_adj_norm	<a href="#">1</a>	Visium	Human	Prostate	Normal	Adjacent Normal of Cancer	Normal	3459	15497	2020	<a href="#">10x website</a>
10x_demo_FFPE_prostate_cancer	<a href="#">1</a>	Visium	Human	Prostate	Prostate Cancer	Malignant	Pathological	4369	15574	2020	<a href="#">10x website</a>
10x_demo_FFPE_prostate	<a href="#">1</a>	Visium	Human	Prostate		Normal	Normal	2542	14840	2020	<a href="#">10x website</a>
10x_demo_GE_breast_cancer_sec2	<a href="#">1</a>	Visium	Human	Breast	Breast Cancer	Malignant	Pathological	3983	21187	2020	<a href="#">10x website</a>
10x_demo_GE_coronal	<a href="#">1</a>	Visium	Mouse	Brain		Normal	Normal	2697	18768	2020	<a href="#">10x website</a>

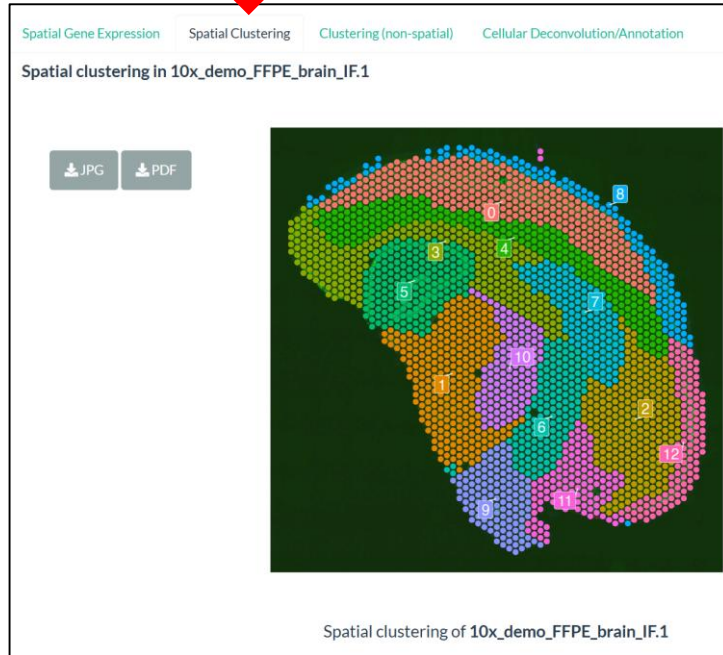
Showing 1 to 10 of 3,461 entries

Previous [1](#) [2](#) [3](#) [4](#) [5](#) ... [347](#) Next

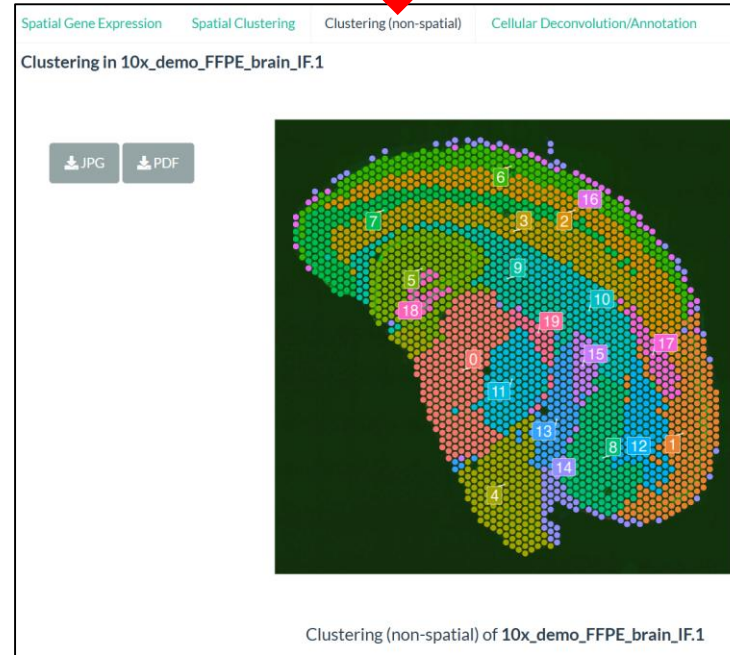


# SOAR – Data Browser (Visium) (2)

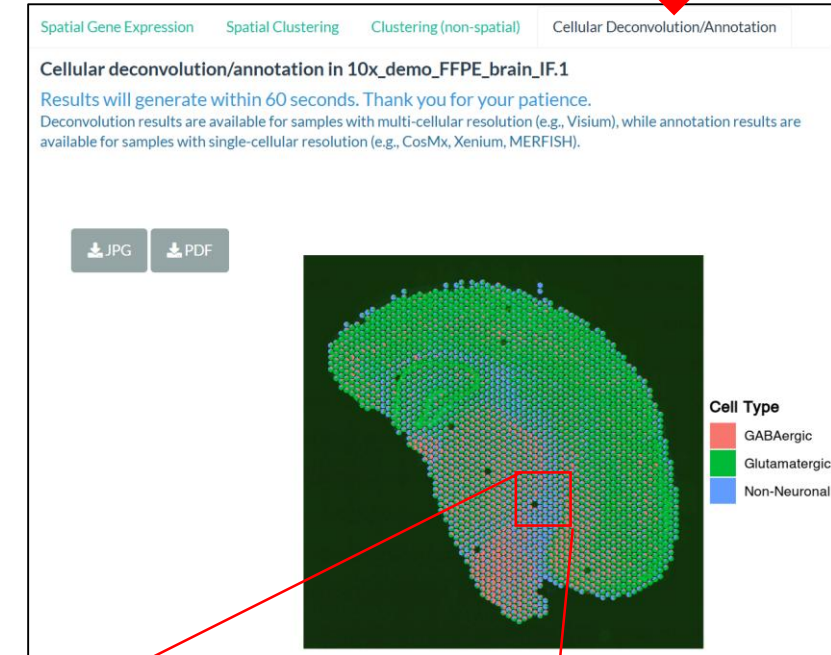
STAGATEを用いた  
spatial domains



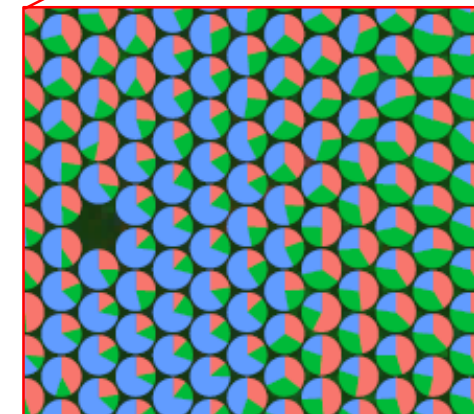
遺伝子発現のみに基づく  
クラスタリング



細胞種予測



予測された細胞種の割合がスポット  
にパイチャートで表示される





# SOAR – Data Browser (Xenium) (1)



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SOAR Data Browser Gene & Cell Analysis Drug Discovery Download Help

**Data Browser**

- Click on a [Sample number](#) to visualize spatial gene expression and view its spatial variability analysis results
- The datasets are categorized into different research topics (the [Topic](#) column), and sample-wise conditions are recorded in the [Condition](#) column

Show 10 entries

Search:

Dataset	Sample	Technology	Species	Organ	Tissue	Condition	Topic	#Spots	#Genes	Publication year	Source
All	All	Xenium x	All	All	All	All	All	All	All	All	All
Schott_2024_Human_Primary_HNSCC_xenium	<a href="#">1</a>	CBSST-Seq CosMx DBiT-seq Decoder-seq EEL-FISH MAGIC-seq MERFISH Open-ST	Human	Head and Neck	Head and Neck Squamous Cell Carcinoma	Malignant	Pathological	4731	377	2024	<a href="#">PMID 38917789</a>
Schott_2024_Metastatic_lymph_node_xenium	<a href="#">1</a>		Human	Lymph Node	Lymph Node Metastasis (HNSCC Patients)	Malignant	Pathological	3503	377	2024	<a href="#">PMID 38917789</a>
Xenium_mouse_brain_WT_AD	<a href="#">1</a>	Xenium	Mouse	Brain	TgCRND8 (AD Model)	Normal / Pathological	60767	347	2023	<a href="#">10x website</a>	
Xenium_mouse_brain_WT_AD	<a href="#">2</a>	Xenium	Mouse	Brain	TgCRND8 (AD Model)	Normal / Pathological	53779	347	2023	<a href="#">10x website</a>	
Xenium_mouse_brain_WT_AD	<a href="#">3</a>	Xenium	Mouse	Brain	TgCRND8 (AD Model)	Normal / Pathological	58620	347	2023	<a href="#">10x website</a>	
Xenium_mouse_brain_WT_AD	<a href="#">4</a>	Xenium	Mouse	Brain	Control	Normal / Pathological	59841	347	2023	<a href="#">10x website</a>	
Xenium_mouse_brain_WT_AD	<a href="#">5</a>	Xenium	Mouse	Brain	Control	Normal / Pathological	57967	347	2023	<a href="#">10x website</a>	
Xenium_mouse_brain_WT_AD	<a href="#">6</a>	Xenium	Mouse	Brain	Control	Normal / Pathological	58493	347	2023	<a href="#">10x website</a>	

Showing 1 to 8 of 8 entries (filtered from 3,461 total entries)

Previous 1 Next

“Xenium”を選ぶ

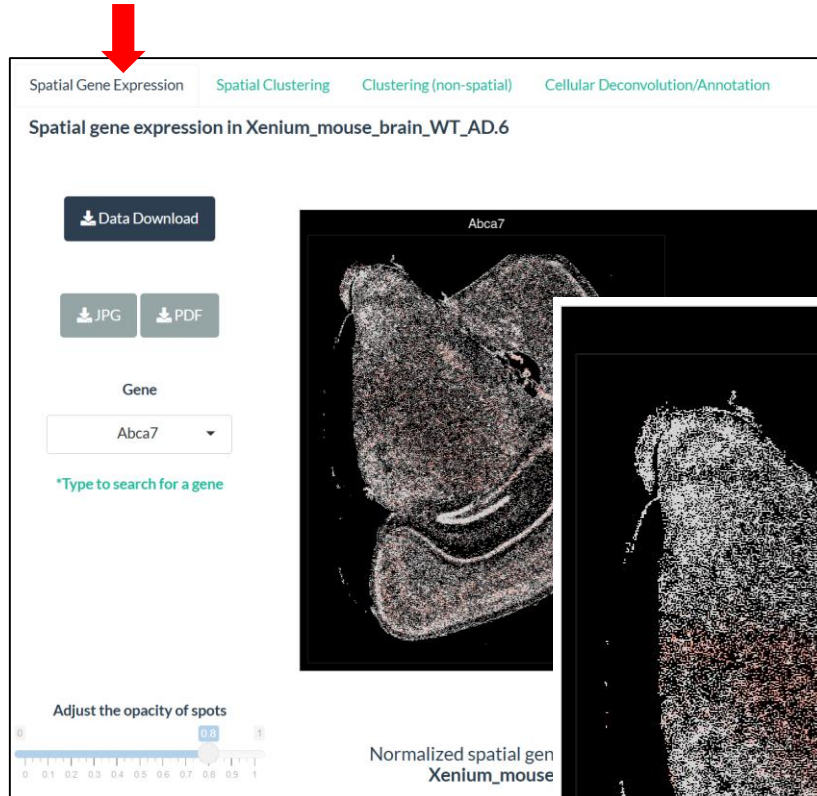
SOAR にはXeniumが  
8サンプル集められている

このマウスの脳サンプルをクリックすると

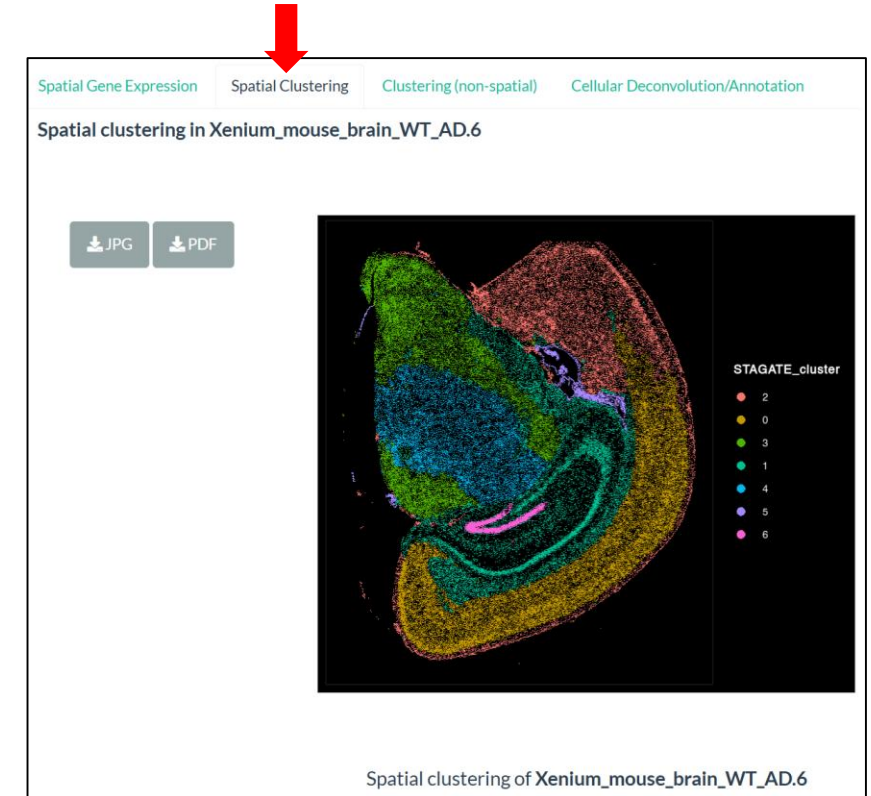


# SOAR – Data Browser (Xenium) (2)

## 遺伝子発現



## STAGATE を用いた 空間的クラスタリング



# 既存のデータベースに共通する特徴



- 優れた点

- 多彩なプラットフォーム
- サンプル数が多い

- だが問題が多い

- 低品質なデータが多く含まれている
- 解析機能が限られている
- 直観的な操作ではない上に反応がしばしば遅い

- Rを使った空間トランスクリプトミクスデータ解析
  - Visium example
  - Xenium example
- 既存の空間トランスクリプトミクスデータベースの紹介
- DeepSpaceDBの紹介
  - Visium interface
  - Xenium interface
- まとめ

## Data Sources



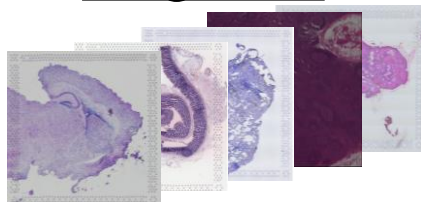
Lung Cell Atlas  
Heart Cell Atlas  
Reproductive Cell Atlas  
Zenodo  
Mendeley Data  
Etc

GEOquery

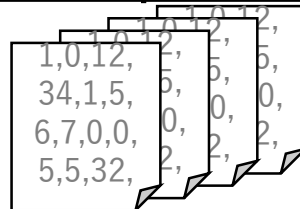
Manual  
collection

## Raw Data

### Image data



### Transcriptome data



### Annotation data

Species, tissue, condition,  
age, sex, publication, etc

## Processed Data

Quality indicators

Curated annotation

Spatially variable genes

Pathway activities

Cell type compositions

Seurat object

## Database



DeepSpaceDB

<https://deepspace-db.com/>

- Samples
- Functions



# アノテーションデータの収集例



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NCBI

Gene Expression Omnibus

HOME | SEARCH | SITE MAP | GEO Publications | FAQ | MIAME | Email GEO

NCBI > GEO > [Accession Display](#) Not logged in | [Login](#)

Scope:  Format:  Amount:  GEO accession:

**Series GSE225766** [Query DataSets for GSE225766](#)

StatusPublic on Jun 16, 2023

TitleA cellular and molecular spatial atlas of dystrophic muscle

Organism[Mus musculus](#)

Experiment typeExpression profiling by high throughput sequencing  
Other

SummaryAsynchronous skeletal muscle degeneration/regeneration is a hallmark feature of Duchenne muscular dystrophy (DMD); however, traditional -omics technologies that lack spatial context make it difficult to study the biological mechanisms of how asynchronous regeneration contributes to disease progression. Here, using the severely dystrophic D2-mdx mouse model, we generated a high-resolution cellular and molecular spatial atlas of dystrophic muscle by integrating spatial transcriptomics and single-cell RNAseq datasets.

Overall designGene expression profiling analysis of spatial transcriptome data taken from wildtype (DBA2/J) and dystrophic (D2-mdx) mouse gastrocnemius/plantaris muscle

Contributor(s)[Stec M, Su Q, Adler C, Zhang L, Ni M, Wei Y, Atwal G, Halasz G](#)

Citation(s)Stec MJ, Su Q, Adler C, Zhang L et al. A cellular and molecular spatial atlas of dystrophic muscle. *Proc Natl Acad Sci U S A* 2023 Jul 18;120(29):e2221249120. PMID: 37410813

Submission dateFeb 21, 2023

Last update dateSep 18, 2023

Contact nameMichael Stec

Organization nameRegeneron Pharmaceuticals

Street address777 Old Saw Mill River Rd

CityTarrytown

State/provinceNY

ZIP/Postal code10591

CountryUSA

Platforms (1)[GPL19057](#) Illumina NextSeq 500 (Mus musculus)

Samples (11)[GSM7055901](#) WT1  
[GSM7055902](#) WT2  
[GSM7055903](#) MDX1  
[GSM7055904](#) MDX2  
[GSM7055905](#) WT3  
[GSM7055906](#) MDX3  
[GSM7055907](#) MDX4

[Less...](#)

**Sample GSM7055907** [Query DataSets for GSM7055907](#)

StatusPublic on Jun 16, 2023

TitleMDX4

Sample typeSRA

Source nameGastrocnemius

Organism[Mus musculus](#)

Characteristics  
tissue: Gastrocnemius  
genotype: MDX

Extracted moleculepolyA RNA

Extraction protocol10x Genomics Visium Spatial Gene Expression for Fresh Frozen Tissue v1.0

Library strategyRNA-Seq

Library sourcetranscriptomic

Library selectioncDNA

Instrument modelIllumina NextSeq 500

Data processing  
Spaceranger 1.3.0  
Assembly: mm10

Submission dateFeb 21, 2023

Last update dateSep 18, 2023

Contact nameMichael Stec

Organization nameRegeneron Pharmaceuticals

Street address777 Old Saw Mill River Rd

CityTarrytown

State/provinceNY

ZIP/Postal code10591

CountryUSA

Platform ID[GPL19057](#)

Series (1)[GSE225766](#) A cellular and molecular spatial atlas of dystrophic muscle

**Relations**  
[BioSample SAMN33402466](#)

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE225766>

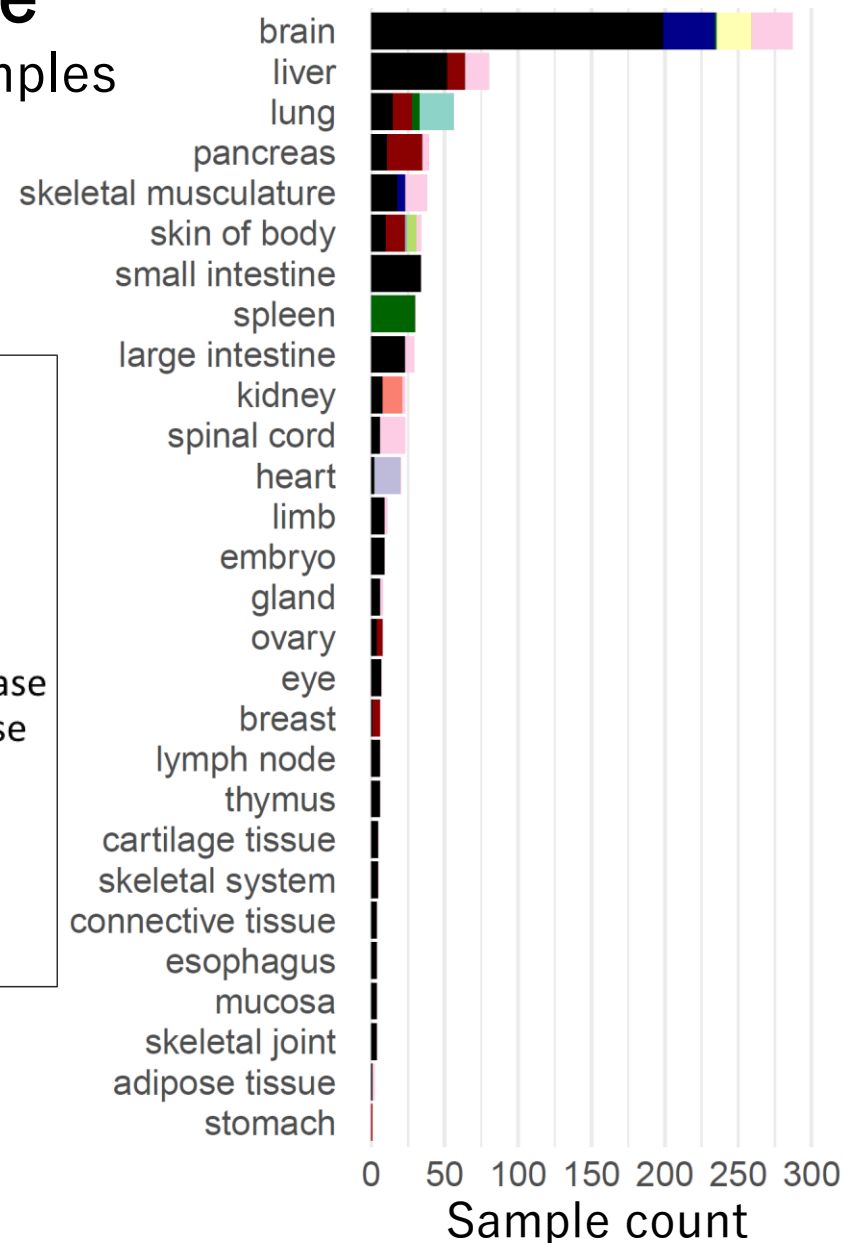
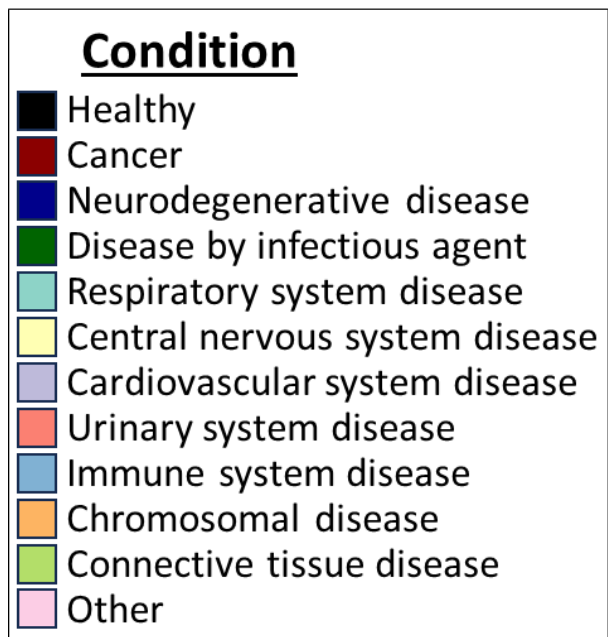
# UBERON anatomy ontology

