

# Rを用いた空間解析の基礎 と 空間データベースの紹介

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大学



 LiMe

# 本日の目標・想定する受講者

空間トランскри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скри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скри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

バンデンボン アレクシス  
**VANDENBON Alexis** 京都大学 医生物学研究所 准教授



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скриプトミクスデータ解析
  - Visium example
  - Other platforms
- 既存の空間トランскри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)

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## Getting Started with Seurat

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

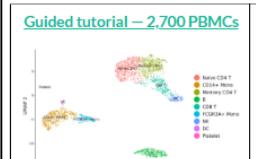
We provide a series of vignettes, tutorials, and analysis walkthroughs to help users get started with Seurat. You can also check out our [Reference page](#) which contains a full list of functions available to users.

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.

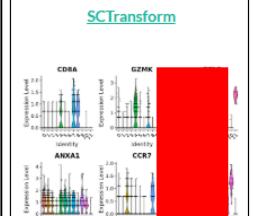
**Guided tutorial – 2,700 PBMCs**



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

**GO**

**SCTransform**



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

**Contents**

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

or

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## Getting Started with Seurat

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

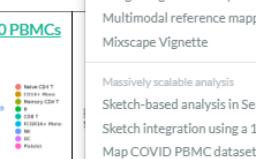
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**Guided tutorial – 2,700 PBMCs**



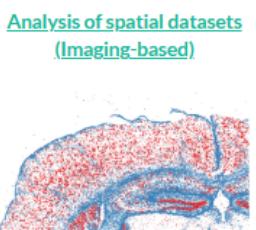
A basic overview of Seurat that includes an introduction to common analytical workflows.

**GO**

**Spatial analysis**

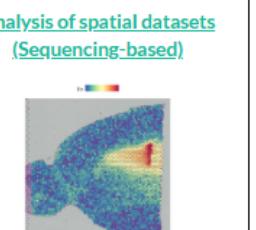
These vignettes will help introduce users to the analysis of spatial datasets in Seurat v5, including technologies that leverage sequencing-based readouts, as well as technologies that leverage in-situ imaging-based readouts. The vignettes introduce data from multiple platforms including 10x Visium,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

**Analysis of spatial datasets (Imaging-based)**



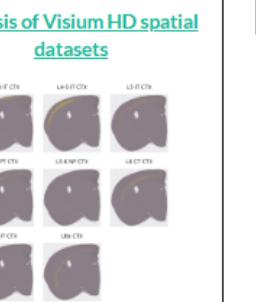
Learn to explore spatially-resolved data from multiplexed imaging technologies, including MERSCOPE, Xenium, CosMx SMI, and CODEX.

**Analysis of spatial datasets (Sequencing-based)**



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

**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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**Spatial analysis**

- Analysis of spatial datasets (Imaging-based)
- Analysis of spatial datasets (Sequencing-based)
- Analysis of Visium HD spatial datasets

**Seurat Object data access**

Pseudobulk analysis

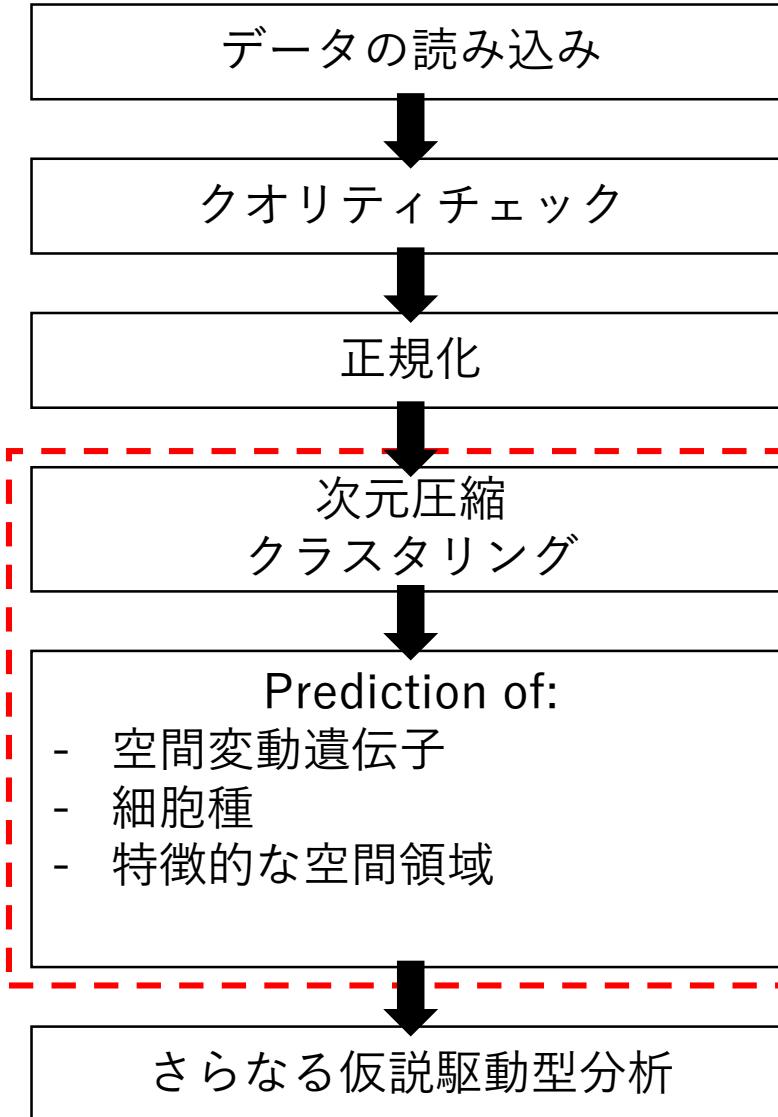
Multi-Assay features

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



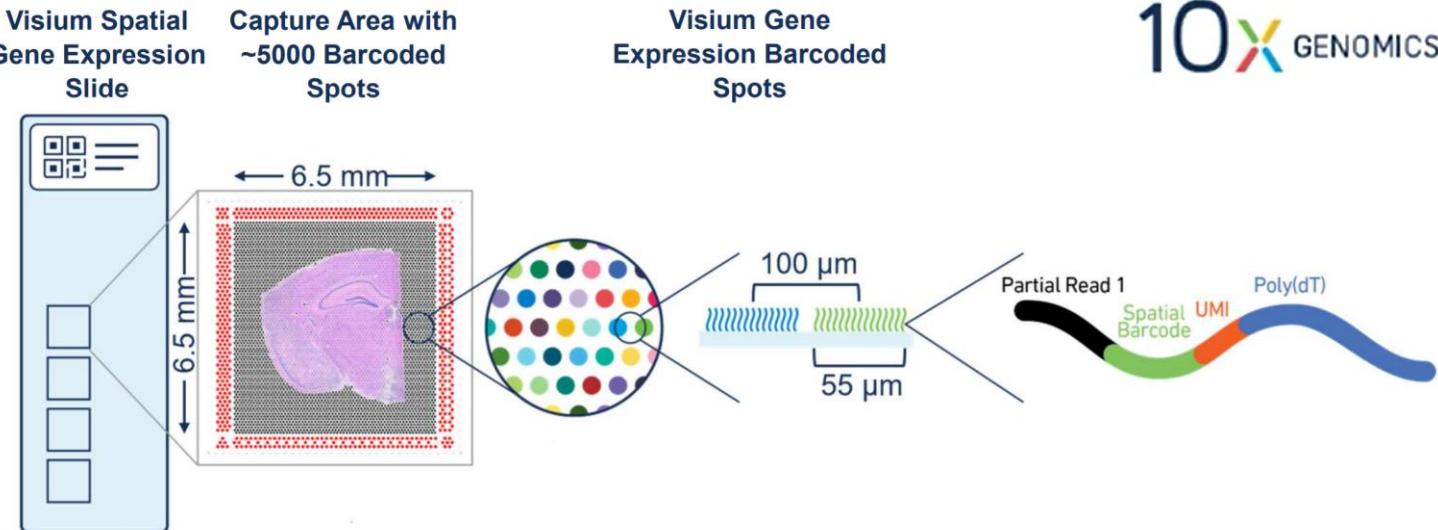
[https://satijalab.org/seurat/articles/spatial\\_vignette](https://satijalab.org/seurat/articles/spatial_vignette)