# Human disease ontology

- アノテーション作業は非常に時間がかかる
- 高度な専門性が必要となる
- LLMsを使い、部分的な自動化を目指したい

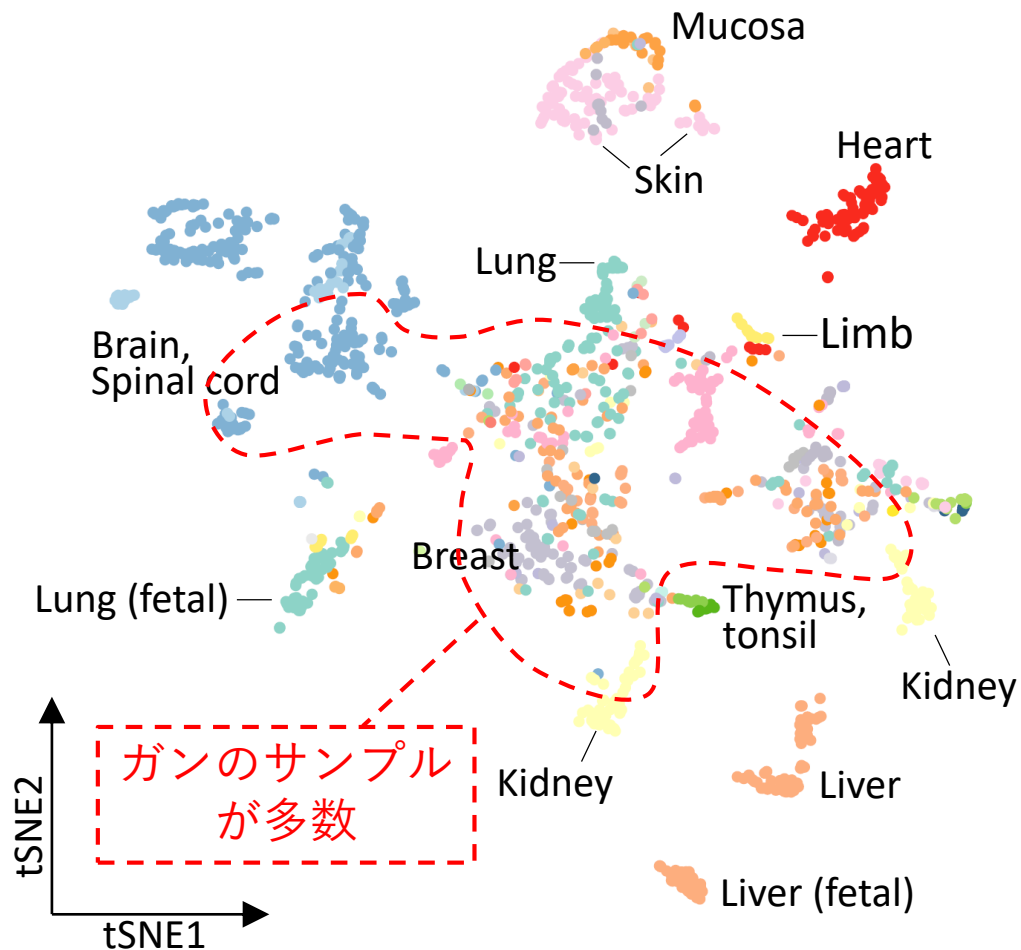
# Mouse

783 samples

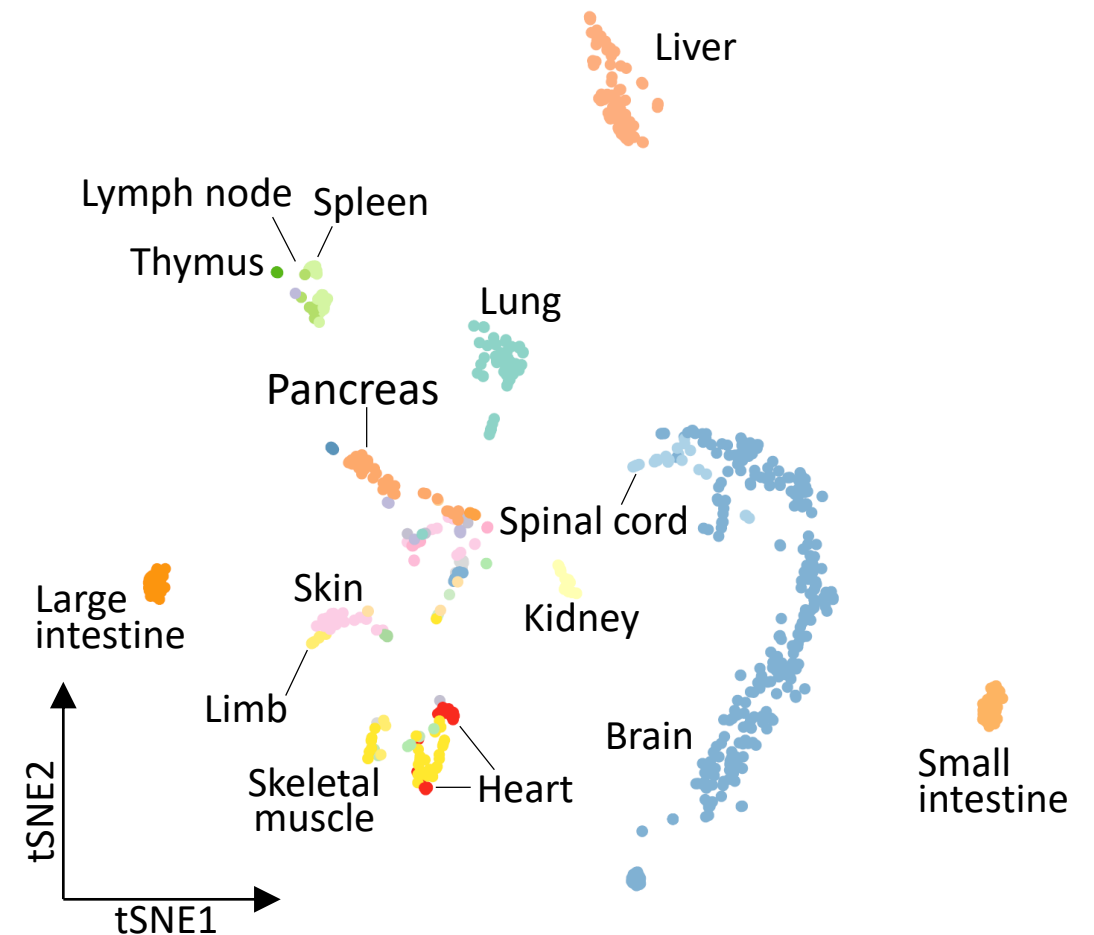


- 全てのサンプルを“pseudo-bulk”として埋め込み2次元に圧縮
- 関連する組織は似た遺伝子発現パターンを示す

## Human tissue slices



## Mouse tissue slices



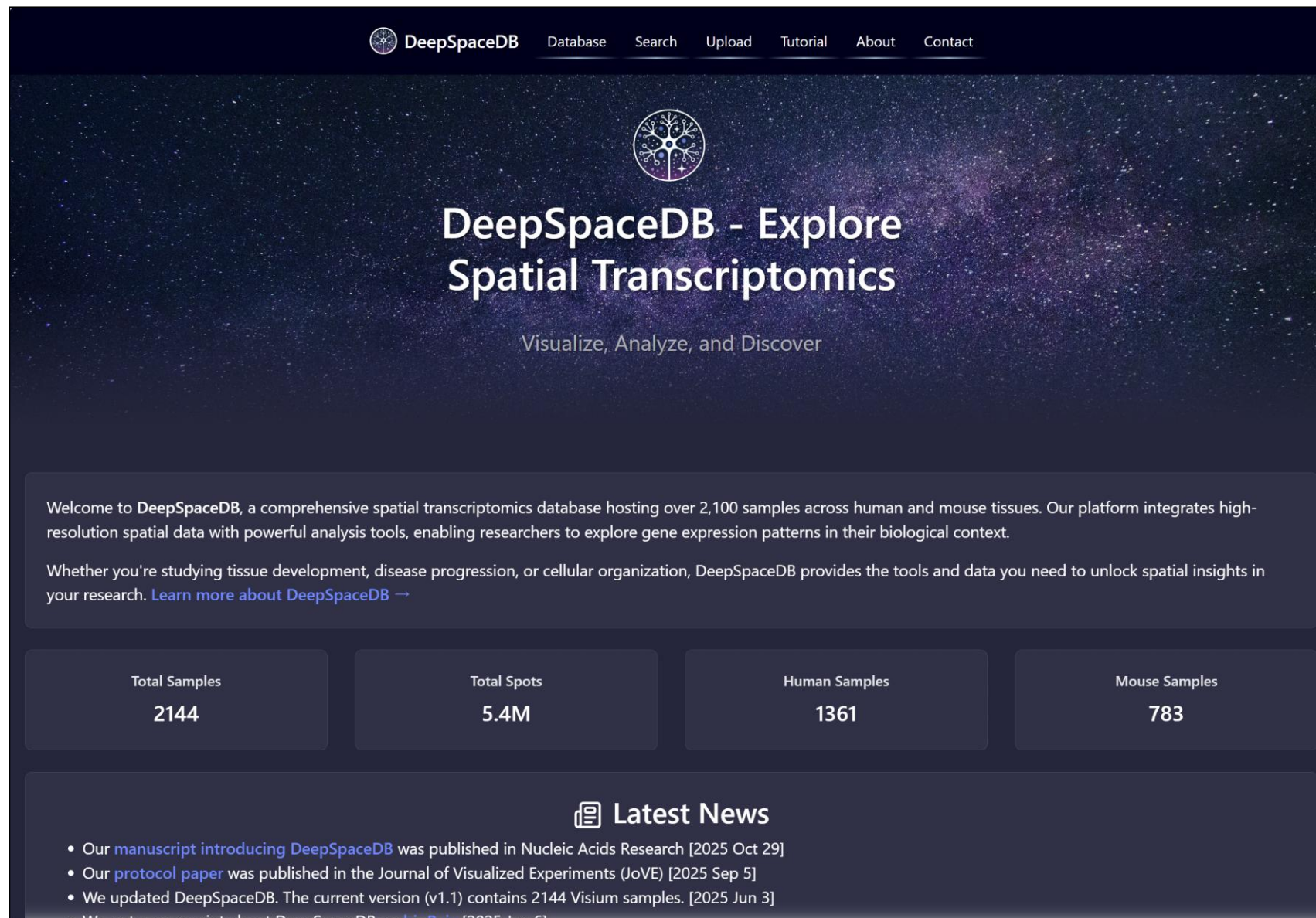


# DeepSpaceDB – Top page



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1. **Database:**  
サンプル検索
2. **Search:**  
遺伝子やパスウェイによる  
検索
3. **Upload:**  
自分のVisium dataをアップ  
ロード
4. **Tutorial:**  
ビデオとFAQs
5. **About:**  
概要研究資金引用
6. **Contact:**  
研究グループおよび研究協  
力者



The screenshot shows the DeepSpaceDB website top page. At the top, there is a navigation bar with the DeepSpaceDB logo and links for Database, Search, Upload, Tutorial, About, and Contact. Below the navigation bar is a large hero section with a dark, starry background. It features the DeepSpaceDB logo, the title "DeepSpaceDB - Explore Spatial Transcriptomics", and the tagline "Visualize, Analyze, and Discover". Below the hero section is a welcome message: "Welcome to DeepSpaceDB, a comprehensive spatial transcriptomics database hosting over 2,100 samples across human and mouse tissues. Our platform integrates high-resolution spatial data with powerful analysis tools, enabling researchers to explore gene expression patterns in their biological context. Whether you're studying tissue development, disease progression, or cellular organization, DeepSpaceDB provides the tools and data you need to unlock spatial insights in your research. [Learn more about DeepSpaceDB](#) →". Below the welcome message is a table with four columns: Total Samples (2144), Total Spots (5.4M), Human Samples (1361), and Mouse Samples (783). At the bottom, there is a "Latest News" section with a list of updates: "Our manuscript introducing DeepSpaceDB was published in Nucleic Acids Research [2025 Oct 29]", "Our protocol paper was published in the Journal of Visualized Experiments (JoVE) [2025 Sep 5]", "We updated DeepSpaceDB. The current version (v1.1) contains 2144 Visium samples. [2025 Jun 3]", and "We put our preprint about DeepSpaceDB on bioRxiv [2025 Jan 6]".

1 2 3 4 5 6

DeepSpaceDB Database Search Upload Tutorial About Contact

DeepSpaceDB - Explore Spatial Transcriptomics

Visualize, Analyze, and Discover

Welcome to DeepSpaceDB, a comprehensive spatial transcriptomics database hosting over 2,100 samples across human and mouse tissues. Our platform integrates high-resolution spatial data with powerful analysis tools, enabling researchers to explore gene expression patterns in their biological context.

Whether you're studying tissue development, disease progression, or cellular organization, DeepSpaceDB provides the tools and data you need to unlock spatial insights in your research. [Learn more about DeepSpaceDB](#) →

Total Samples	Total Spots	Human Samples	Mouse Samples
2144	5.4M	1361	783

Latest News

- Our [manuscript introducing DeepSpaceDB](#) was published in Nucleic Acids Research [2025 Oct 29]
- Our [protocol paper](#) was published in the Journal of Visualized Experiments (JoVE) [2025 Sep 5]
- We updated DeepSpaceDB. The current version (v1.1) contains 2144 Visium samples. [2025 Jun 3]
- We put our preprint about DeepSpaceDB on [bioRxiv](#) [2025 Jan 6]

# DeepSpaceDB – Demonstration (動画)



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DeepSpaceDB

[Database](#)

[Search](#)

[Upload](#)

[Tutorial](#)

[About](#)

[Contact](#)



## DeepSpaceDB - Explore Spatial Transcriptomics

Visualize, Analyze, and Discover

Welcome to **DeepSpaceDB**, a comprehensive spatial transcriptomics database hosting over 2,100 samples across human and mouse tissues. Our platform integrates high-resolution spatial data with powerful analysis tools, enabling researchers to explore gene expression patterns in their biological context.

Whether you're studying tissue development, disease progression, or cellular organization, DeepSpaceDB provides the tools and data you need to unlock spatial insights in your research. [Learn more about DeepSpaceDB](#) →

Total Samples

2144

Total Spots

5.4M

Human Samples

1361

Mouse Samples

783

### Latest News

- We updated DeepSpaceDB. The current version (v1.1) contains 2144 Visium samples. [2025 Jun 3]
- We put our preprint about DeepSpaceDB on [bioRxiv](#) [2025 Jan 6]
- A short article about DeepSpaceDB was published in 客観日本 ([Simplified Chinese](#) and [Traditional Chinese](#)) [2024 Dec 13]
- A short article about DeepSpaceDB was published in [JST News \(Japanese\)](#) [2024 Dec 2]



# DeepSpaceDB – Database tab (1)



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キーワード検索 (and)

各種フィルター

DeepSpaceDB Database Search Upload Tutorial About Contact

Filters

- Organism
- Organ
- Detailed Organ
- Condition
- Detailed Condition
- Sex
- Source
- Platform

Search Clear Filters Compare Download

DS ID	Organism	Condition	Organ	Source	PMID	Date Published	
<a href="#">DSID000001</a>	human	cancer	skin of body	<a href="#">GEO</a>	<a href="#">32579974</a>	2020-06-22	
<a href="#">DSID000002</a>	human	cancer	skin of body	<a href="#">GEO</a>	<a href="#">32579974</a>	2020-06-22	
<a href="#">DSID000003</a>	human	cancer	skin of body	<a href="#">GEO</a>	<a href="#">32579974</a>	2020-06-22	
<a href="#">DSID000004</a>	human	cancer	skin of body	<a href="#">GEO</a>	<a href="#">32579974</a>	2020-06-22	
<a href="#">DSID000005</a>	mouse	--	brain	<a href="#">GEO</a>	<a href="#">34413515</a>	2021-06-03	
<a href="#">DSID000006</a>	mouse	--	brain	<a href="#">GEO</a>	<a href="#">34413515</a>	2021-06-03	
<a href="#">DSID000007</a>	mouse	--	brain	<a href="#">GEO</a>	<a href="#">34413515</a>	2021-06-03	
<a href="#">DSID000008</a>	mouse	--	brain	<a href="#">GEO</a>	<a href="#">34413515</a>	2021-06-03	
<a href="#">DSID000009</a>	mouse	--	brain	<a href="#">GEO</a>	<a href="#">34413515</a>	2021-06-03	
<a href="#">DSID000010</a>	mouse	--	brain	<a href="#">GEO</a>	<a href="#">34413515</a>	2021-06-03	

2,144 results found < 1 2 3 4 5 ... 215 > Show 10 entries

Preview

DeepSpace ID DSID000001

Organism human

Processed Organ skin of body

Condition cancer

Condition Detailed squamous cell carcinoma

Details cutaneous squamous cell carcinoma; same patient as sample GSM4565824

Sample Page

— 現在選んでいる  
サンプルのサマリー

サンプルテーブル

# DeepSpaceDB – Database tab (2)



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フィルターにてヒト乳がんを選択した例

The screenshot shows the DeepSpaceDB interface. On the left, the 'Filters' panel is expanded, showing 'human (1361)' selected under 'Organism' and 'breast (99)' selected under 'Condition'. Below these, a list of diseases is shown, with 'cancer (715)' selected. A red box highlights the 'human (1361)' and 'breast (99)' filters. Another red box highlights the 'cancer (715)' filter. A third red box highlights the 'benign neoplasm (14)' filter. A fourth red box highlights the 'cancer (715)' filter. A fifth red box highlights the 'cancer (715)' filter. A sixth red box highlights the 'cancer (715)' filter. A seventh red box highlights the 'cancer (715)' filter. A eighth red box highlights the 'cancer (715)' filter. A ninth red box highlights the 'cancer (715)' filter. A tenth red box highlights the 'cancer (715)' filter. A eleventh red box highlights the 'cancer (715)' filter. A twelfth red box highlights the 'cancer (715)' filter. A thirteenth red box highlights the 'cancer (715)' filter. A fourteenth red box highlights the 'cancer (715)' filter. A fifteenth red box highlights the 'cancer (715)' filter. A sixteenth red box highlights the 'cancer (715)' filter. A seventeenth red box highlights the 'cancer (715)' filter. An eighteenth red box highlights the 'cancer (715)' filter. A nineteenth red box highlights the 'cancer (715)' filter. A twentieth red box highlights the 'cancer (715)' filter. A twenty-first red box highlights the 'cancer (715)' filter. A twenty-second red box highlights the 'cancer (715)' filter. A twenty-third red box highlights the 'cancer (715)' filter. A twenty-fourth red box highlights the 'cancer (715)' filter. A twenty-fifth red box highlights the 'cancer (715)' filter. A twenty-sixth red box highlights the 'cancer (715)' filter. A twenty-seventh red box highlights the 'cancer (715)' filter. A twenty-eighth red box highlights the 'cancer (715)' filter. A twenty-ninth red box highlights the 'cancer (715)' filter. A thirtieth red box highlights the 'cancer (715)' filter. A thirty-first red box highlights the 'cancer (715)' filter. A thirty-second red box highlights the 'cancer (715)' filter. A thirty-third red box highlights the 'cancer (715)' filter. A thirty-fourth red box highlights the 'cancer (715)' filter. A thirty-fifth red box highlights the 'cancer (715)' filter. A thirty-sixth red box highlights the 'cancer (715)' filter. A thirty-seventh red box highlights the 'cancer (715)' filter. A thirty-eighth red box highlights the 'cancer (715)' filter. A thirty-ninth red box highlights the 'cancer (715)' filter. A fortieth red box highlights the 'cancer (715)' filter. A forty-first red box highlights the 'cancer (715)' filter. A forty-second red box highlights the 'cancer (715)' filter. A forty-third red box highlights the 'cancer (715)' filter. A forty-fourth red box highlights the 'cancer (715)' filter. A forty-fifth red box highlights the 'cancer (715)' filter. A forty-sixth red box highlights the 'cancer (715)' filter. A forty-seventh red box highlights the 'cancer (715)' filter. A forty-eighth red box highlights the 'cancer (715)' filter. A forty-ninth red box highlights the 'cancer (715)' filter. A fiftieth red box highlights the 'cancer (715)' filter. A fifty-first red box highlights the 'cancer (715)' filter. A fifty-second red box highlights the 'cancer (715)' filter. A fifty-third red box highlights the 'cancer (715)' filter. A fifty-fourth red box highlights the 'cancer (715)' filter. A fifty-fifth red box highlights the 'cancer (715)' filter. A fifty-sixth red box highlights the 'cancer (715)' filter. A fifty-seventh red box highlights the 'cancer (715)' filter. A fifty-eighth red box highlights the 'cancer (715)' filter. A fifty-ninth red box highlights the 'cancer (715)' filter. A sixtieth red box highlights the 'cancer (715)' filter. A sixty-first red box highlights the 'cancer (715)' filter. A sixty-second red box highlights the 'cancer (715)' filter. A sixty-third red box highlights the 'cancer (715)' filter. A sixty-fourth red box highlights the 'cancer (715)' filter. A sixty-fifth red box highlights the 'cancer (715)' filter. A sixty-sixth red box highlights the 'cancer (715)' filter. A sixty-seventh red box highlights the 'cancer (715)' filter. A sixty-eighth red box highlights the 'cancer (715)' filter. A sixty-ninth red box highlights the 'cancer (715)' filter. A seventieth red box highlights the 'cancer (715)' filter. A seventy-first red box highlights the 'cancer (715)' filter. A seventy-second red box highlights the 'cancer (715)' filter. A seventy-third red box highlights the 'cancer (715)' filter. A seventy-fourth red box highlights the 'cancer (715)' filter. A seventy-fifth red box highlights the 'cancer (715)' filter. A seventy-sixth red box highlights the 'cancer (715)' filter. A seventy-seventh red box highlights the 'cancer (715)' filter. A seventy-eighth red box highlights the 'cancer (715)' filter. A seventy-ninth red box highlights the 'cancer (715)' filter. An eightieth red box highlights the 'cancer (715)' filter. An eighty-first red box highlights the 'cancer (715)' filter. An eighty-second red box highlights the 'cancer (715)' filter. An eighty-third red box highlights the 'cancer (715)' filter. An eighty-fourth red box highlights the 'cancer (715)' filter. An eighty-fifth red box highlights the 'cancer (715)' filter. An eighty-sixth red box highlights the 'cancer (715)' filter. An eighty-seventh red box highlights the 'cancer (715)' filter. An eighty-eighth red box highlights the 'cancer (715)' filter. An eighty-ninth red box highlights the 'cancer (715)' filter. A ninetieth red box highlights the 'cancer (715)' filter. A ninety-first red box highlights the 'cancer (715)' filter. A ninety-second red box highlights the 'cancer (715)' filter. A ninety-third red box highlights the 'cancer (715)' filter. A ninety-fourth red box highlights the 'cancer (715)' filter. A ninety-fifth red box highlights the 'cancer (715)' filter. A ninety-sixth red box highlights the 'cancer (715)' filter. A ninety-seventh red box highlights the 'cancer (715)' filter. A ninety-eighth red box highlights the 'cancer (715)' filter. A ninety-ninth red box highlights the 'cancer (715)' filter. A hundredth red box highlights the 'cancer (715)' filter.

★ 星印は病理専門家のアノテーションが付いている事を示す

ページスクロール

選んだサンプルへのリンク



# DeepSpaceDB – Sample page (1)

様々な情報を見  
ることが出来る

DeepSpaceDB

Database

Search

Upload

Tutorial

About

Contact

Sample

Location

Quality

Image annotation

Clusters

Genes

Pathways

Cell types


Tissue Explorer

CCI

Download

Metadata of DSID000600

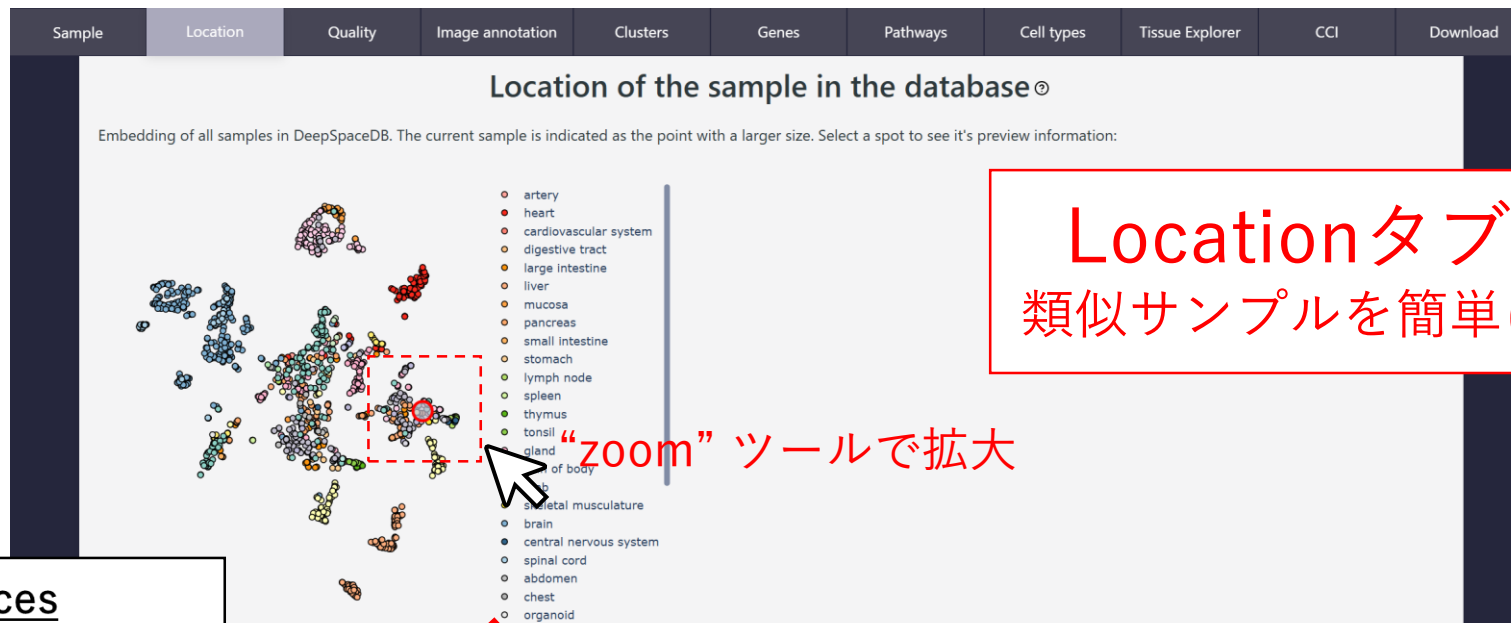
DeepSpace ID	DSID000600
Sample ID	GSM7782699
Series ID	GSE243275
Platform	Visium V2
Organism	human
Organ	<a href="#">breast</a>
Organ Detailed	--
Condition	<a href="#">cancer</a>
Condition Detailed	<a href="#">breast cancer</a>
Sex	--
Age or Stage	--
Post Mortem	--
Ethnicity or Strain	--
Description	--
Source	GEO
Source URL	<a href="#">GSE243275</a>
PMID URL:	<a href="#">38114474</a>
Date Published:	2023-10-09



# DeepSpaceDB – Sample page (2)



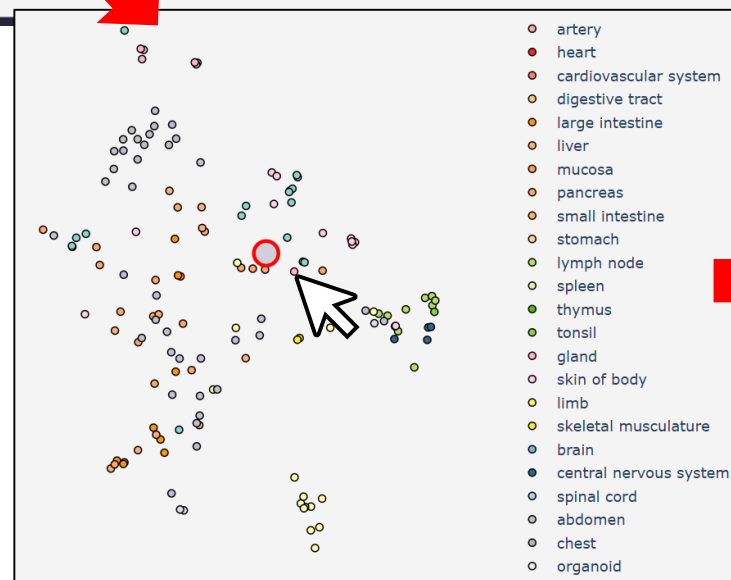
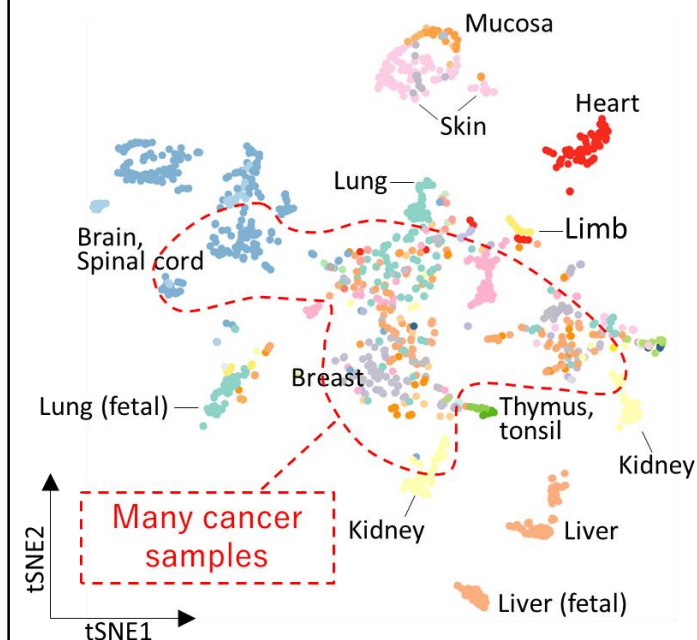
58



Locationタブでは、ユーザーは類似サンプルを簡単に探すことができる

“zoom” ツールで拡大

## Human tissue slices



クリックでサンプルのプレビューが出る

Information about selected sample:

DeepSpace ID: [DSID001012](#)

Organism: human

Organ: [gland](#)

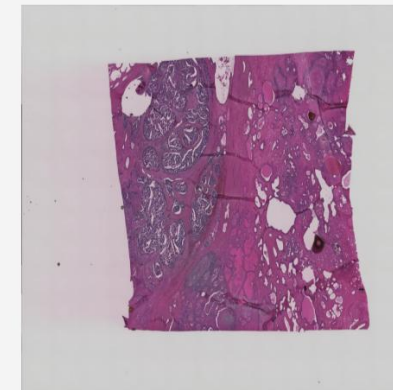
Condition: [cancer](#)

Detailed Condition: [prostate cancer](#)

Details: prostatic cancer; NEPC pT4N1M0 and ARPC pT2aN0M0, Gleason score of 4+4

Close

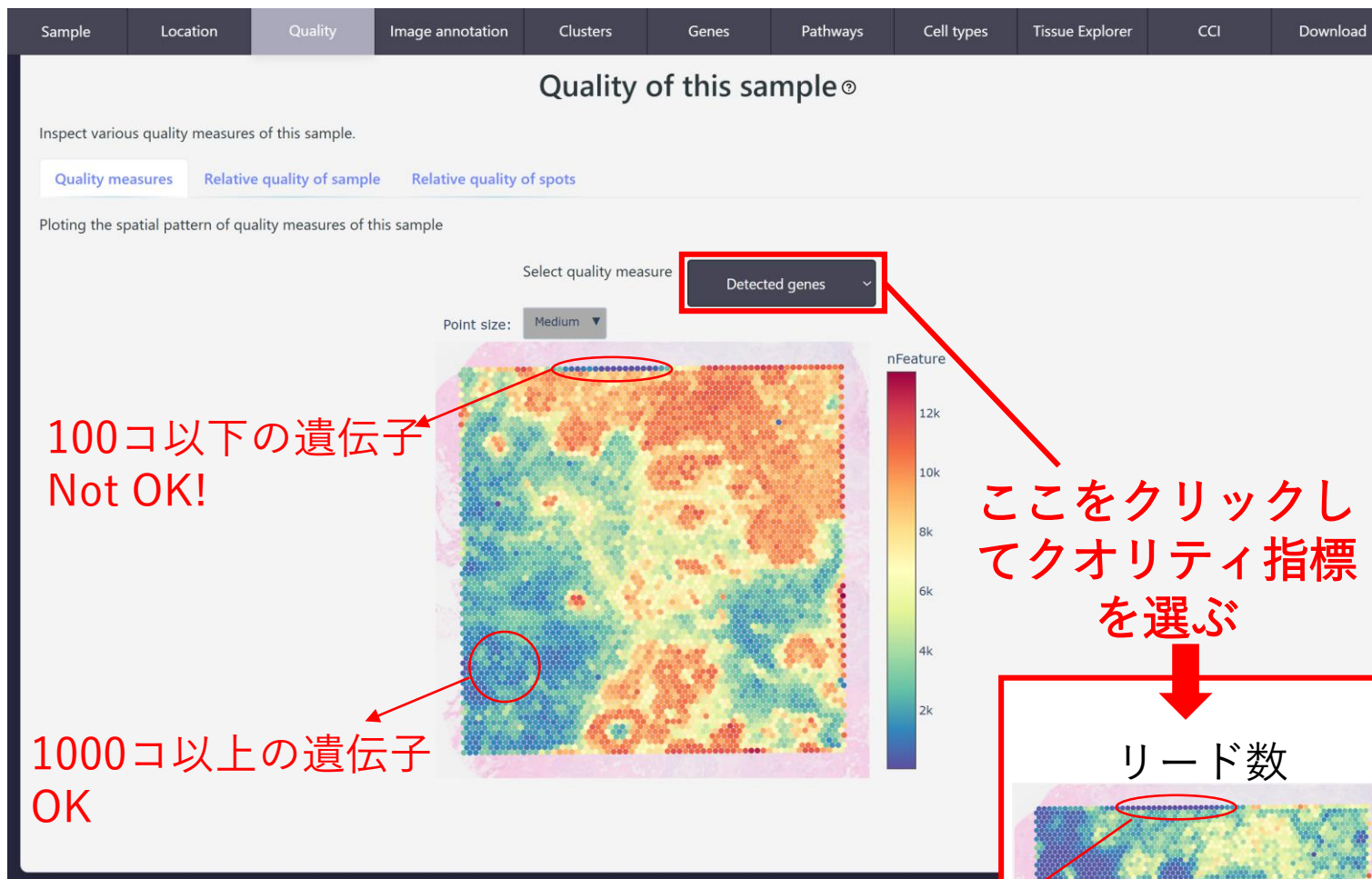
Sample Page



# DeepSpaceDB – Sample page (3)



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Qualityタブでは、サンプルのクオリティ（検出された遺伝子数やリード数など）を確認できる。クオリティは技術的な問題による事も多いが、生物学的因子（細胞密度や細胞種など）によっても大きく左右される。

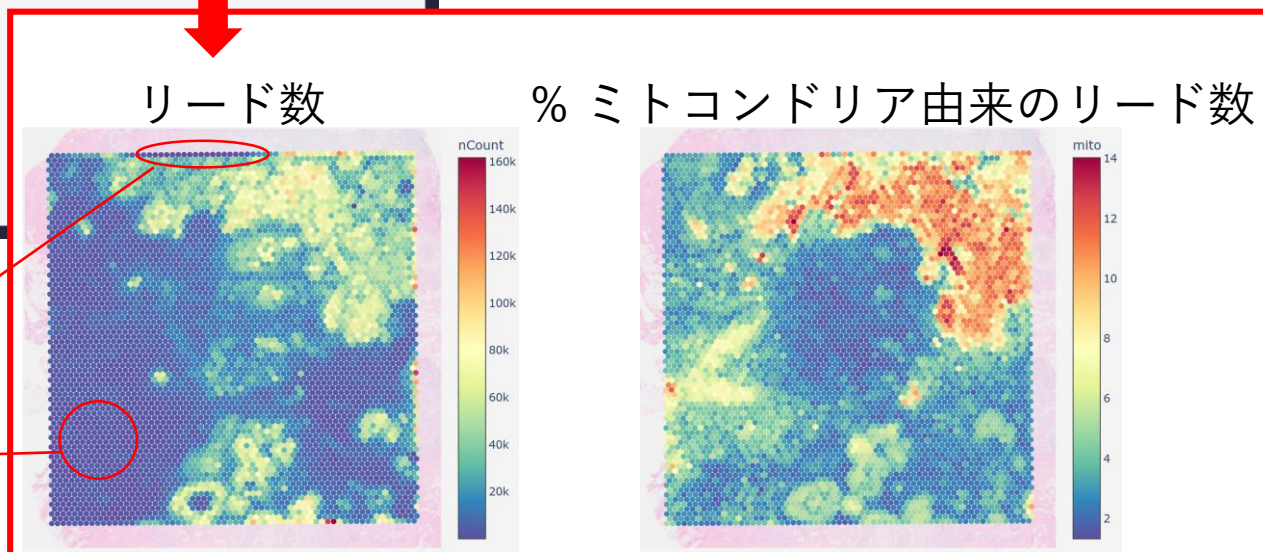
ここをクリックしてクオリティ指標を選ぶ

リード数

% ミトコンドリア由来のリード数

100本以下のリード数 = Not OK!

1500本以上のリード数 = OK

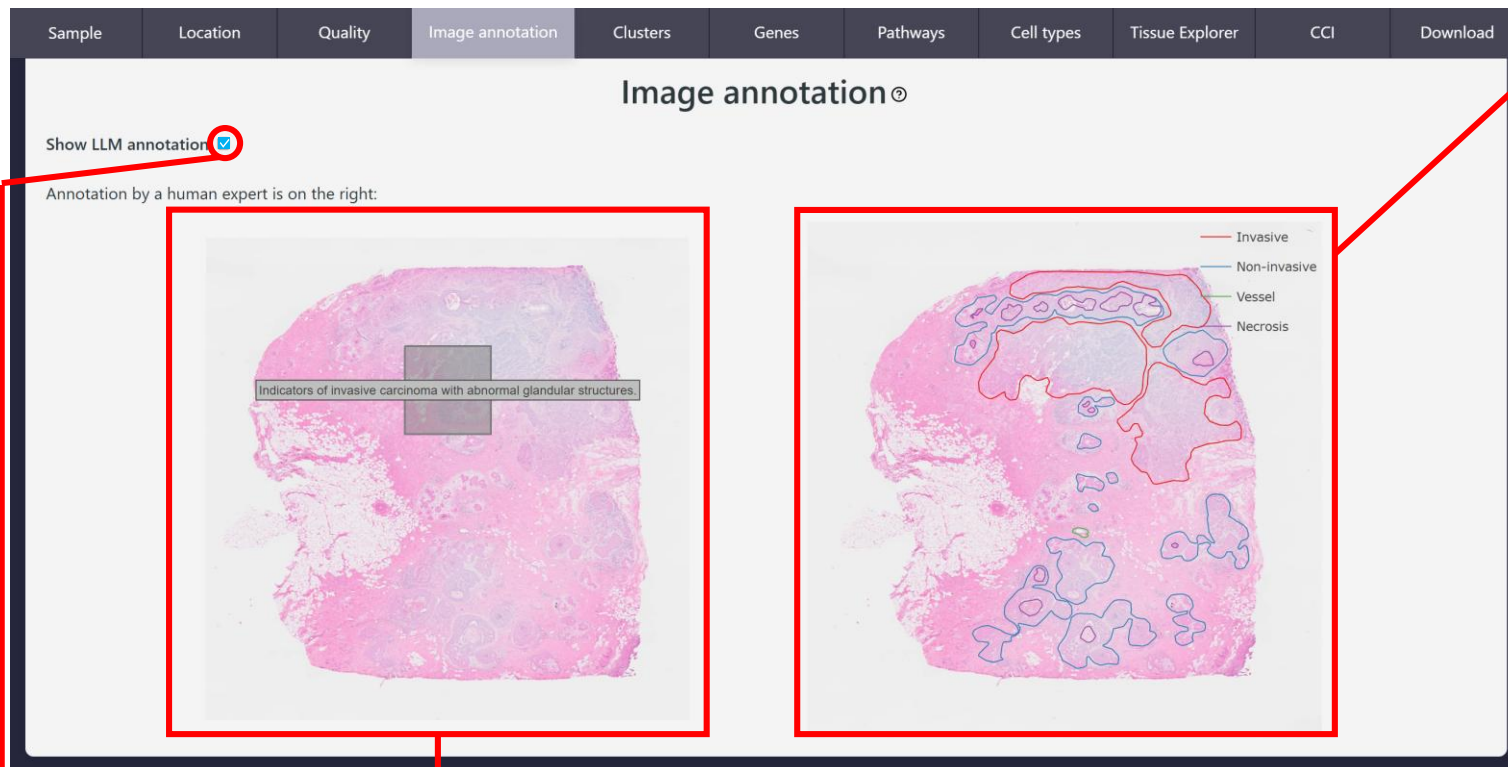




# DeepSpaceDB – Sample page (4)



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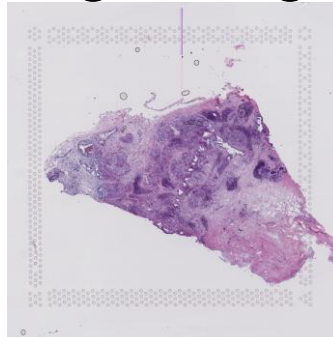
## Image annotationタブ