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

## データ探索

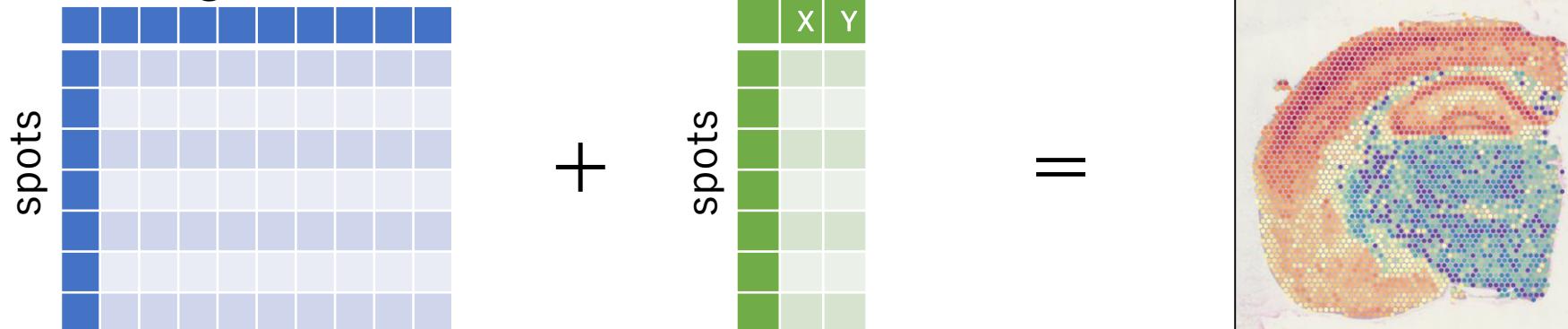
- 高次元データの解析で特に重要な
- データの品質評価や異常値の特定
- データ中の主要な構造を見つける
- 仮説の生成と検証
- 単純に正解をだすような解法は無い

# 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



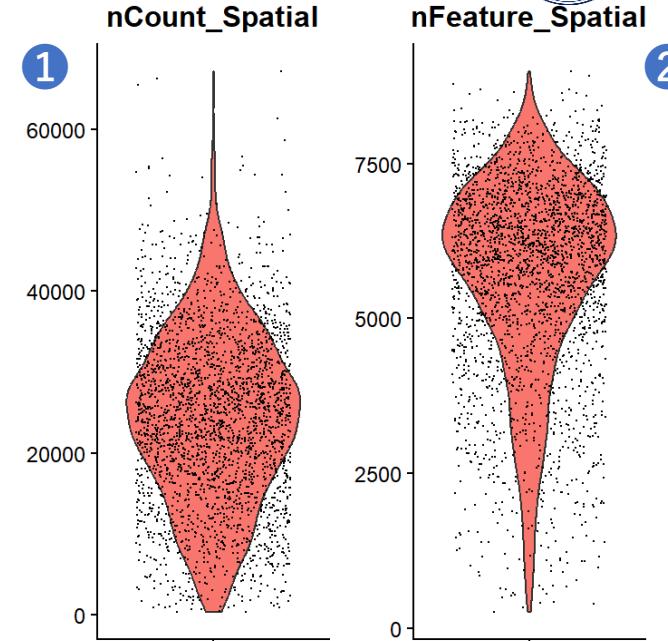
# Seurat tutorial – クオリティチェック (1)



```
#### 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
```