乳がん69サンプルは堀本義哉博士（東京医科大学乳腺科学）によるアノテーションがついている。

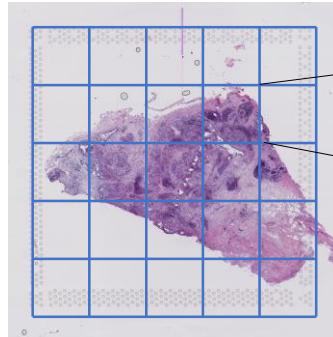
Visium H&E 画像は通常の診断用画像に比べて低画質であることが多いため、アノテーションは研究目的に限定されており、慎重に取り扱う必要がある

## LLM（大規模言語モデル）ベースのアノテーション

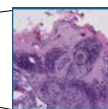
Original image



5 x 5 tiles



GPT-4oへのプロンプト



*This is a part of an H&E image of a [...]  
Describe any tissue features or signs of  
pathology in at most 100 characters. If there is  
not enough tissue to say anything, write 'empty'.*

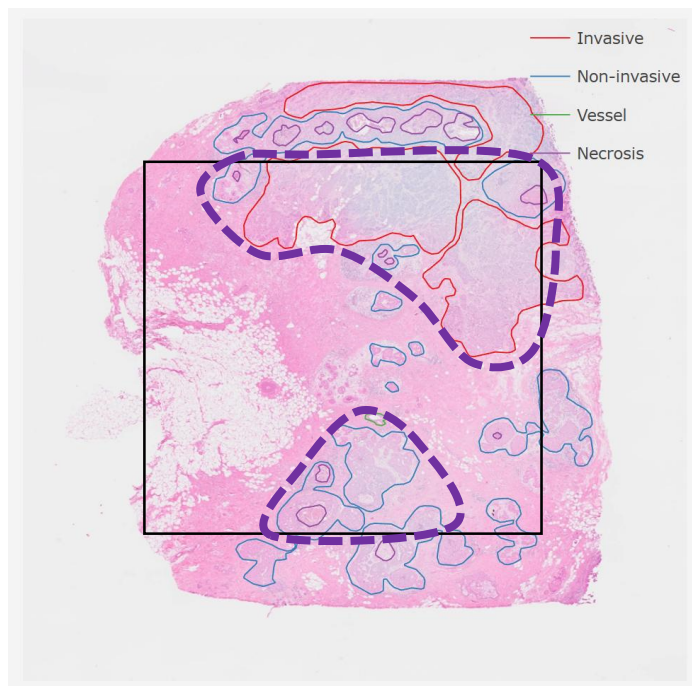
➡ 返答を収集



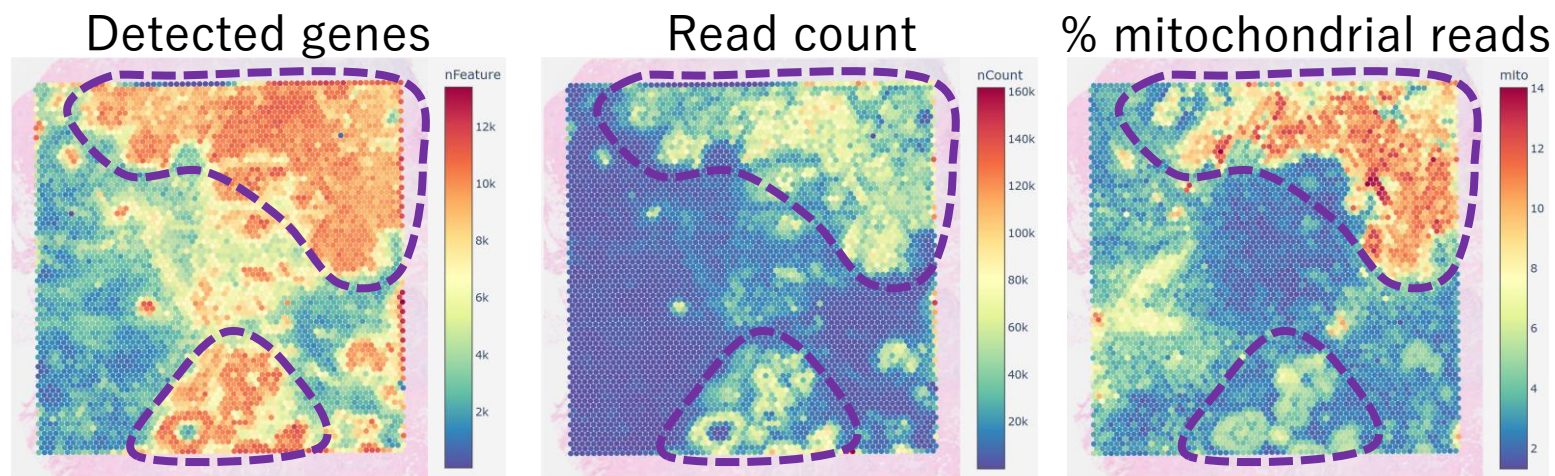
LLMベースのアノテーションは  
注意が必要



Image annotation



クオリティ指標

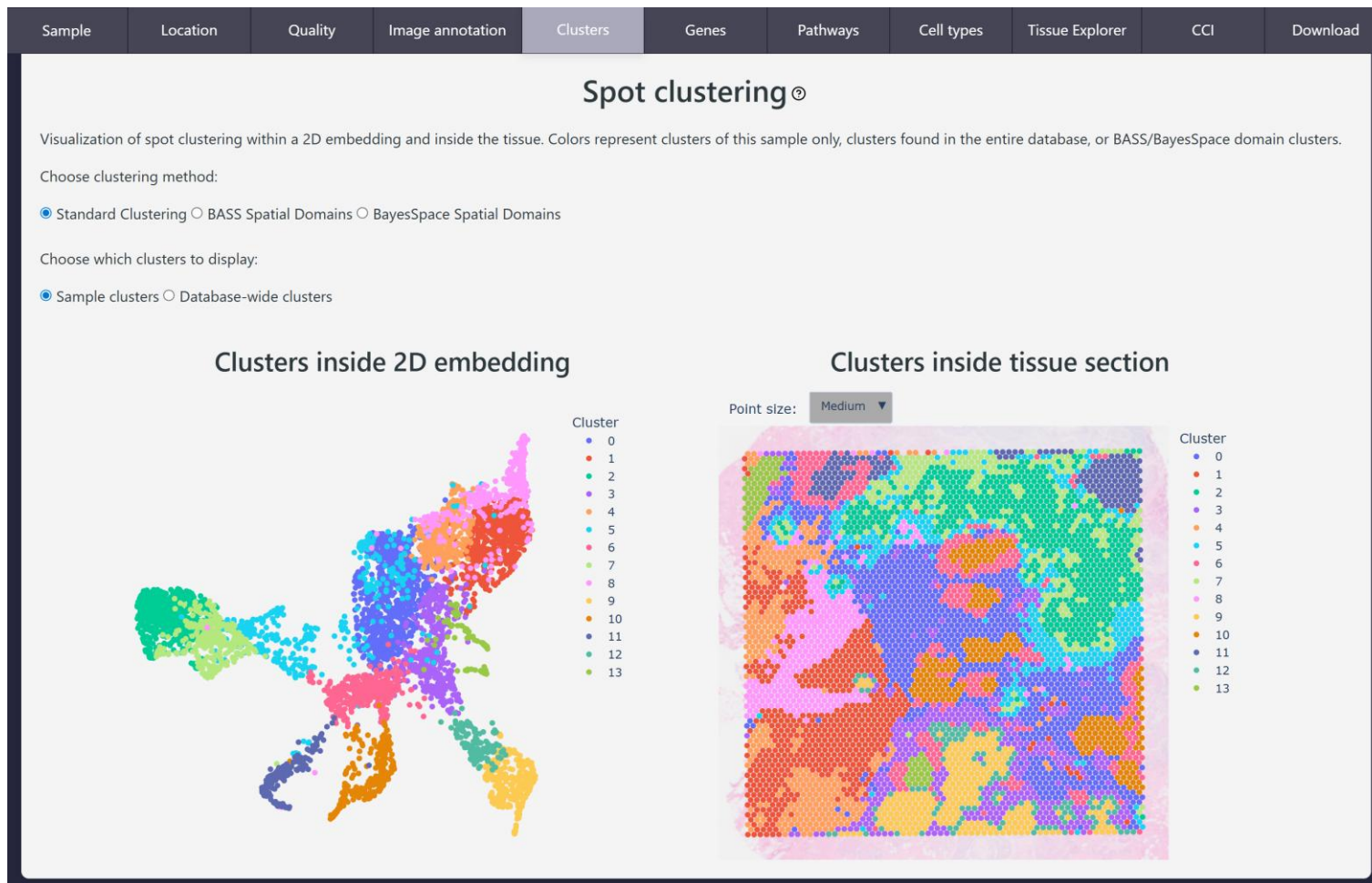


浸潤性、非浸潤性に関わらずガン組織は発現遺伝子数やリード数が多く、ミトコンドリア由来リード数も多いことが分かる。

# DeepSpaceDB – Sample page (6)

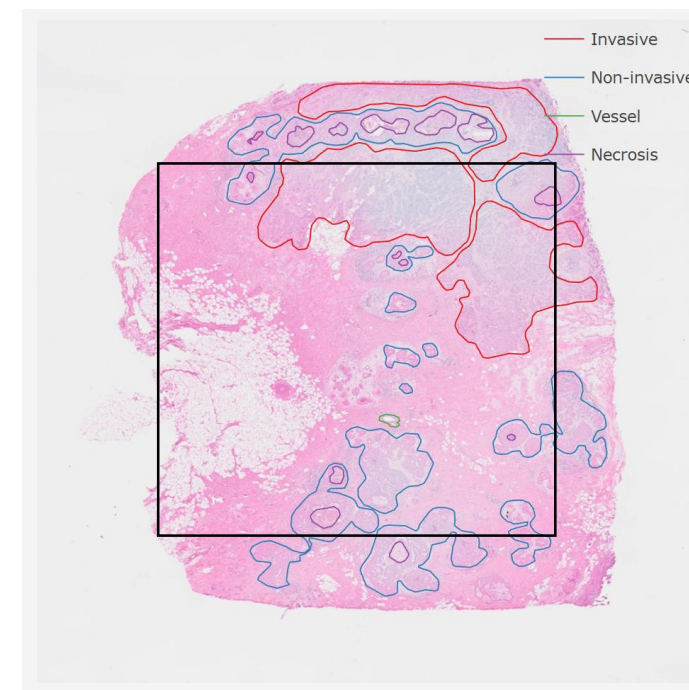


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## Clustersタブ

### Image annotation

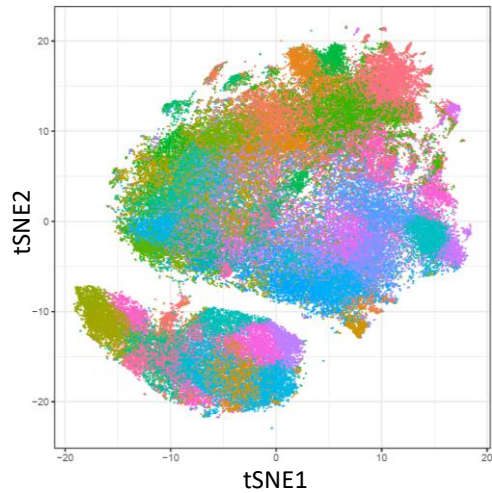


- サンプルのスポットは遺伝子発現パターンの類似性によりクラスタリングされる
- クラスタは生物学的特性をしばしば反映している（細胞種やガン組織など）

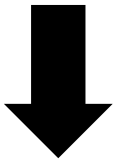


# データベースワイドのクラスターアノテーション

ヒトの全サンプルデータ



これらのクラスターは  
何を意味しているのか?



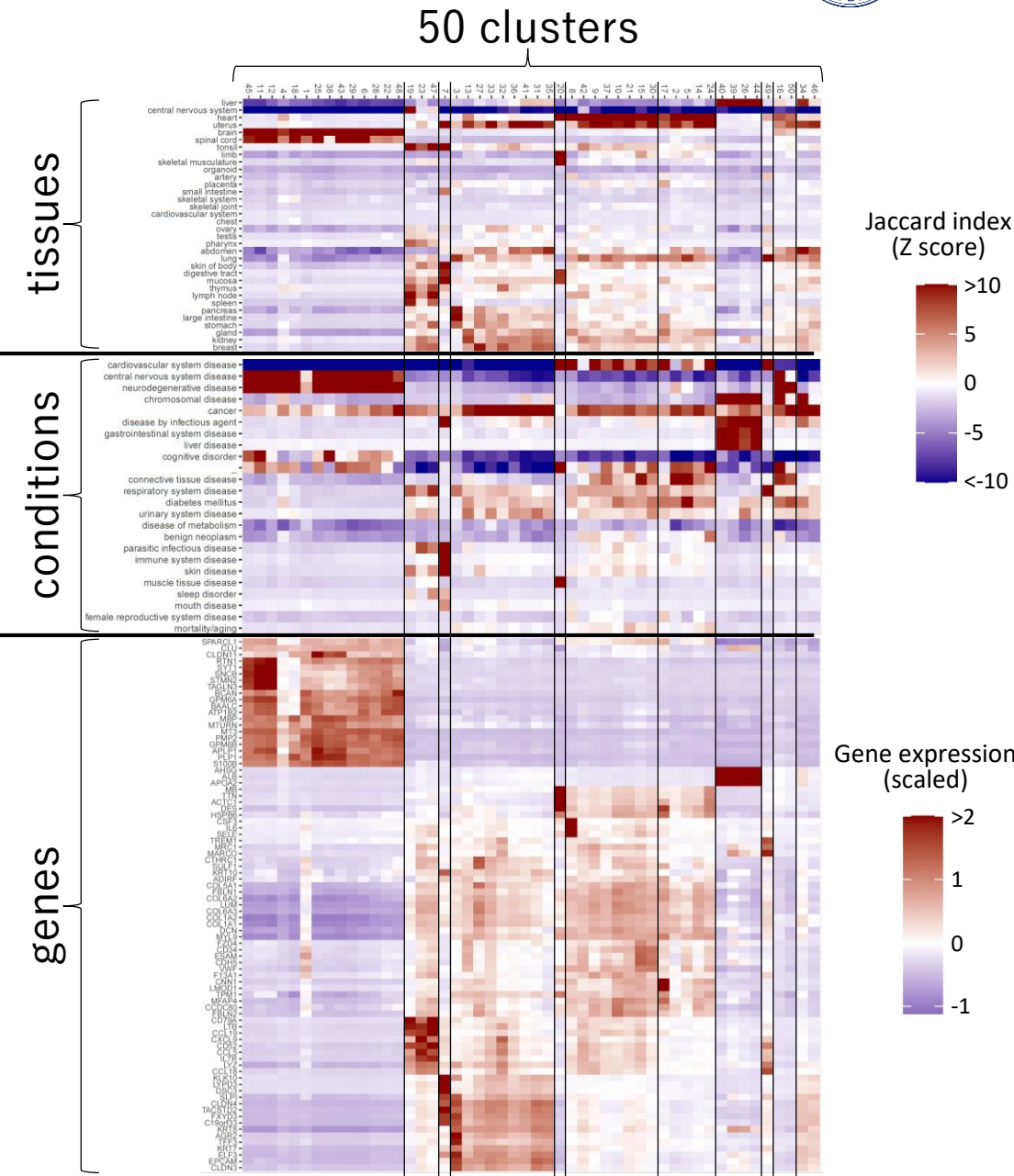
スポットクラスターの  
アノテーション

(神経、ガン、上皮細胞など)

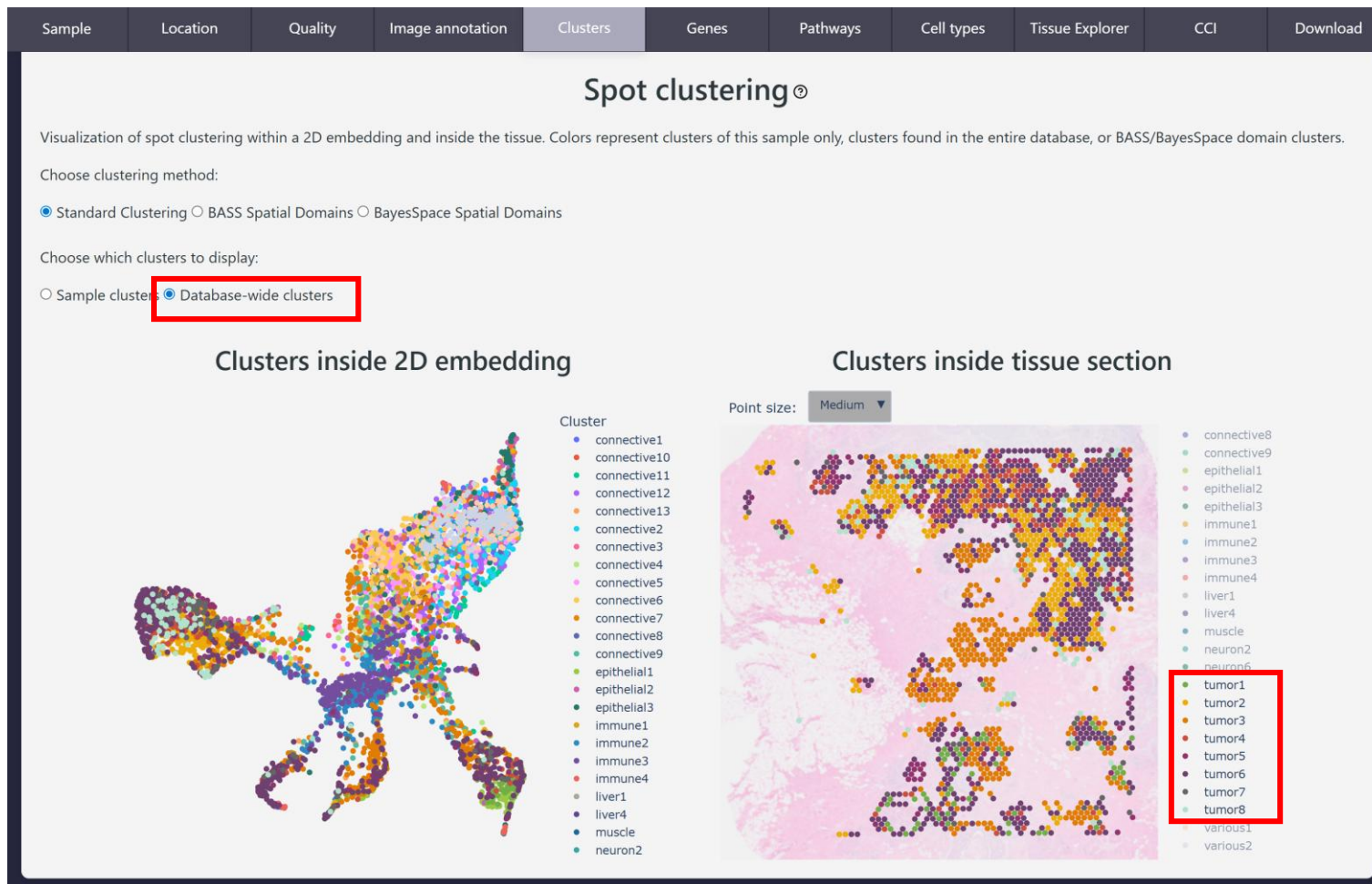
組織ごとのクラスターの  
オーバーラップは?

色々な条件ごとのクラスター  
のオーバーラップは?

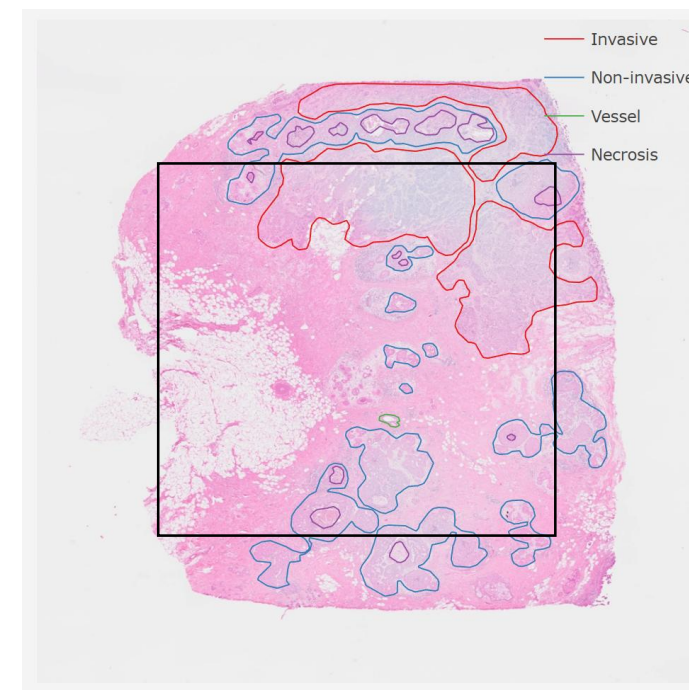
それぞれのクラスターの  
マーカー遺伝子は?