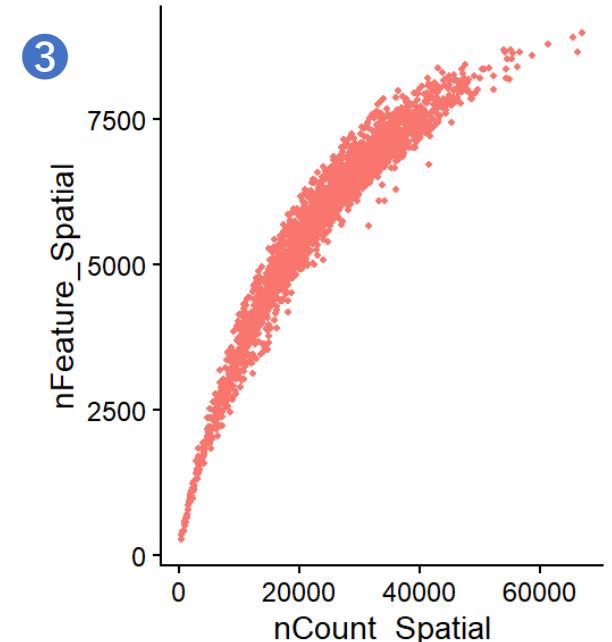
クオリティの指標として使われるもの

- 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")  
SpatialFeaturePlot(brain, features = "nFeature_Spatial")
```

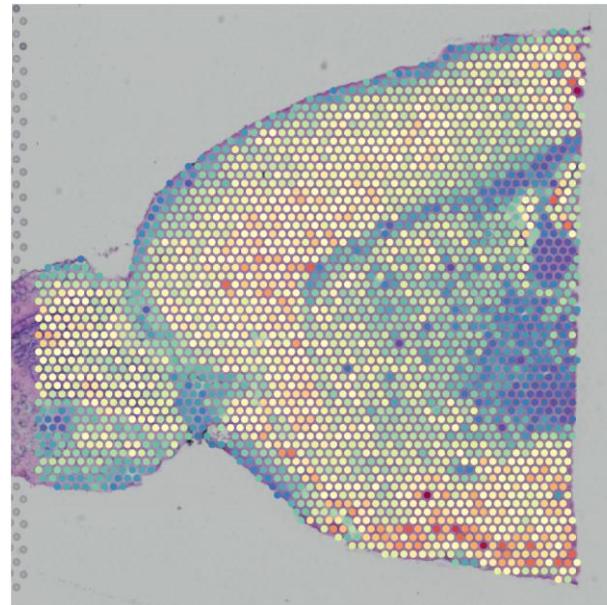
- クオリティの指標として使われるもの

- 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

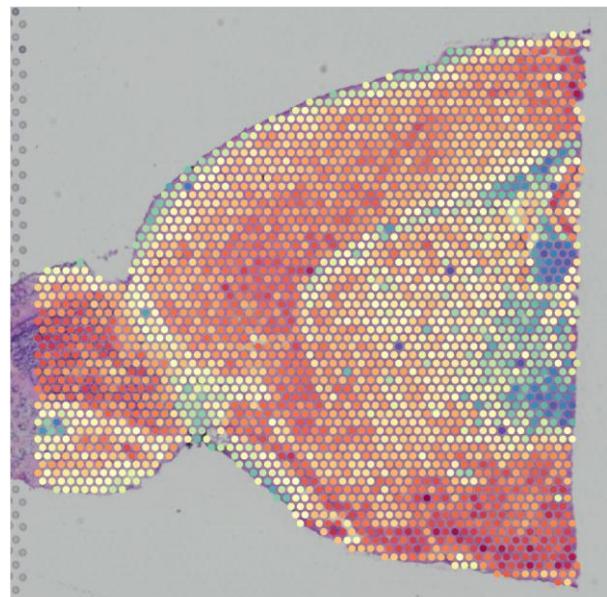
- シングルセル解析以上に注意深い解釈が必要となる

- 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



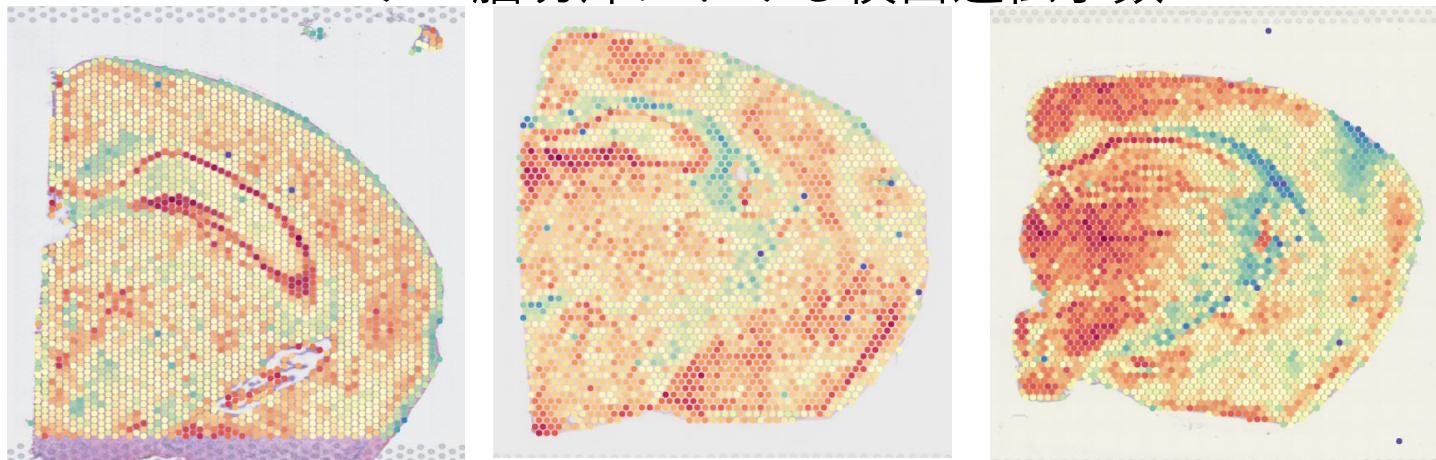
nCount\_Spatial  
60000  
40000  
20000

nFeature\_Spatial  
7500  
5000  
2500

# クオリティ値の空間パターン

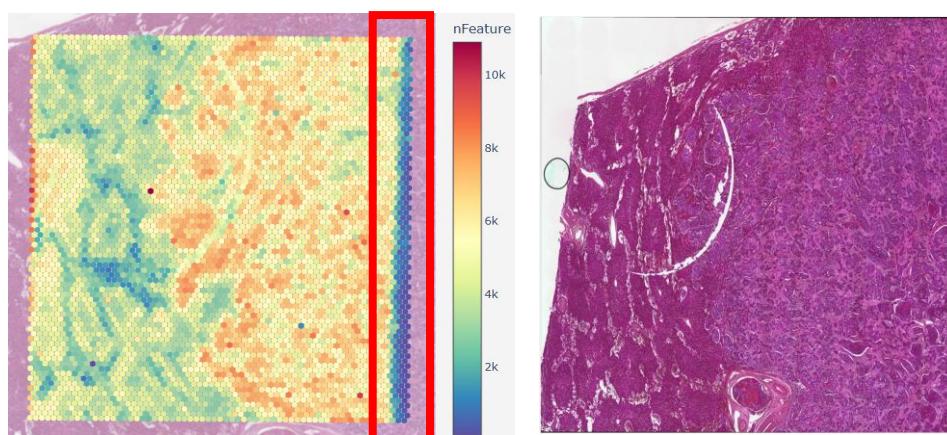
- DeepSpaceDBからの例
- 一部のパターンでは生物学的な特徴を反映している
  - 脳の神経解剖学的構造
  - ガン組織の存在

マウス脳切片における検出遺伝子数

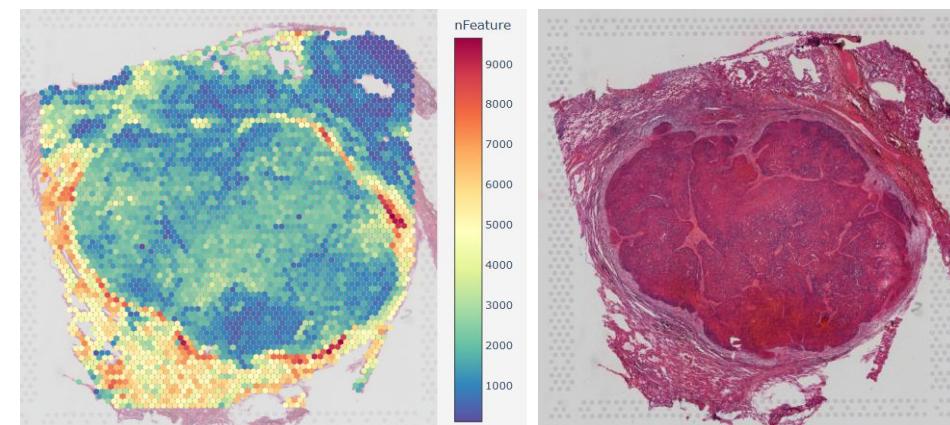


技術的な問題でパターンが生じることもある

乳がん由来の肝臓転移  
(sample ID DSID001370)



肝芽腫 (sample ID DSID001904)



# Seurat チュートリアル – 正規化

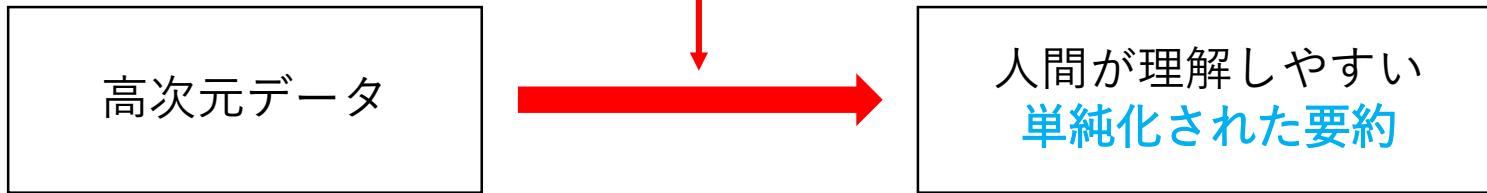
- 生データのUMIカウントは、スポット間のシークエンシング深度の違いに左右される
- スポット間の比較を妥当とするには正規化が必要である
- オプション:
  - Option 2. ライブラリサイズ（シークエンシング深度）による正規化
  - Option 1. SCTransform 負の二項分布に基づく複雑な正規化アプローチ

```
#### 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

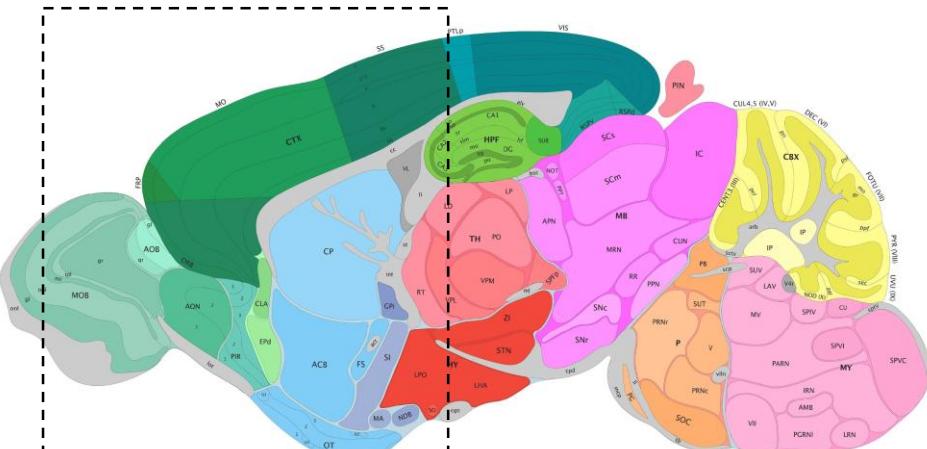
# 探索的データ解析



## #### 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) ←
```

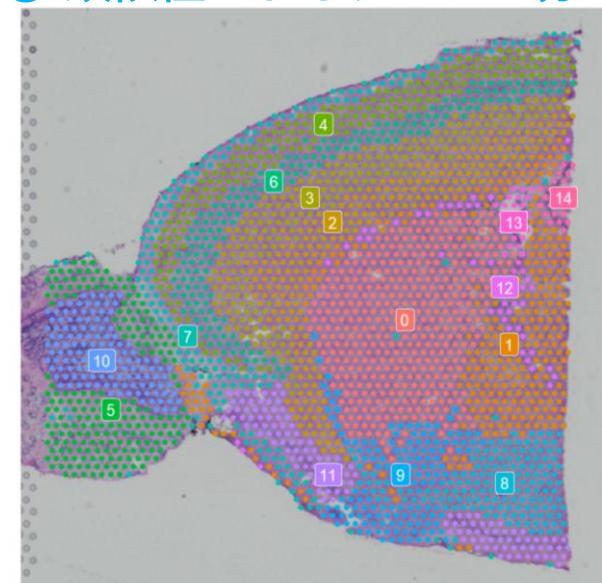


マウス脳 サジタル断面 (Image from Allen brain atlas)



# 人間が理解しやすい 単純化された要約

## ① 類似性によるグループ分け



## 2 次元圧縮

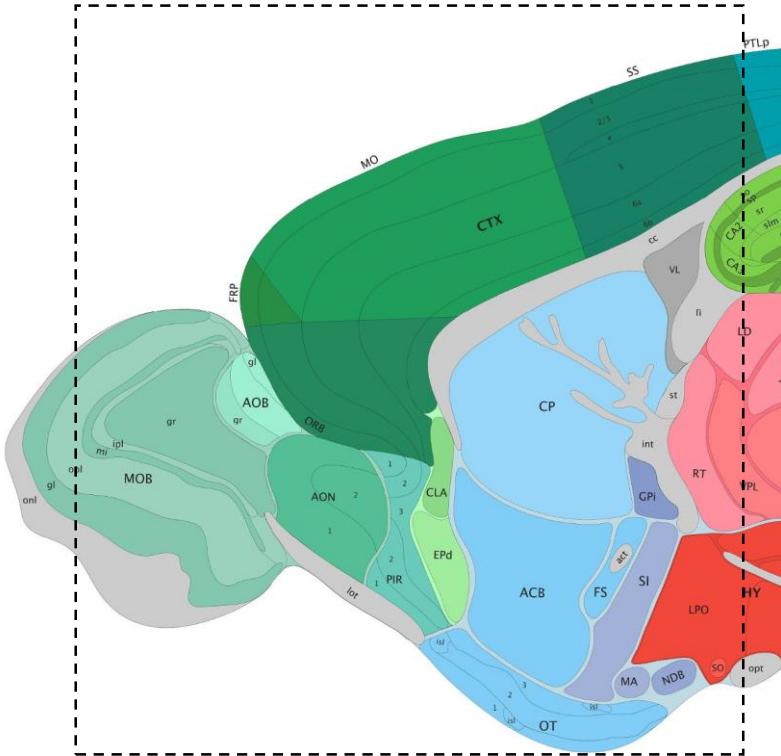
## ② 次元圧縮

# Seurat tutorial – クラスタリング結果の検証



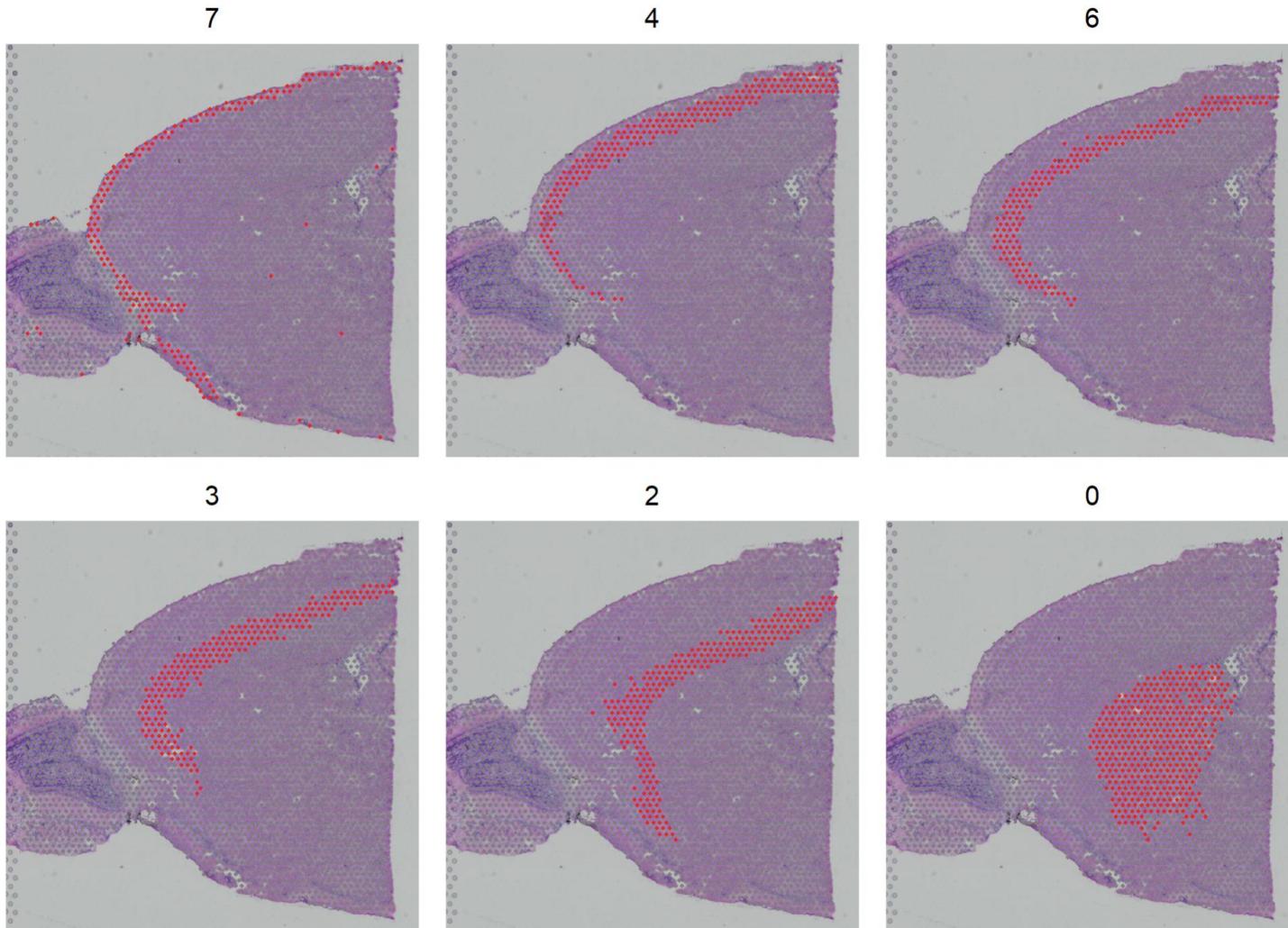
```
# highlighting clusters
```

```
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にのみ基づいており、空間的情報は一切用いていない