# DeepSpaceDB – Sample page (7)



## Image annotation



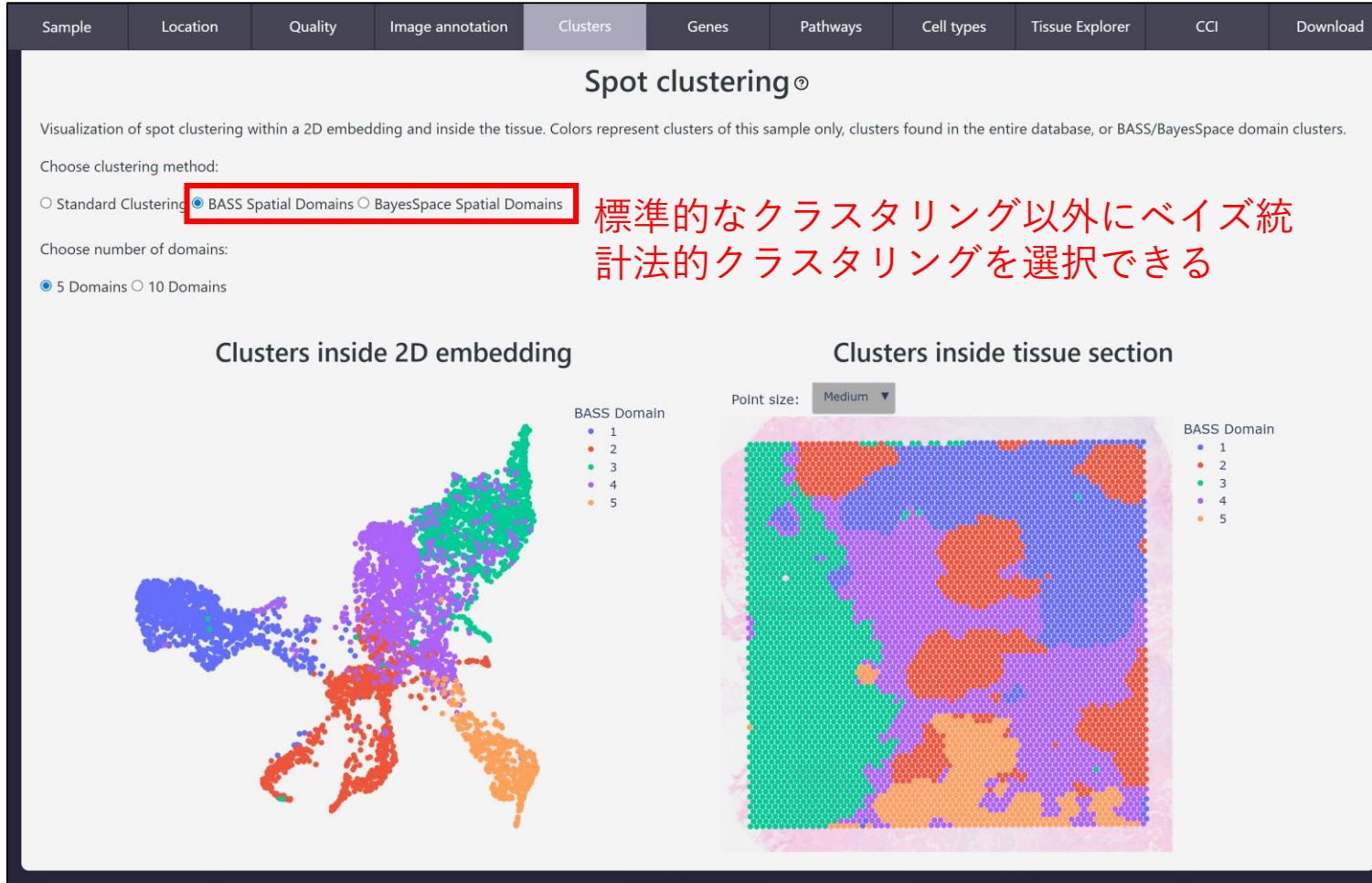
- データベースワイドのクラスターは Visium サンプルの組織構造を解釈する際に有益である。
- ここではtumorクラスター(1から8)がサンプルのガン組織上に局在する



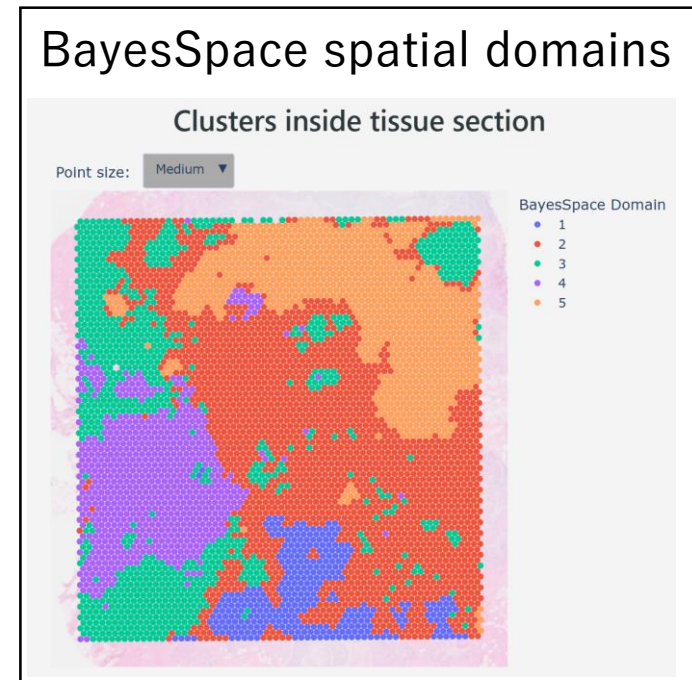
# DeepSpaceDB – Sample page (8)



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標準的なクラスタリング以外にベイズ統計法的クラスタリングを選択できる

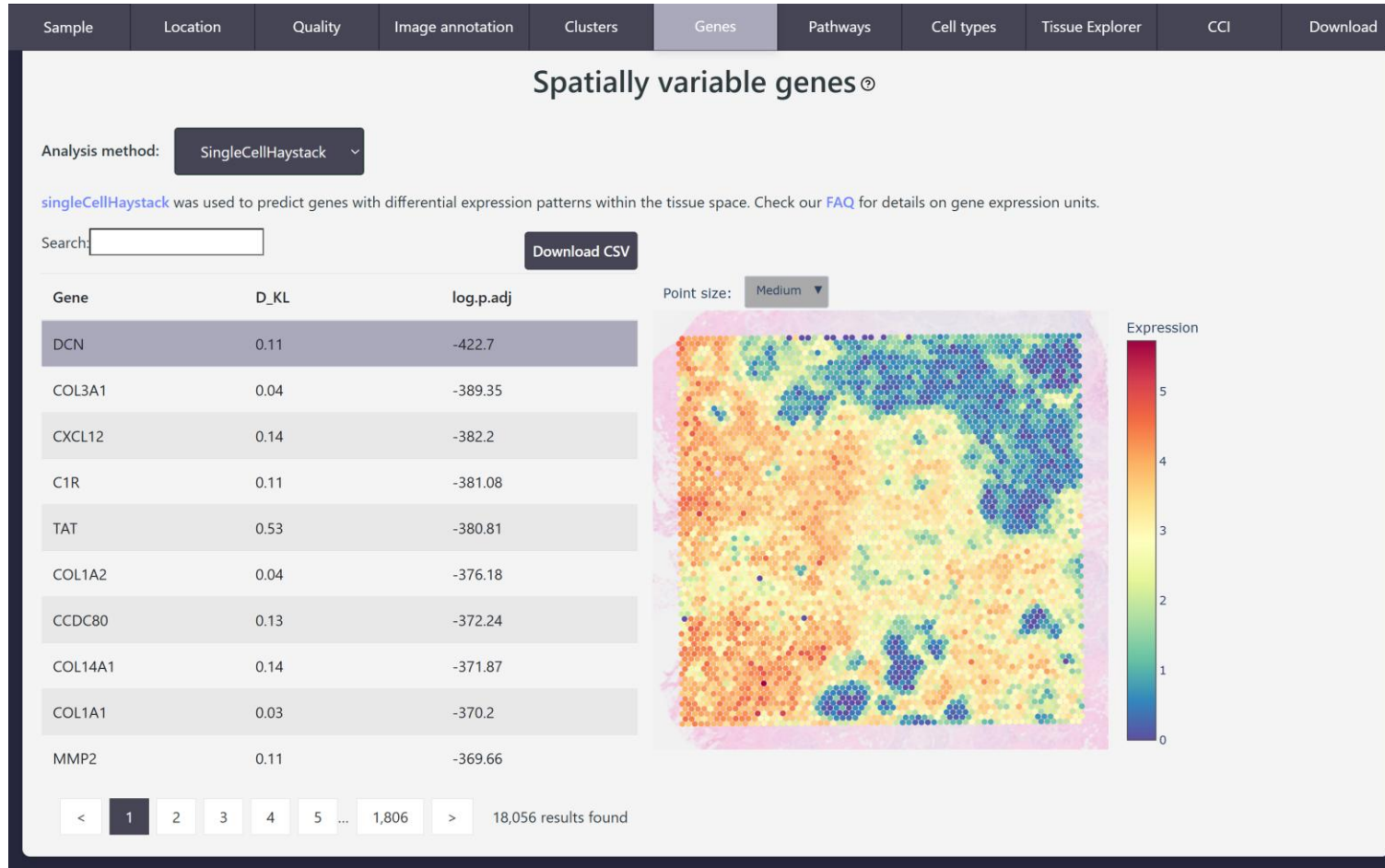
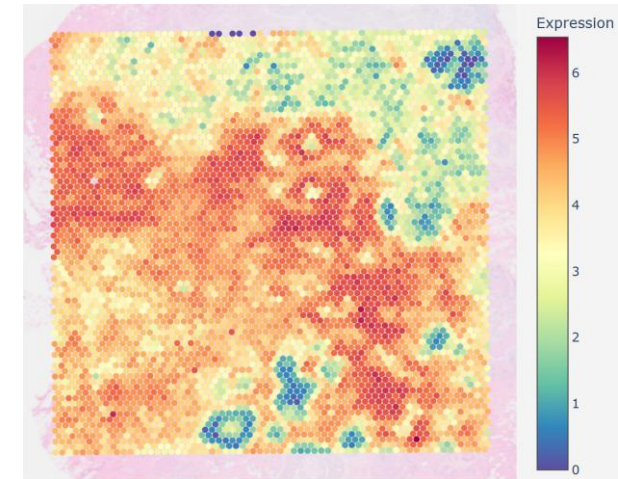
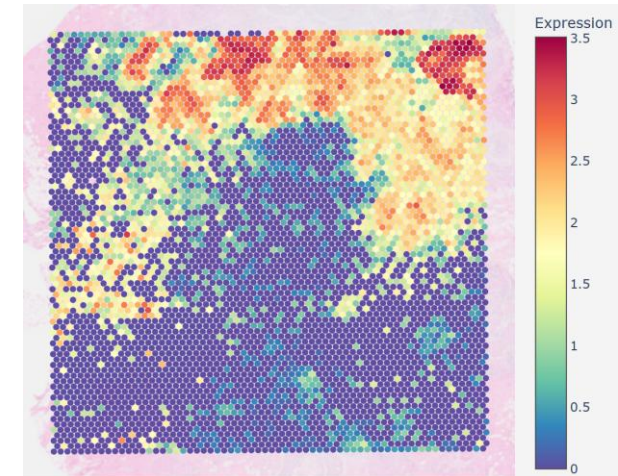


- **Spatial domains** は遺伝子発現情報に加えて空間情報を用いてクラスタリングを行う。
- DeepSpaceDB はBASS や BayesSpaceを用いたクラスタリングを提供している
- 解析から得られたドメインは生物学的特性をしばしば表している
- **当ウェビナー後半 酒井俊輔博士の講演**

# DeepSpaceDB – Sample page (9)



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*COL3A1**TAT*

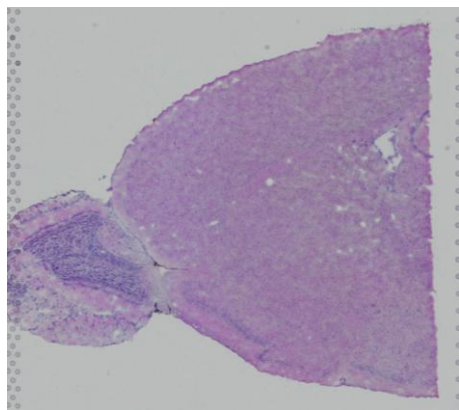
- Genesタブでは空間変動遺伝子 (SVG) を予測できる  
SVGとは明確な空間パターンをもつ遺伝子である
- DeepSpaceDB ではSVG予測プログラムのうち  
**singleCellHaystack** **SPARK-X** **BinSpect**が利用可能



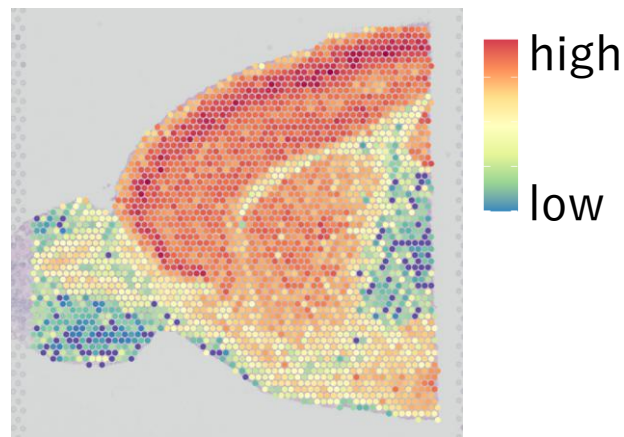
# singleCellHaystack 方法論

singleCellHaystack は細胞や遺伝子発現の分布の偏りに基づき空間的発現変動遺伝子を予測する

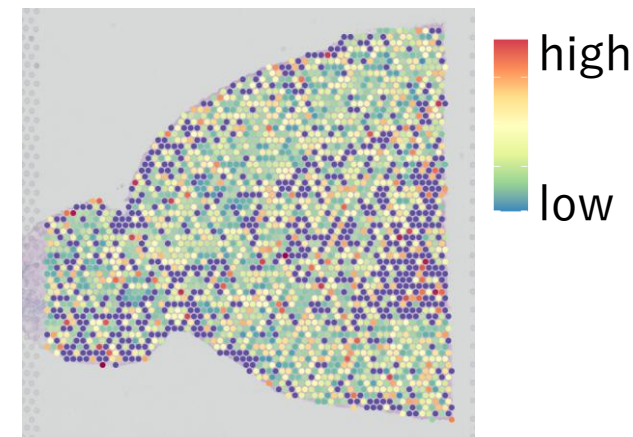
与えられた空間



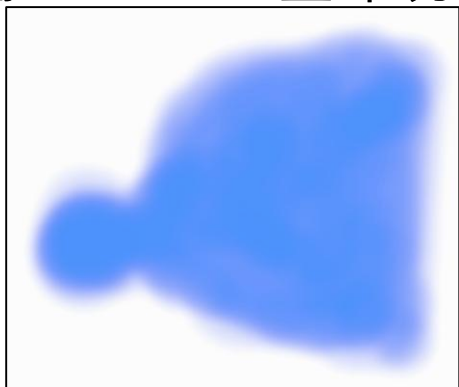
SVG



SVGではない

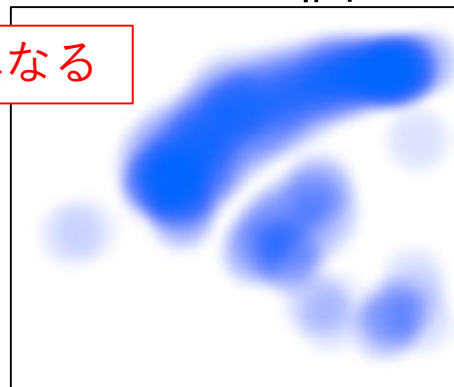


偏りのない基準分布

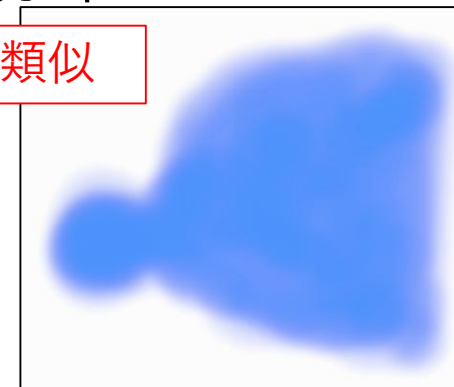


個々の遺伝子発現の分布

基準と異なる



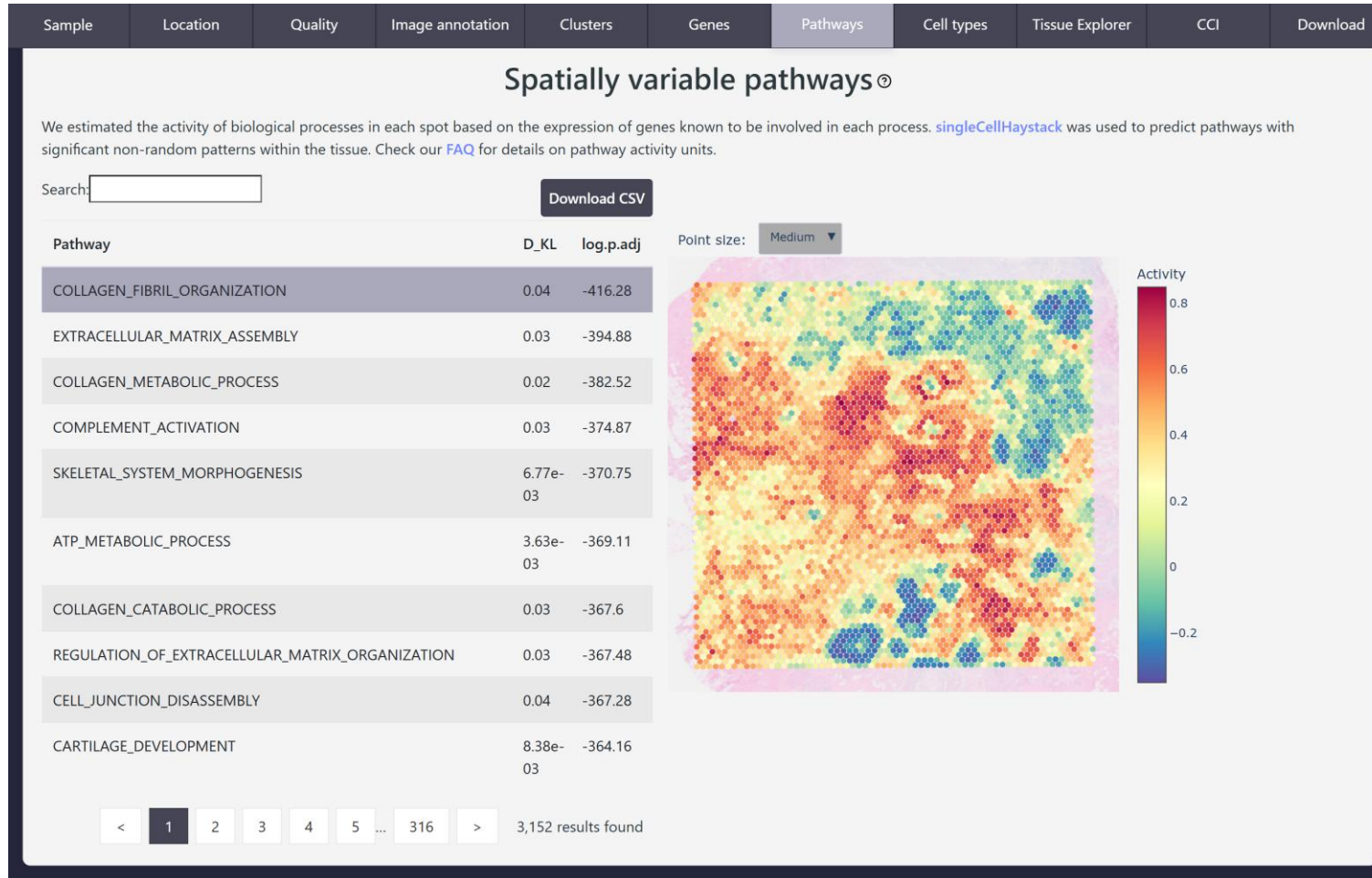
基準に類似



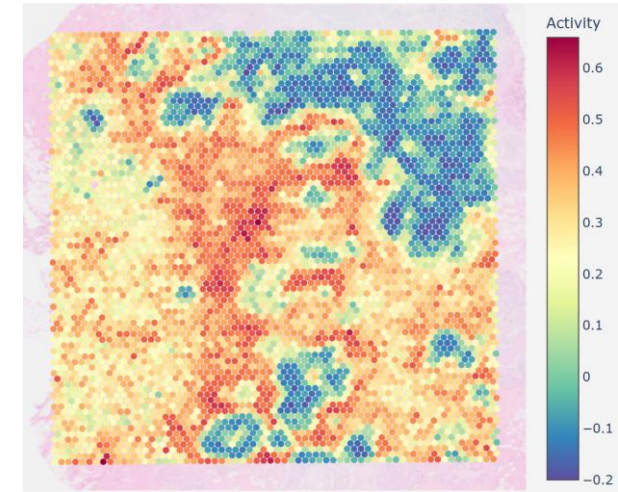
# DeepSpaceDB – Sample page (10)