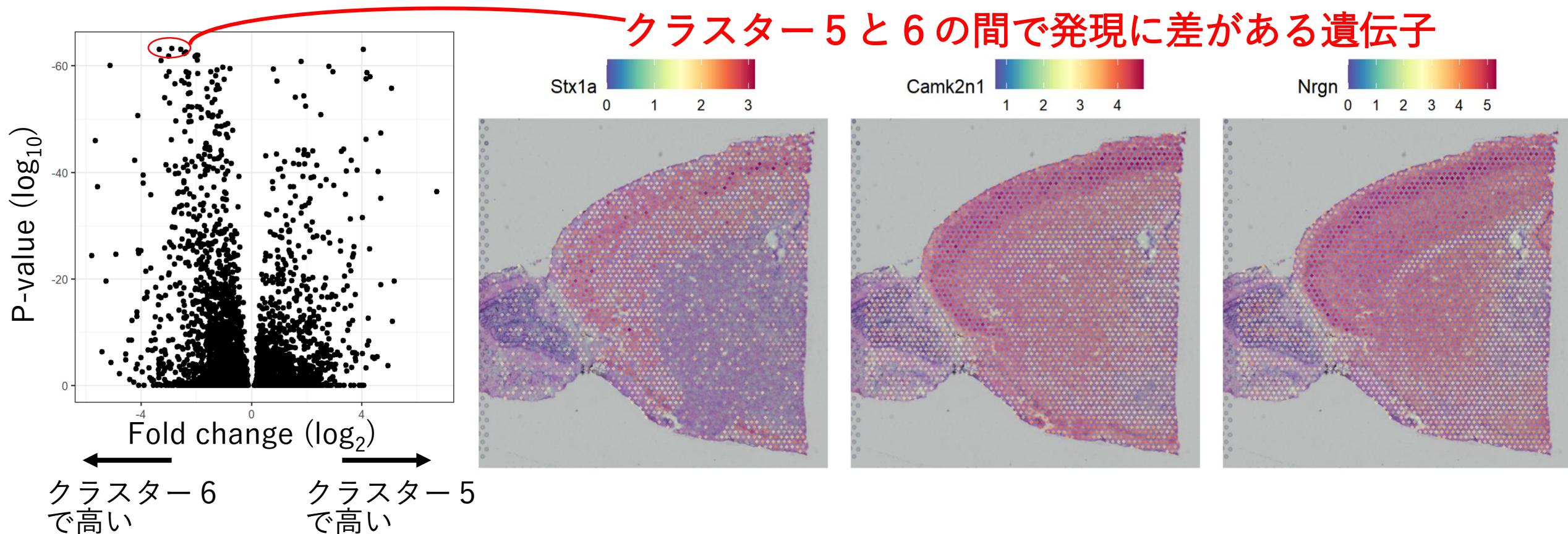


# Seurat tutorial – 空間的変動遺伝子 (SVG) (1)



```
#### 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



# Seurat tutorial – 空間的変動遺伝子 (SVG) (2)



## 空間情報を取り込んだSVG 予測法

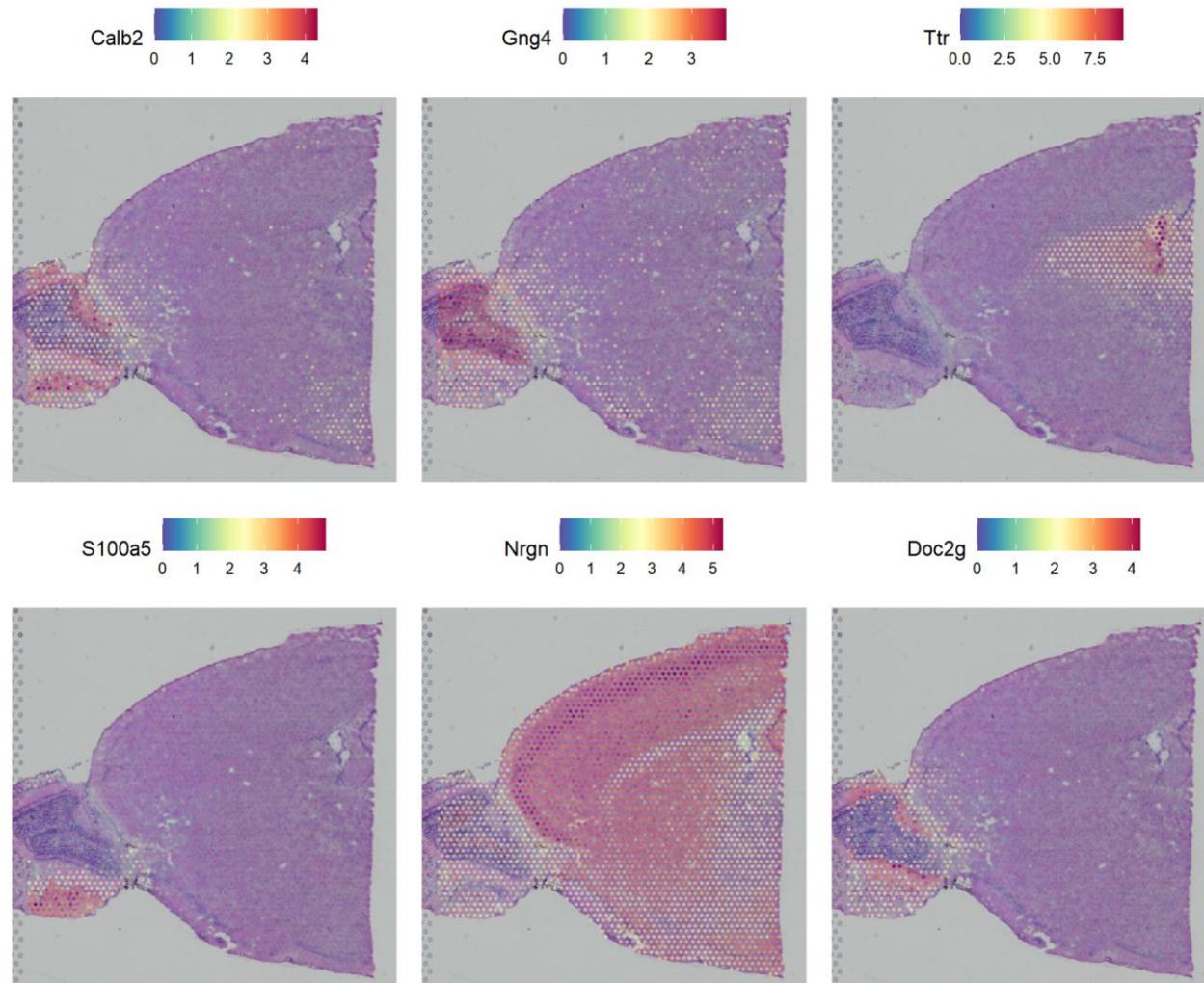
- Moran's I (used in this tutorial)
- SPARK-X (Zhu *et al.*, Genome Biol, 2021)
- binSpect (Giotto package; Dries *et al.*, Genome Biol, 2021)
- singleCellHaystack (Vandenbon and Diez, Nat Commun, 2020)

```
# 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



- Rを使った空間トランскриプトミクスデータ解析
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# 他のプラットフォームについて

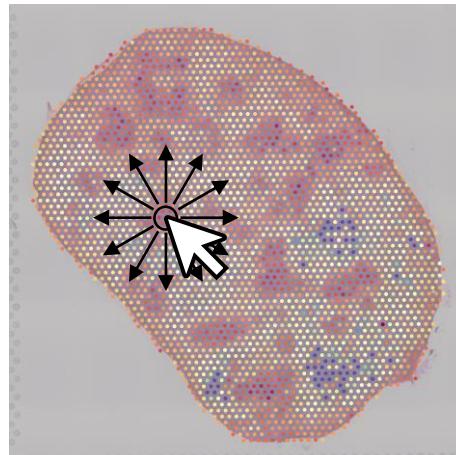
- The Seuratのウェブサイト上のチュートリアルはシーケンスベースのプラットフォームを対象としている
  - Visium
  - Slide-seq
- しかし、イメージベースのプラットフォームも同様のワークフローで解析可能である
  - Vizgen MERSCOPE
  - Xenium
  - Nanostring CosMx Spatial Molecular Imager
  - Akoya CODEX

# Seurat tutorial – 結論

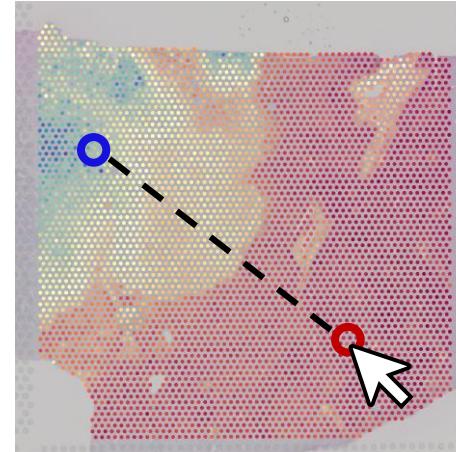


- Seurat は空間データ解析ツールとして大変優れている
- 解析の大部分はscRNA-seq 解析と同様の流れである
- しかし空間的な要素を完全には活用していない
- インタラクティブな探索には限界がある