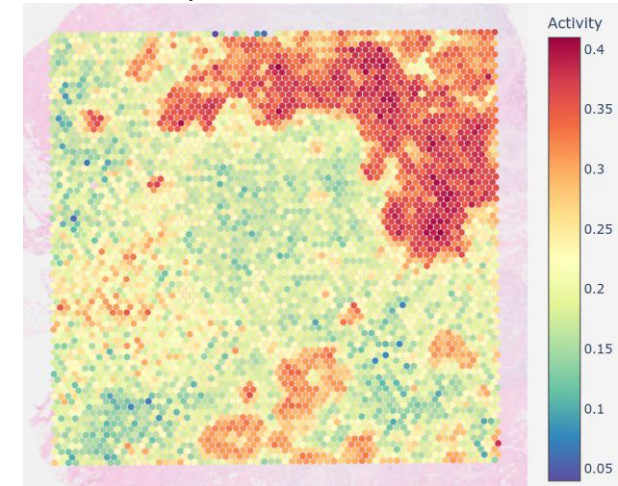
68



補体活性化



ATP 代謝プロセス



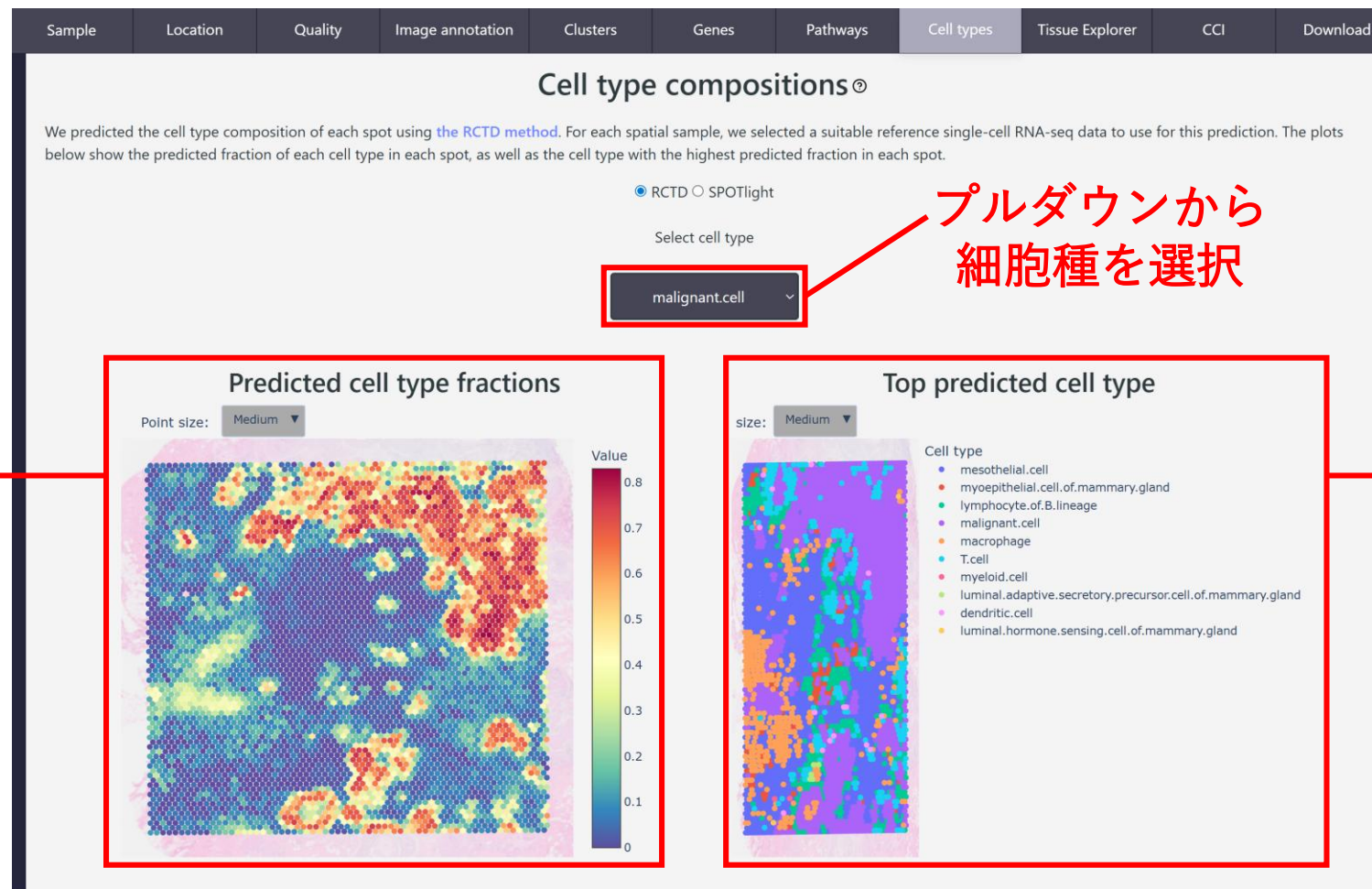
- **空間的変動パスウェイ**とはその活性が空間的に異なる分布を示すパスウェイである。
- 活性はそのパスウェイに関わる遺伝子群の発現に基づいている
- 予測は **singleCellHaystack**に基づいている



# DeepSpaceDB – Sample page (11)



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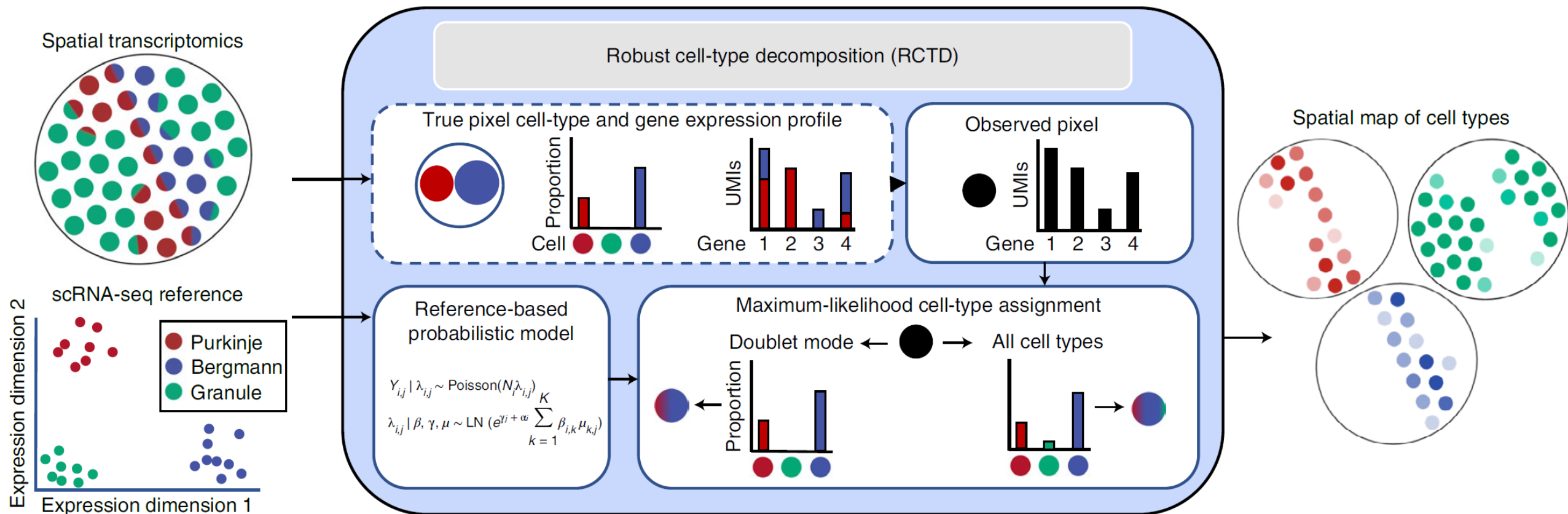


プルダウンから  
細胞種を選択

スポットごとの  
malignant cells(悪  
性細胞)である確率  
が表現されている

スポットごとの  
予測細胞種  
(hard to see)

- Cell typesタブでは**RCTD** または **SPOTlight**を用いて細胞種を予測
- これらの予測はシングルセルRNA-seqデータとの比較に基づいている



- RCTD は参照となる細胞種データを基に各スポットを細胞種の比率へと変換する
- Visium サンプルごとに最適の参照データセットを用意する事が重要

# DeepSpaceDB – Sample page (12)



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“Tissue Explorer”タブではユーザーインタラクティブな比較が可能である

興味のある領域を自由に選択できる

Manual Selection

Cluster Selection

1. 選択した領域をSet # という名前にして

Select a set:

☒ Set 1  
Number of spots in Set 1: 1127

☐ Set 2  
Number of spots in Set 2: 752

Make a new set

Remove set

Reset all sets

Add to set

Remove from set

Reset set

Compare gene expression

Compare pathway activity

現在の選択領域

2. 比較リストに加え

3. セット間の差異を調べる



# DeepSpaceDB – Sample page (13)



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比較結果は“Tissue Explorer”タブの下方に表示される

## 遺伝子発現テーブル:

- 選択領域それぞれの平均値
- 発現の差
- P-value (t-test)
- Adjusted p-value

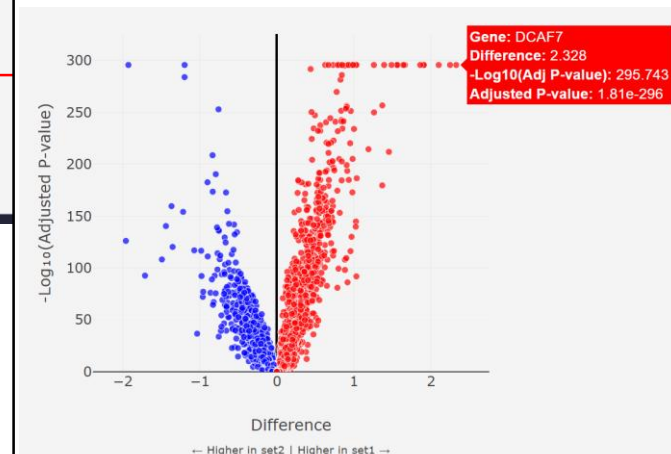


もし3つ以上の領域を選択した場合は、プルダウンでそのセットを表示するか選ぶことができる

## Visualization:

- scatter plot
- volcano plot

## The result in a volcano plot

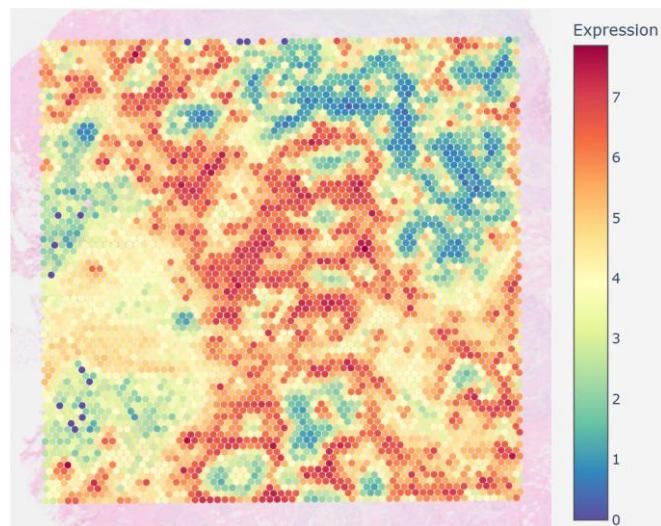




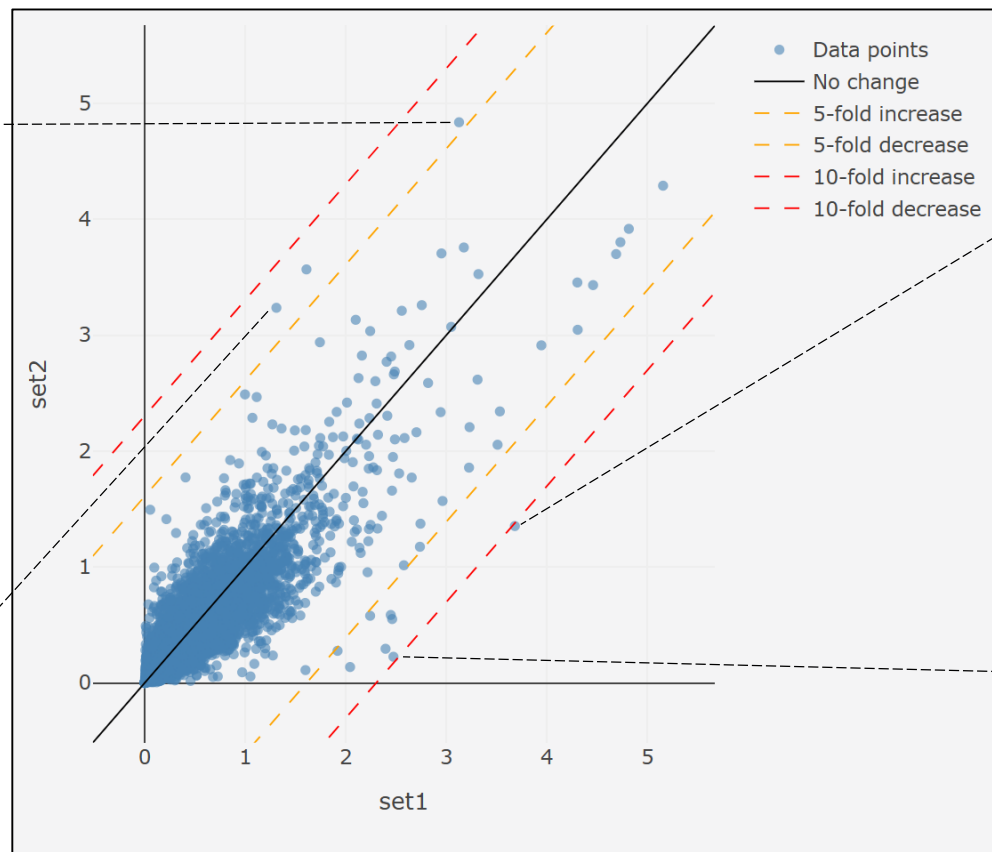
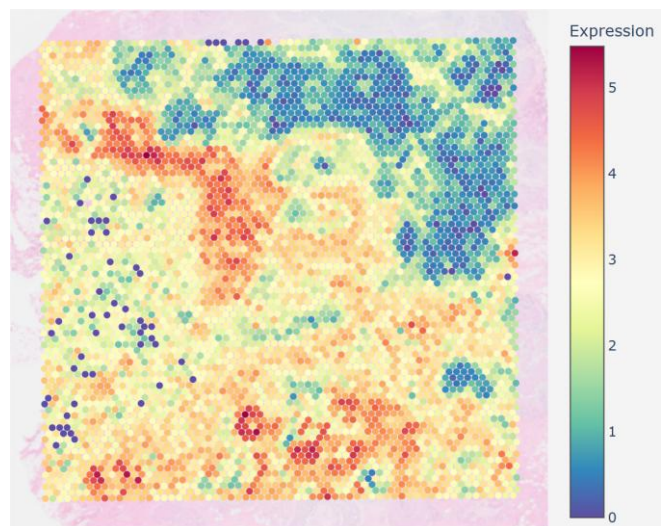
# DeepSpaceDB – Sample page (14)

比較で得た結果は“Genes” タブで確認することができる

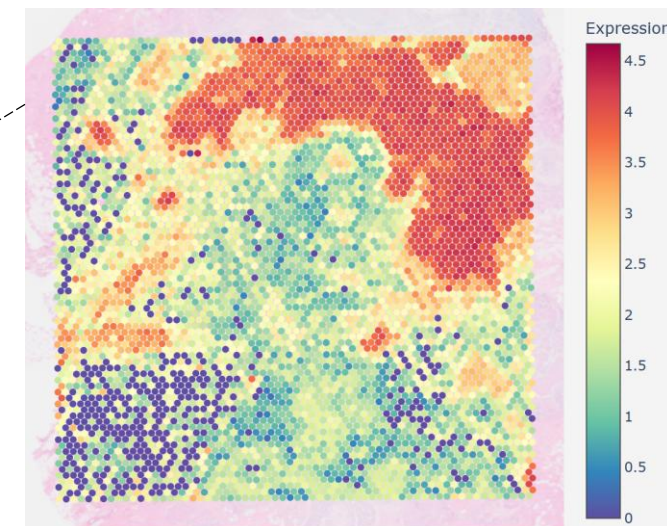
*IGKC*



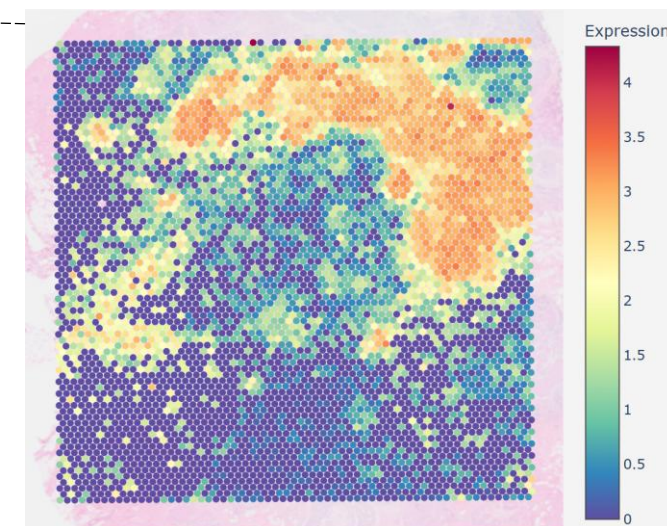
*MGP*



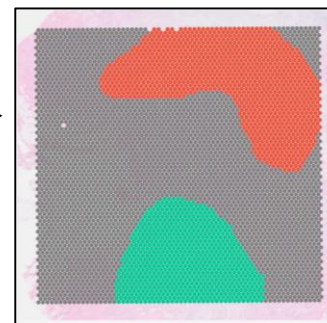
*DCAF7*



*CDH2*



マウス操作で選んだ領域→



## Cell-cell Communication

Cell-cell communication analysis results from CellChat.

[Download CellChat Results \(CellChat.csv\)](#)

## Download data

[Download filtered\\_feature\\_bc\\_matrix.h5](#)  
[Download seurat\\_processed.rds](#)  
[Download seurat\\_raw.rds](#)  
[Download moduleScores.csv](#)  
[Download haystack\\_genes.csv](#)  
[Download haystack\\_moduleScores.csv](#)  
[Download SPARKX.csv](#)  
[Download BinSpect.csv](#)  
[Download BASS.csv](#)  
[Download BayesSpace.csv](#)  
[Download CellChat.csv](#)  
[Download cell\\_type\\_prediction\\_SPOTlight.csv](#)  
[Download cell\\_type\\_prediction\\_RCTD.csv](#)  
[Download spatial/tissue\\_lowres\\_image.png](#)  
[Download spatial/tissue\\_hires\\_image.png](#)  
[Download spatial/scalefactors\\_json.json](#)  
[Download spatial/tissue\\_positions\\_list.csv](#)  
[Download All Files](#)

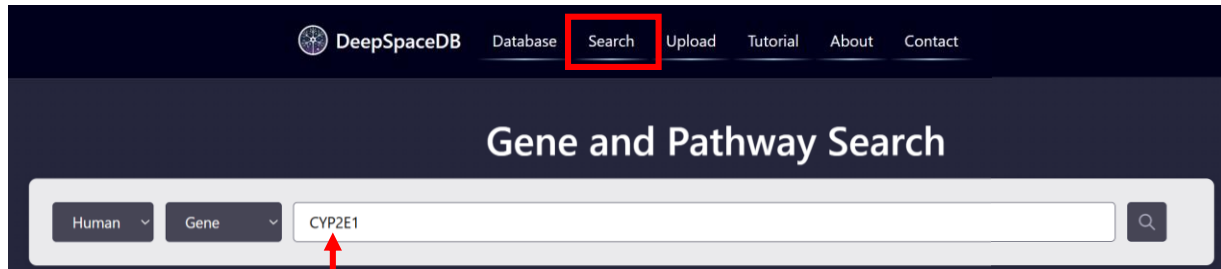
CellChatによる細胞間相  
相互作用予測  
(Jin *et al.*, Nat Protocols, 2024)

データや解析結果をダウン  
ロードできる

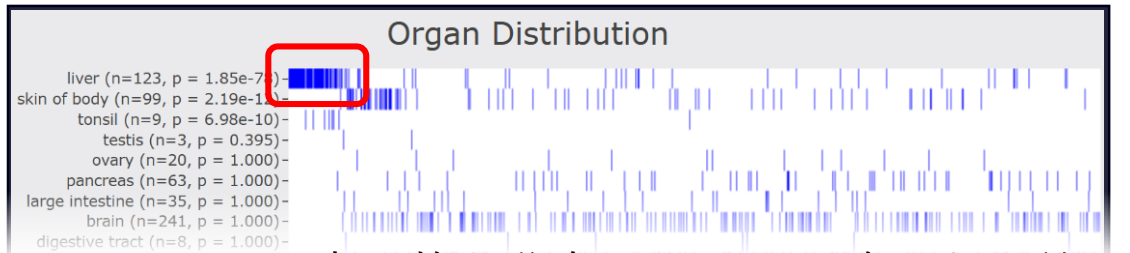
一日あたりダウンロードで  
きるファイル数は制限あり



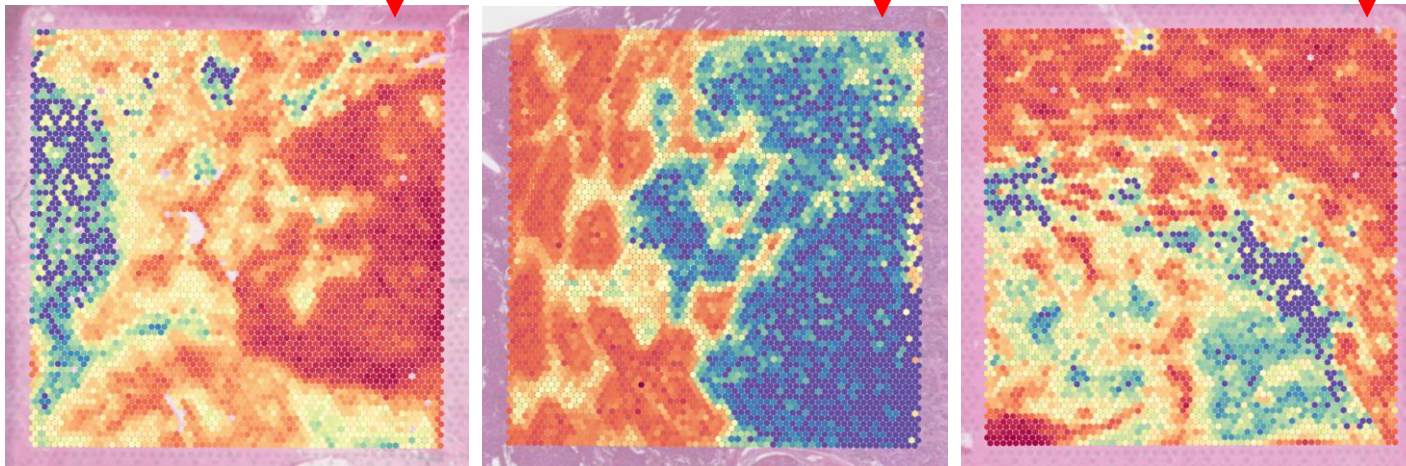
# Search tool: データベース全体から検索



検索したい遺伝子やパスウェイを入力



空間的な分布パターンが強い順に並ぶ



- 遺伝子の機能について深い洞察へのヒントとなる
- 明確な分布パターンを持つサンプルを容易に検索できる

DS ID	Organ	Condition	Source	PMID	log.p.adj
<a href="#">DSID001919</a>	liver	cancer	<a href="#">GEO</a>	<a href="#">39900120</a>	-536.15
<a href="#">DSID001370</a>	liver	cancer	<a href="#">GEO</a>	--	-487.46
<a href="#">DSID001917</a>	liver	cancer	<a href="#">GEO</a>	<a href="#">39900120</a>	-415.15
<a href="#">DSID000838</a>	liver	cancer	<a href="#">GEO</a>	<a href="#">36652202</a>	-365.63
<a href="#">DSID001916</a>	liver	cancer	<a href="#">GEO</a>	<a href="#">39900120</a>	-355.89
<a href="#">DSID001913</a>	liver	cancer	<a href="#">GEO</a>	<a href="#">39900120</a>	-346.59
<a href="#">DSID001912</a>	liver	cancer	<a href="#">GEO</a>	<a href="#">39900120</a>	-336.28
<a href="#">DSID001914</a>	liver	cancer	<a href="#">GEO</a>	<a href="#">39900120</a>	-322.7
<a href="#">DSID001918</a>	liver	cancer	<a href="#">GEO</a>	<a href="#">39900120</a>	-306.73
<a href="#">DSID001915</a>	liver	cancer	<a href="#">GEO</a>	<a href="#">39900120</a>	-298.14

1,337 results found < 1 2 3 4 5 ... 134 > Show 10 entries

# Upload tool

データベースに保存されないのご安心下さい



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解析結果 →

**Upload Center**

Upload your data to get instant insights. Our analysis tools help you understand your data better with detailed visualizations and reports.

Job Label:  Select Species: Human Mouse Select Image Resolution: High Low Load example: Load Example Data

[Advanced Settings](#)

**Barcodes File**  
Upload your barcodes file (.tsv.gz)  
Select Barcodes File

**Features File**  
Upload your features file (.tsv.gz)  
Select Features File

**Matrix File**  
Upload your matrix file (.mtx.gz)  
Select Matrix File

**Image File**  
Upload your tissue image file (.png)  
Select Image File

**Scalefactors File**  
Upload your scalefactors file (.json)  
Select Scalefactors File

**Tissue Position File**  
Upload your tissue position file (.csv)  
Select Tissue Position File

☐ I'm not a robot

Upload & Analyze

Please complete the captcha

**Recent Jobs (Last 7 Days)**

Job ID	Label	Created	Status	Actions
c6b1f79d-d7fb-40a4-883d-365d84cd747b	Mouse Brain Sample	2/7/2025, 1:40:29 PM GMT+9	completed	<span>Compare</span> <span>Download Data</span> <span>🗑️</span> <span>📄</span> <span>🗑️</span>

アップロード  
オプション

アップロードする  
ファイルを選ぶ

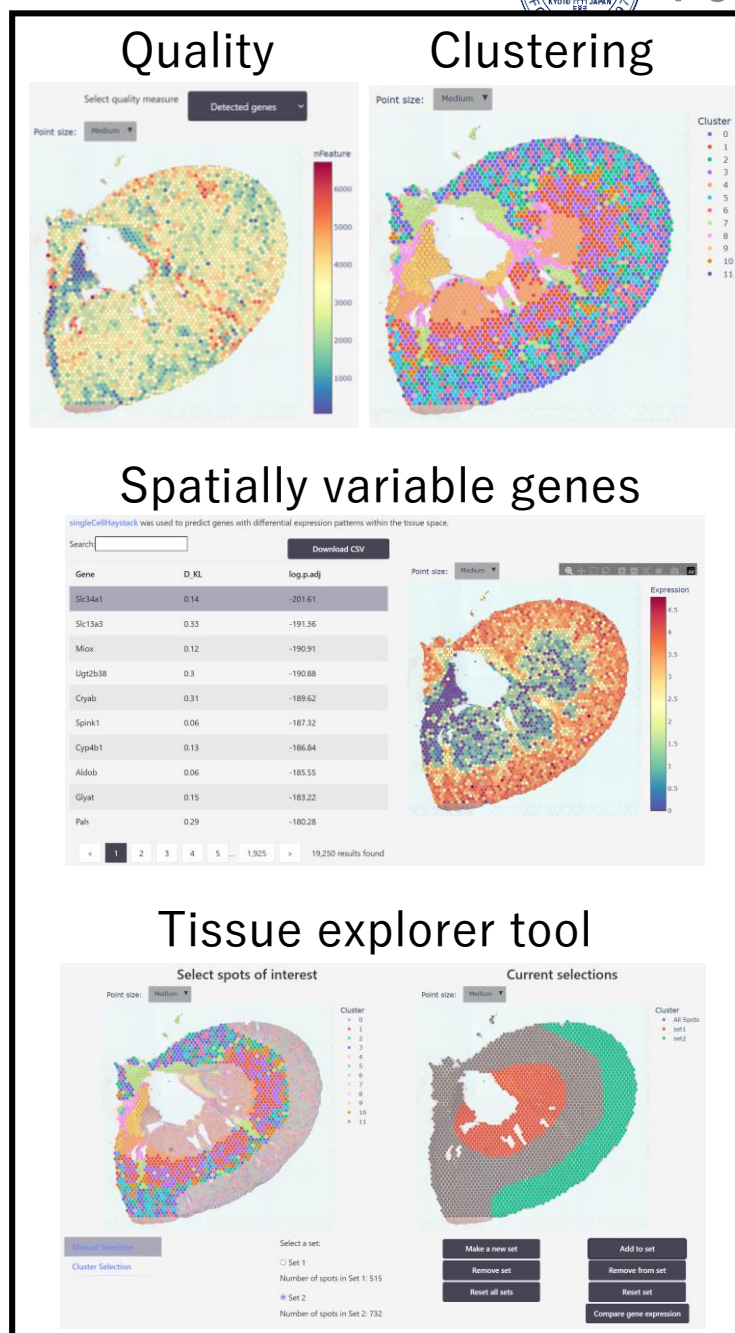
アップロード及び解析

最近アップロードされ  
たサンプル履歴

解析結果を表示

プロセッシングステータス

サーバーからの消去  
結果のダウンロード  
他サンプルとの比較





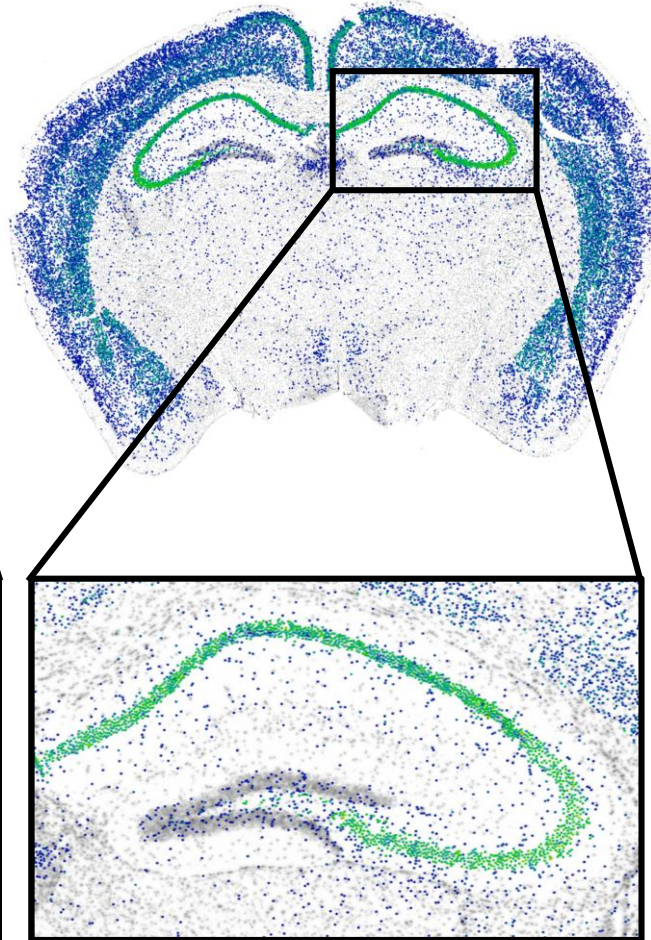
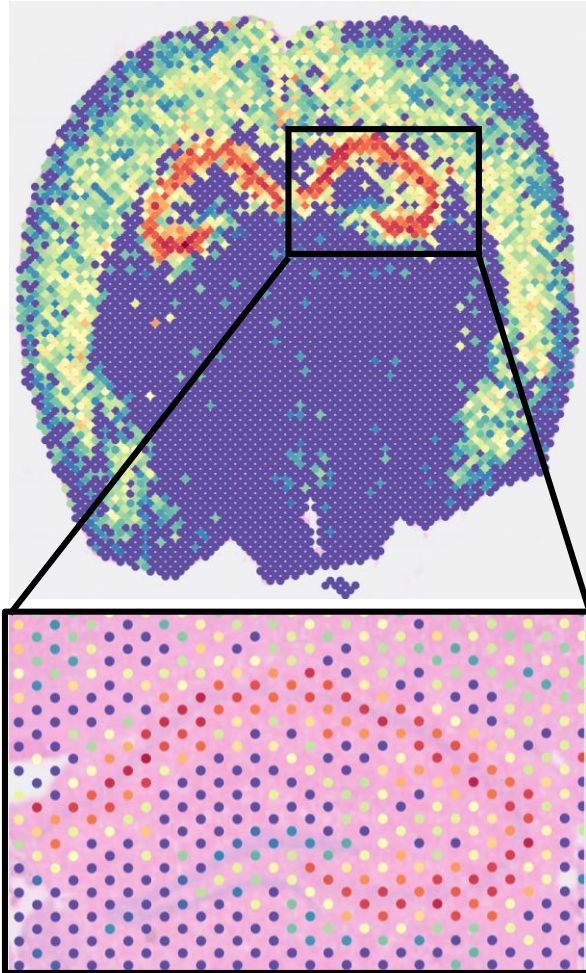
- Rを使った空間トランスクリプトミクスデータ解析
  - Visium example
  - Xenium example
- 既存の空間トランスクリプトミクスデータベースの紹介
- DeepSpaceDBの紹介
  - Visium interface
  - Xenium interface
- まとめ

# VisiumとXeniumの比較例

*Neurod6*

Visium

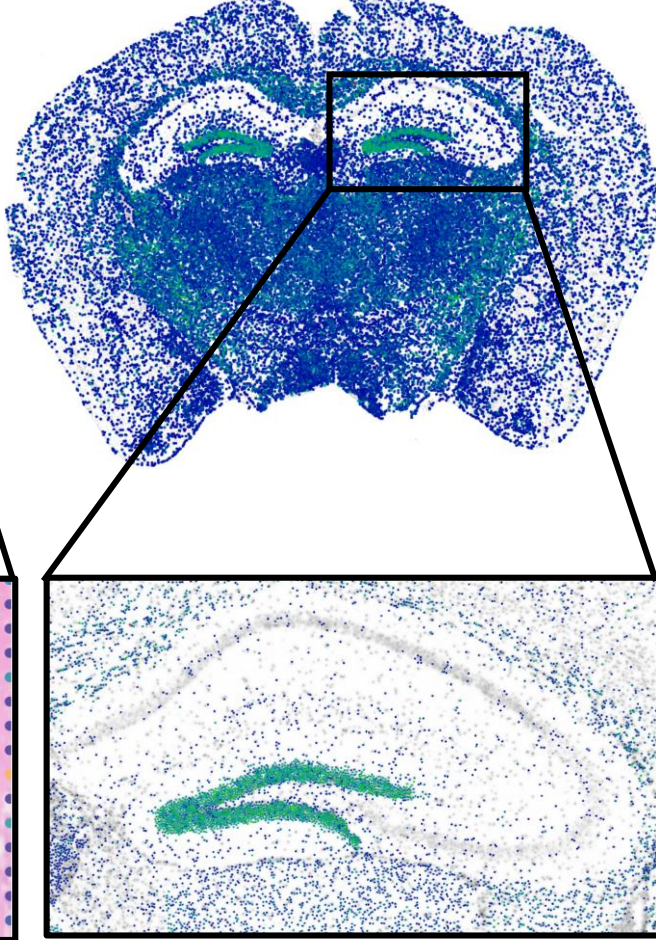
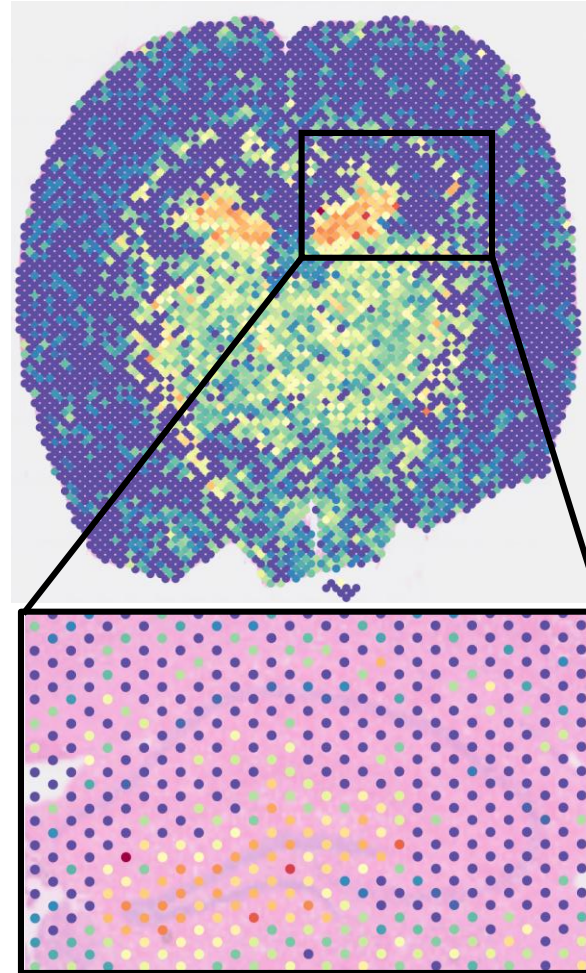
Xenium



*Prox1*

Visium

Xenium





# Xeniumのワークフロー

## Data Sources



## Raw Data

Transcripts  
Cell locations  
Cell shapes  
Image data  
etc

### Annotation data

Species, tissue,  
condition, age,  
sex, publication,  
etc

## Processed

Quality check

PCA, tSNE,  
UMAP  
Clustering

Zarr stores

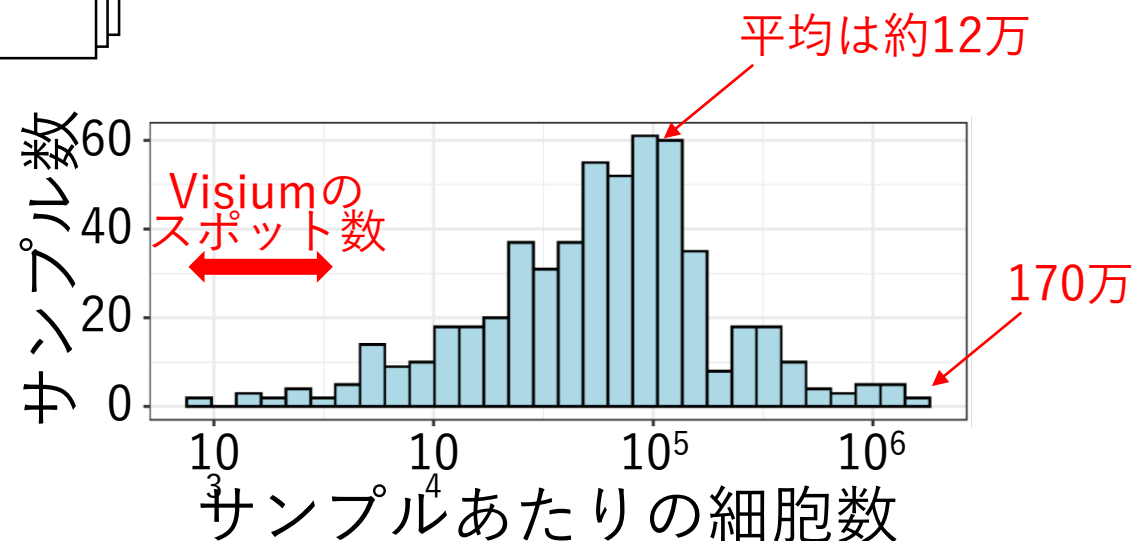
## Database



<https://deepspacedb.com/>

- Samples
- Functions

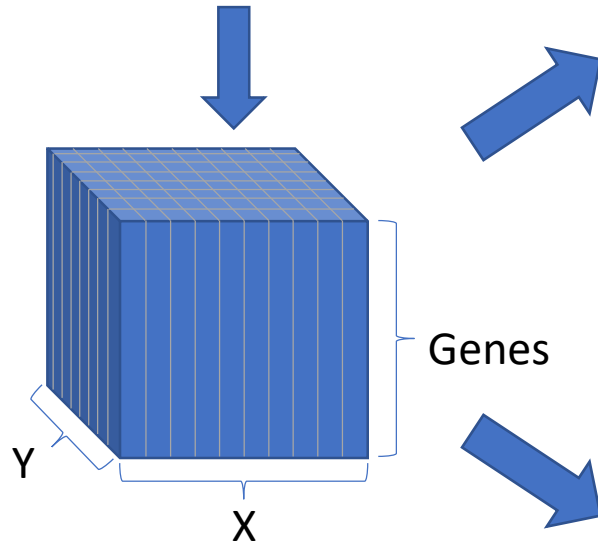
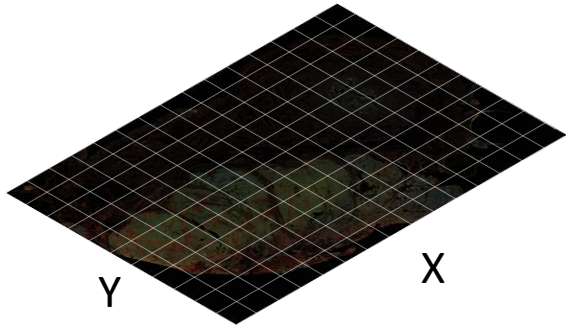
- Xeniumサンプル約600件を処理済み
- 高速アクセス実現のための工夫が必要