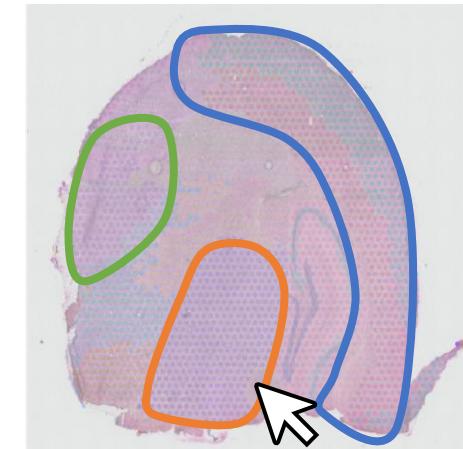
遺伝子発現は、ある点からの距離に応じてどのように変化するのか？



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	Gene 2	Gene 3
●	0.26	0.98	0.99
○	0.15	0.63	0.39
○	0.70	0.05	0.41
○	0.74	1.00	0.63
○	0.79	0.84	0.56
○	0.55	0.44	0.79
○	0.67	0.74	0.93
○	0.24	0.52	0.06
○	0.28	0.92	0.53
○	0.63	0.51	0.85

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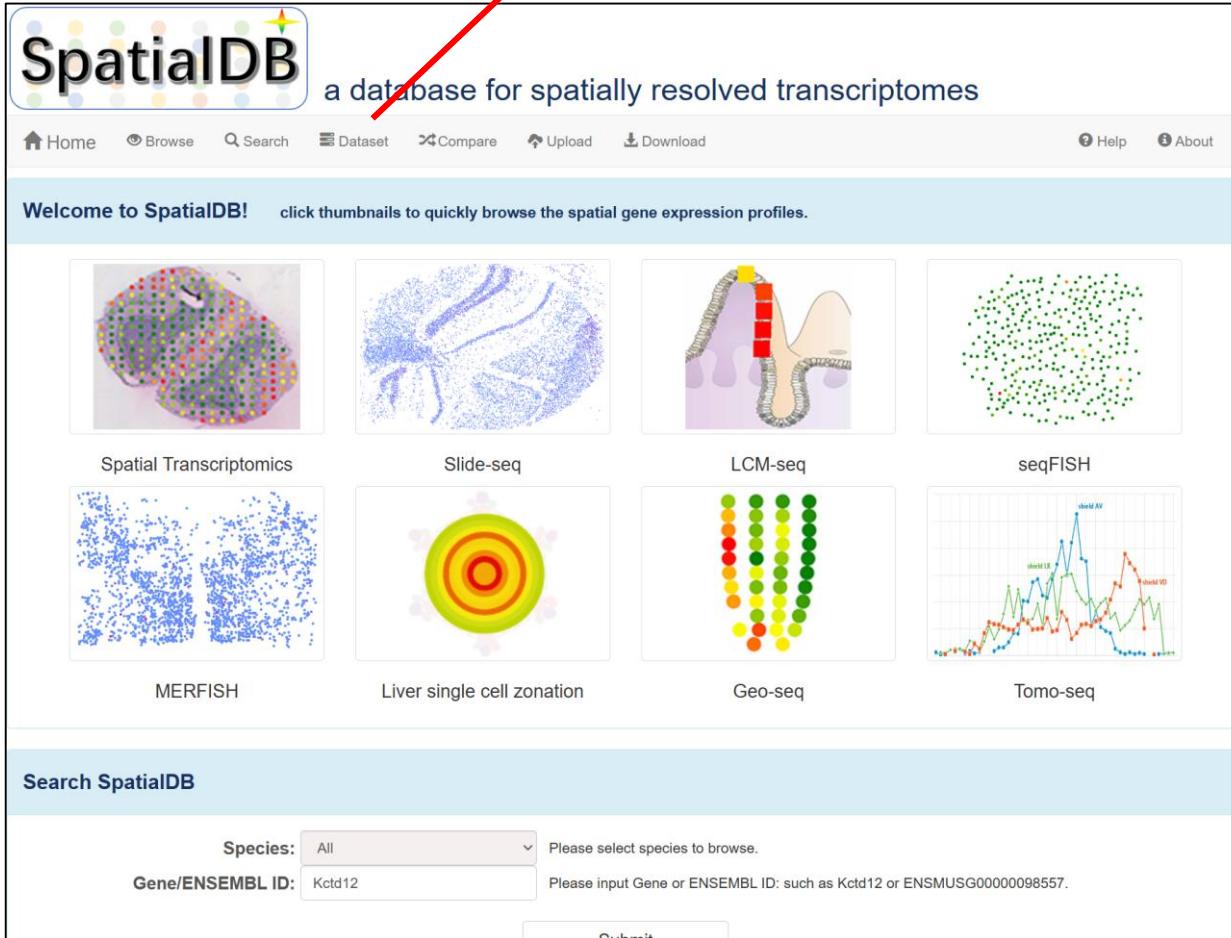
# Spatial transcriptomics databases

- 多くのデータベースが公開されている

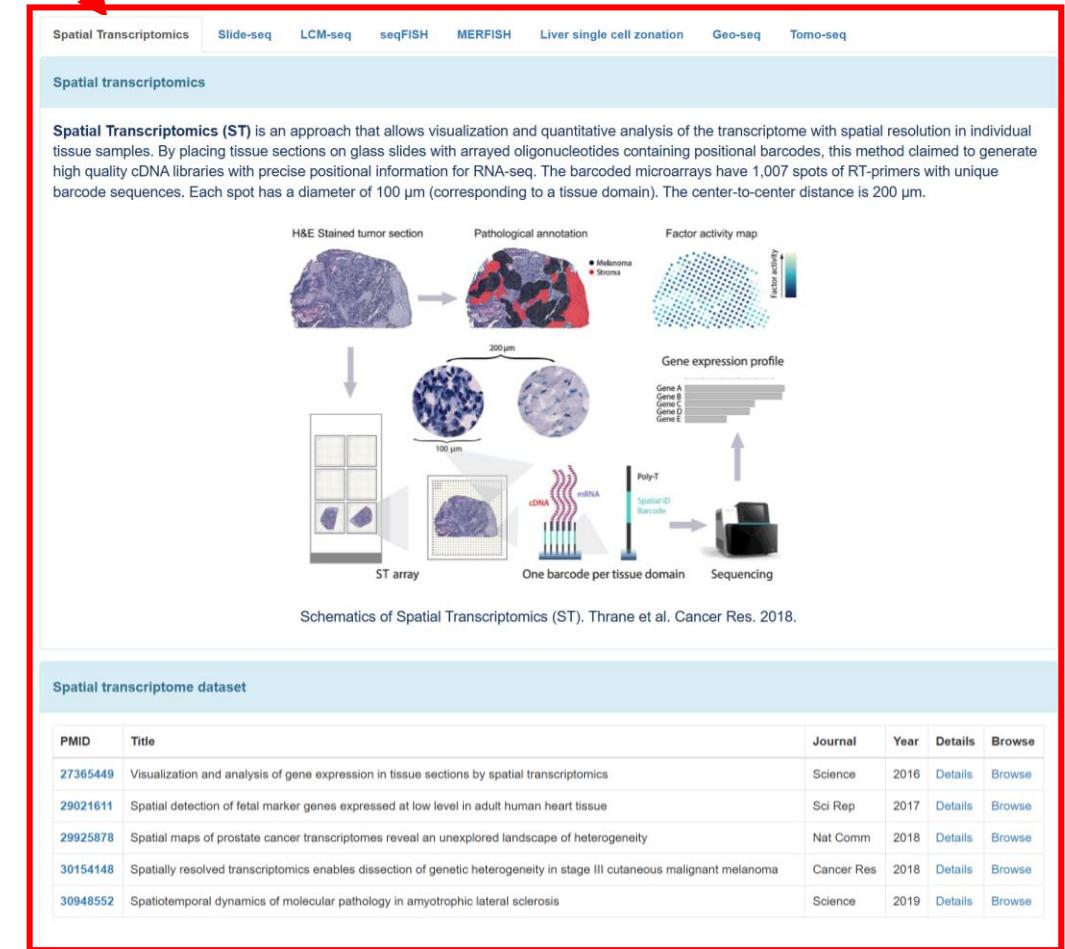
Database	URL	Publication	PMID	Comment
SpatialDB	<a href="#">link</a>	Nucleic Acids Res, 2020	<a href="#">31713629</a>	No longer maintained?
SODB	<a href="#">link</a>	Nat Methods, 2023	<a href="#">36797409</a>	Sometimes long load times
SCAR	<a href="#">link</a>	Nucleic Acids Res, 2024	<a href="#">37739405</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

# SpatialDB



異なる実験手法・技術からなるサンプル



- 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) "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](#).