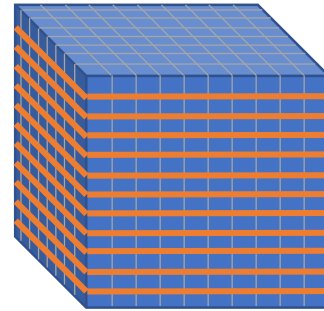
# 目的ごとに最適化されたフォーマットを採用

Xenium sample

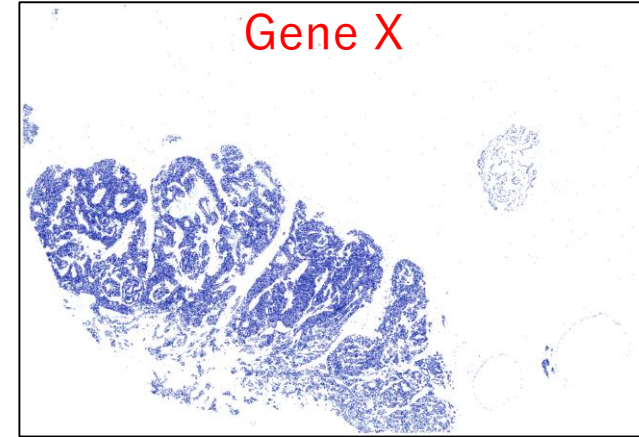


1つの遺伝子の可視化 -> その遺伝子の情報のみ読み込む

Zarr store #1



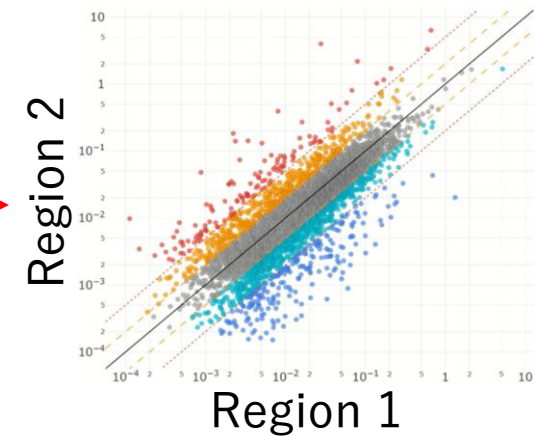
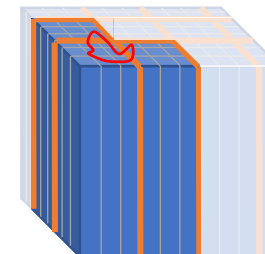
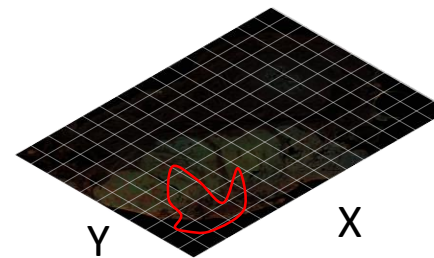
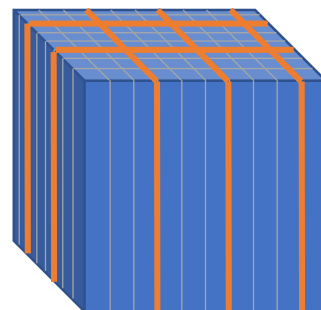
Gene X



ある領域の全遺伝子の平均値

-> その領域の情報のみ読み込む

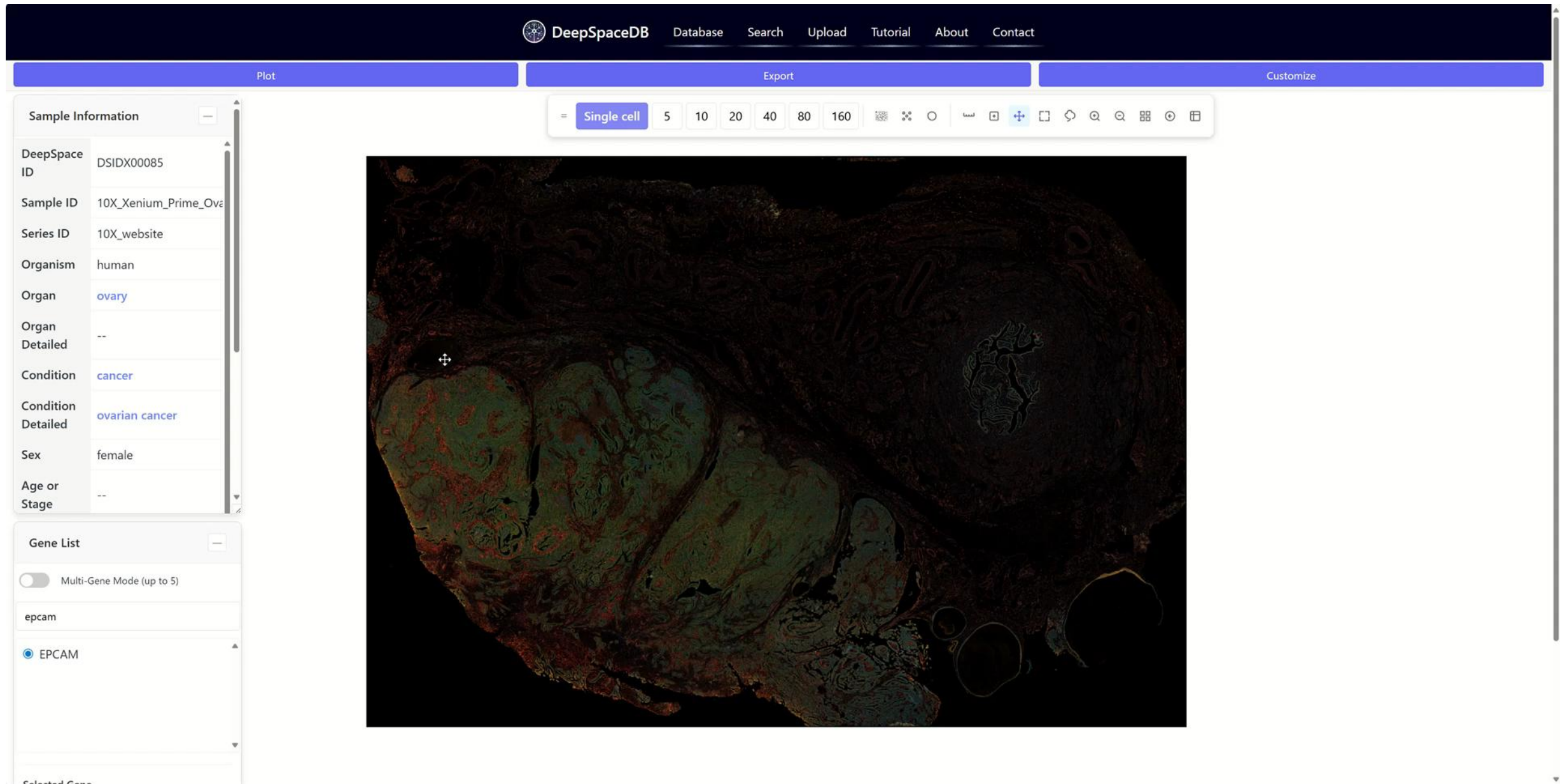
Zarr store #2



# Xenium interface – demonstration (動画)

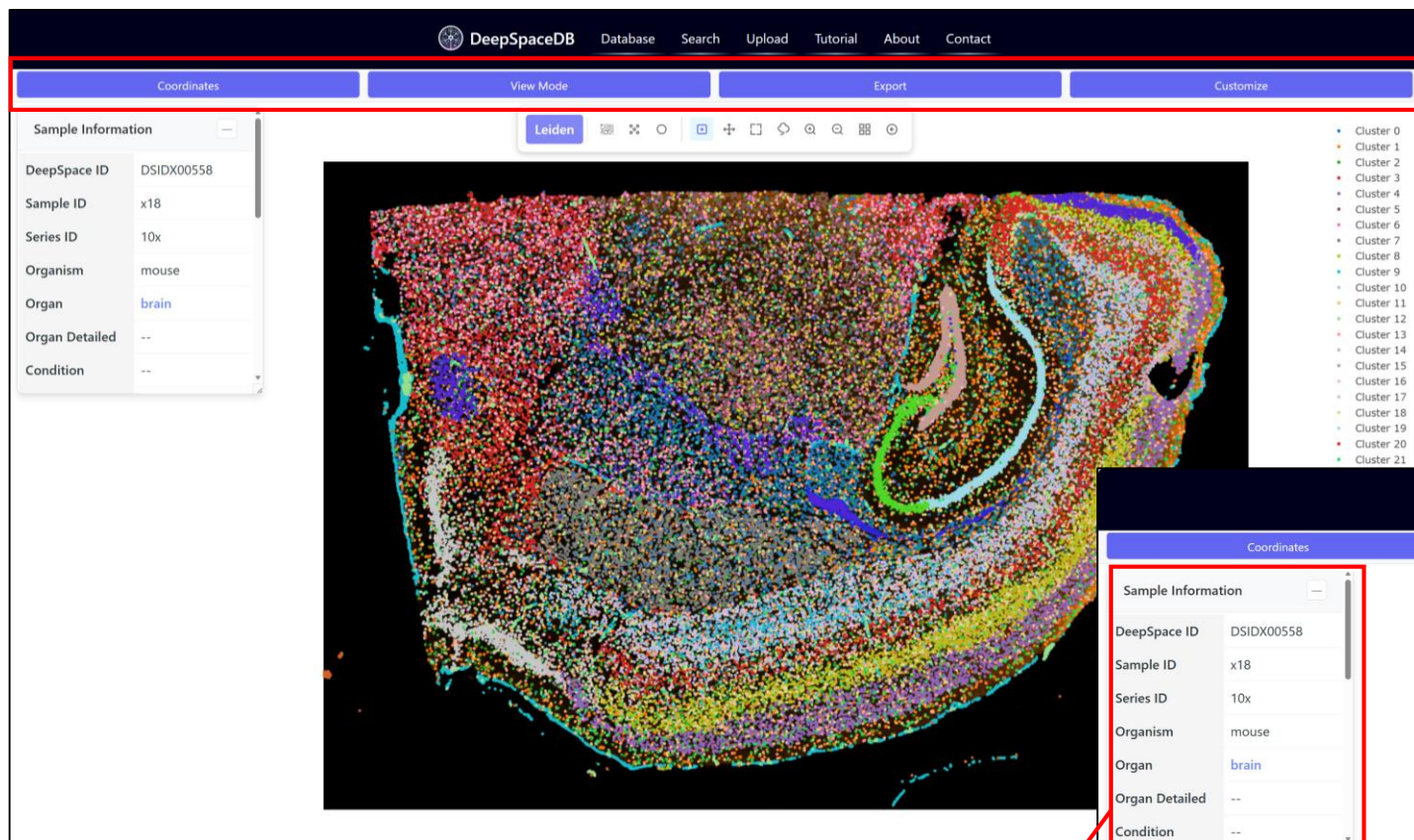


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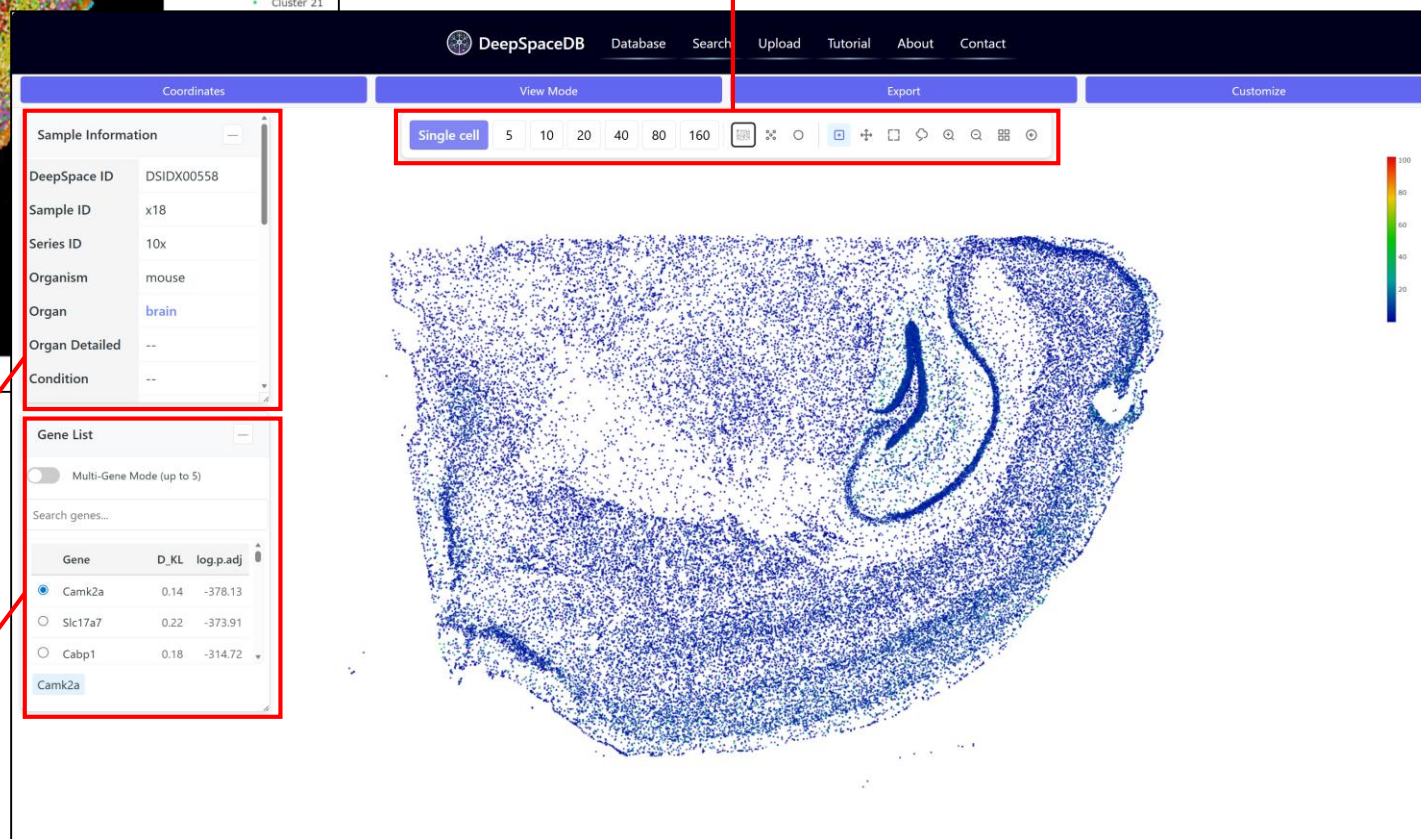
# Xenium interface (1)



メニュー:

- クラスタリング
- 品質指標
- 遺伝子発現パターン

多様な操作ツール  
(zoom in/out、画像表示切替など)



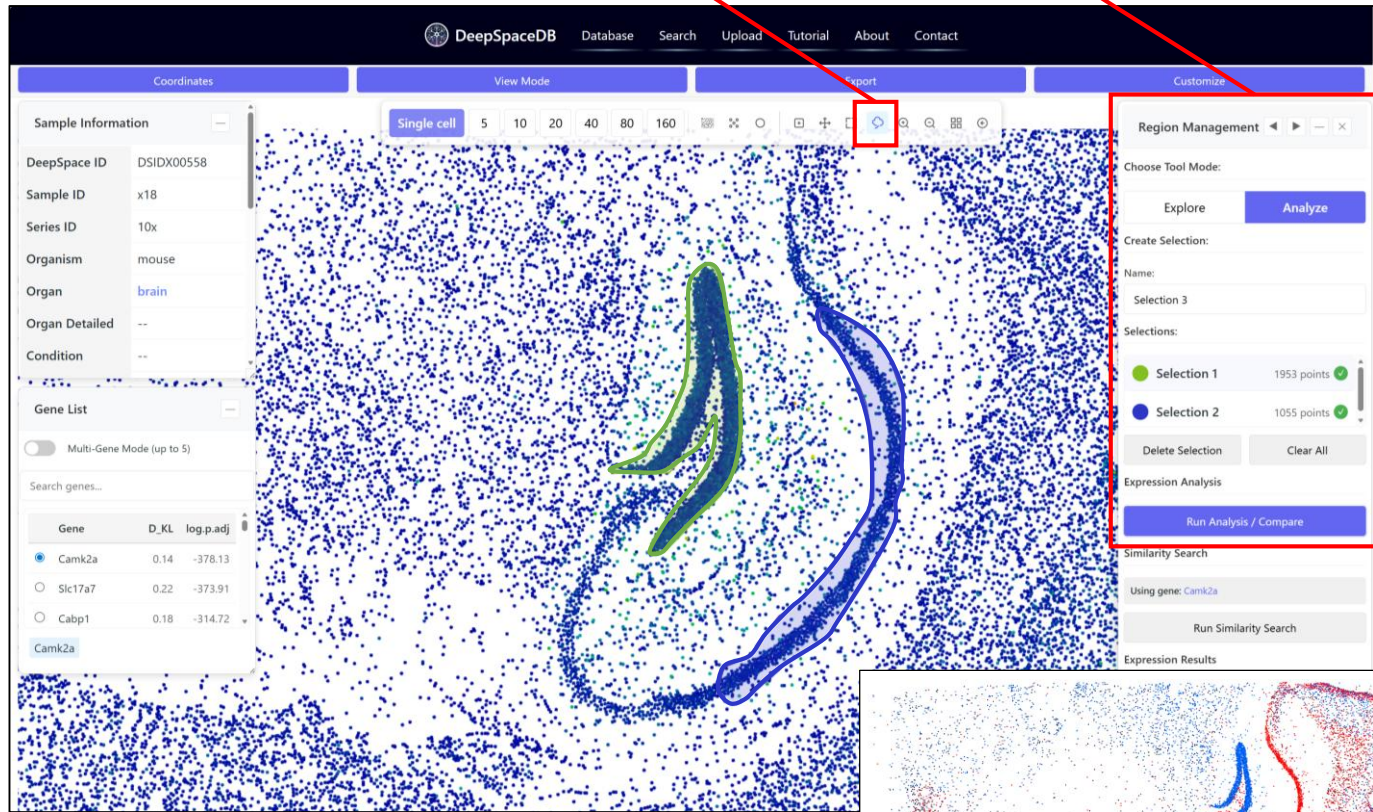
アノテーションデータ

singleCellHaystackを使って空間的変動遺伝子を前もって予測計算している

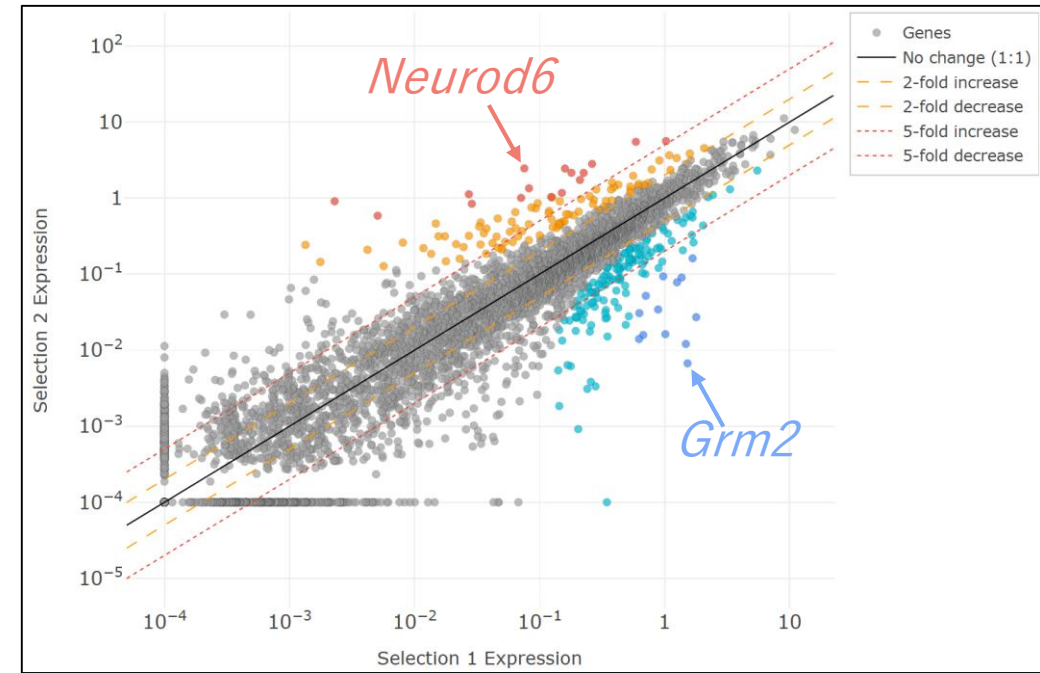


# Xenium interface (2)

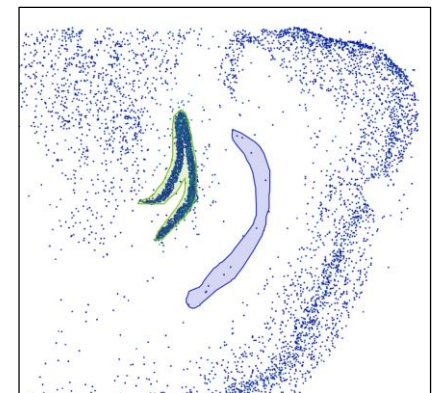
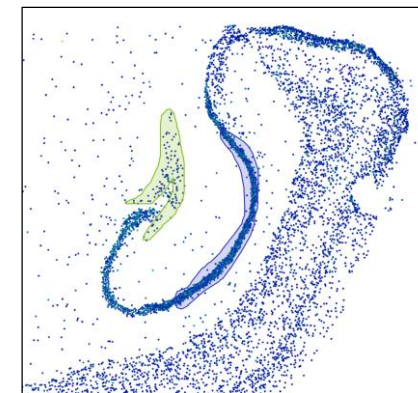
ユーザーは興味のある領域を自由に選択できる



選択した領域間の比較



複数の遺伝子発現プロット  
*Neurod6* *Grm2*



- Rを使った空間トランスクリプトミクスデータ解析
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- まとめ

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# DeepSpaceDBのまとめ

- 空間トランスクリプトームのデータベース構築
- 様々な組織や病歴を含んだ2,000以上の Visium サンプル
- インタラクティブかつ探索的な検索が可能
- 今後の計画:
  - Xenium用のインターフェースの公開
  - 解析ツールの追加
  - 他のプラットフォームも検討

Paper in *Nucleic Acids Research Database Issue*

🔍 deepspacedb nar or [link](#)