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

**External links**

- Single Cell PORTAL
- HTAN 10X GENOMICS
- SPATIAL research
- zenodo
- Dropbox
- ImmunoAtlas

**Visitors**

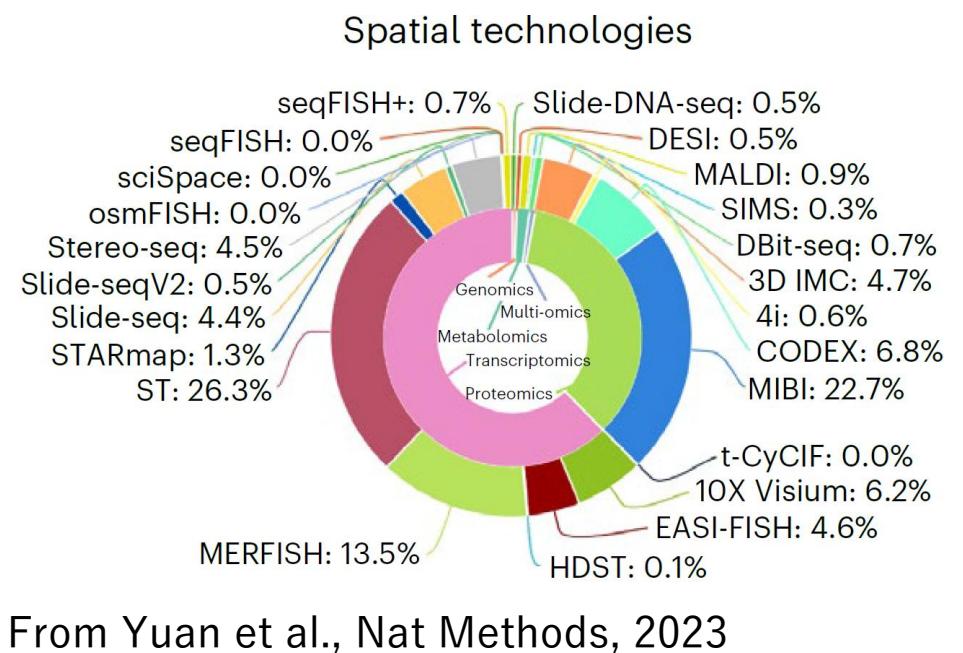
INTRODUCTION BROWSE SEARCH STATISTICS TUTORIAL NEWS

Biotech Categories ▾ Spatial Transcriptomics

10X Visium    Slide-seq    MERFISH    osmFISH

seqFISH    seqFISH+    seqScope    STARmap

- 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

Dataset Name	Date	doi	Country	Operations
The spatial transcriptomic landscape of the healing mouse intestine following 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>

[Subm.](#)

Species  Tissue

Axolotl  
Arabidopsis  
mouse  
Cell Line  
Drosophila  
None  
cell line  
Mouse

NCTC1469/Hepa1-6  
colon cancer  
Lymph Node  
Cell Line  
Spleen  
Kidney Organoid  
neocortex  
spinal cords

Red arrows indicate the flow from the search filters on the left to the dataset list in the center, and from the dataset list to the detailed view on the right.

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: Guilliams, M., Bonnardel, J., Haest, B., Vanderborght, B., Wagner, C., Remmerie, A., Bujko, 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. Dalmeyer, K. Geldhof, P. Casaert, S. Deplancke, B., Ten Dijke, P., Hoorens, A., Vanlander, A., Berrevoet, F., Van Nieuwenhove, Y., Saeyns, 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: GSM576442\_ 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 Confirm  
 Reverse Colors

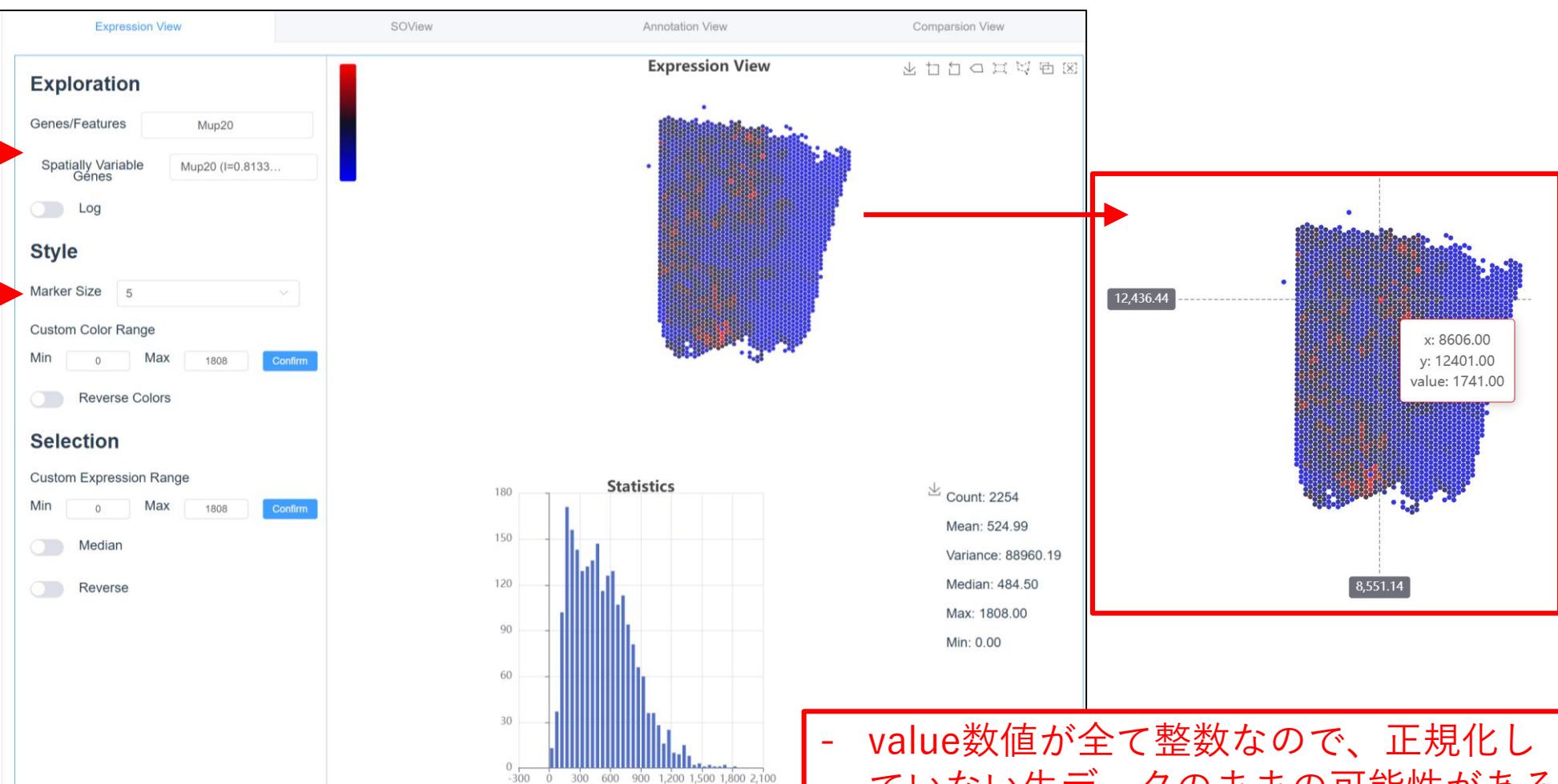
Expression View

# SODB – Expression View

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 →



**Expression View**

**Exploration**

- Genes/Features: Mup20
- Spatially Variable Genes: Mup20 (I=0.8133...)
- Log:

**Style**

- Marker Size: 5
- Custom Color Range: Min 0 Max 1808 Confirm
- Reverse Colors:

**Selection**

- Custom Expression Range: Min 0 Max 1808 Confirm
- Median:
- Reverse:

**Statistics**

	Count: 2254
Mean:	524.99
Variance:	88960.19
Median:	484.50
Max:	1808.00
Min:	0.00

12,436.44

x: 8606.00  
y: 12401.00  
value: 1741.00

8,551.14

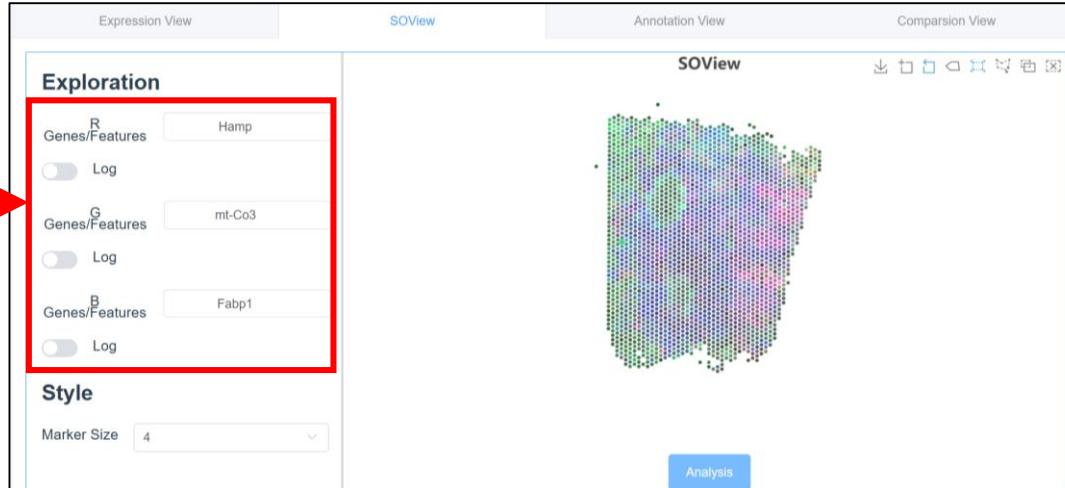
- value数値が全て整数なので、正規化していない生データのままの可能性がある
- 切片画像データが付いていない

# SODB – SOView



25

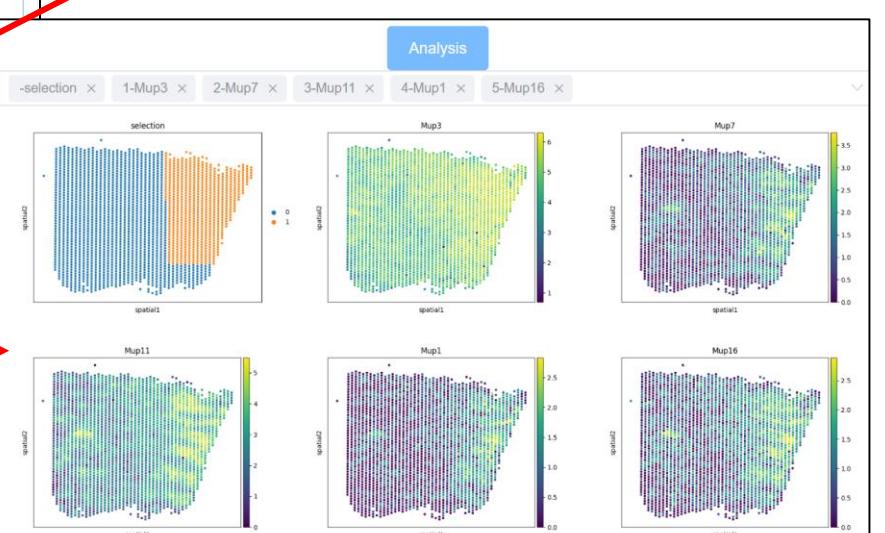
遺伝子発現分布を  
3つまで表示する  
ことができる（赤青  
緑）



興味ある領域を選んで“Analysis”  
をクリックすると



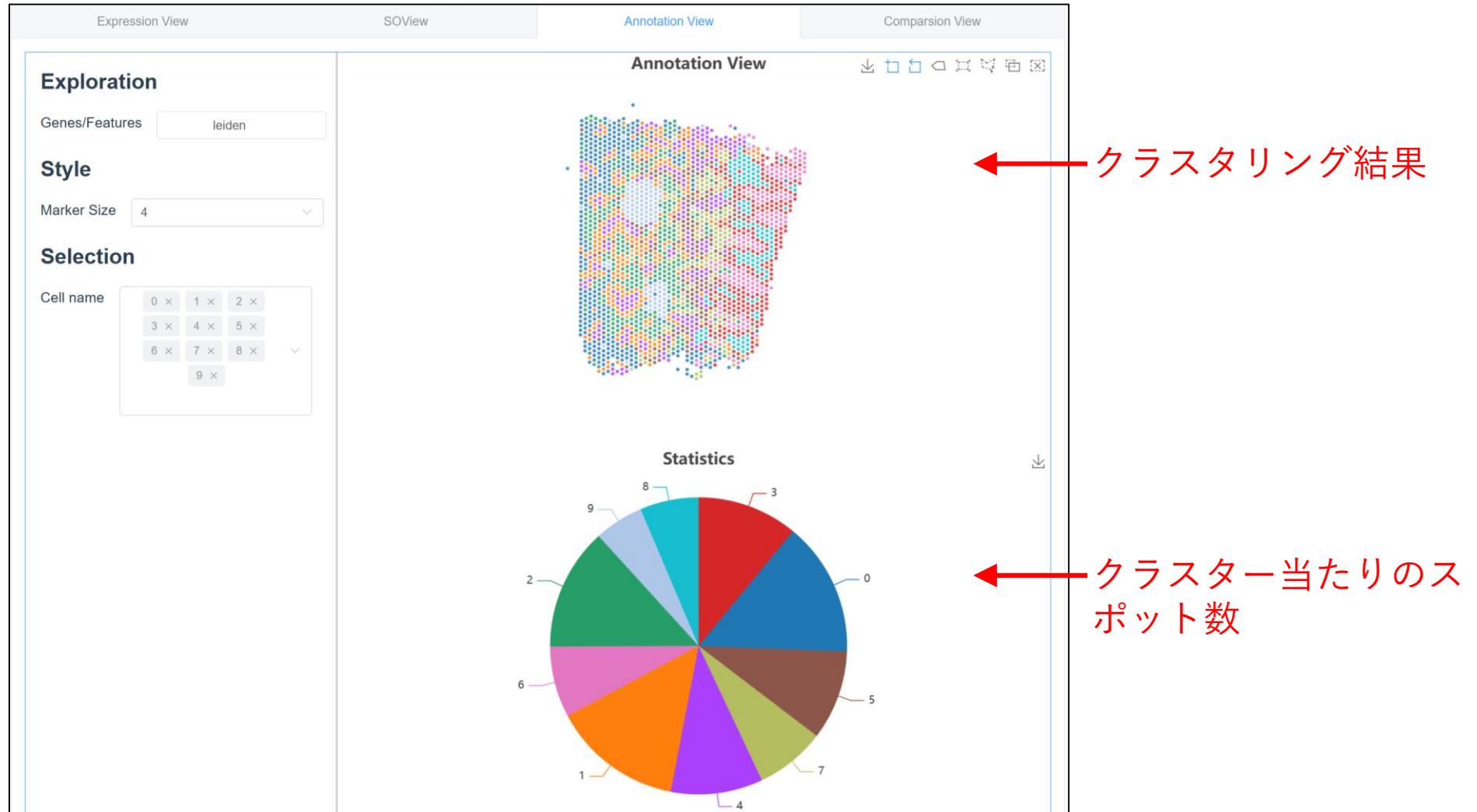
選択した領域内で発現が高い遺伝子が  
表示される。



# SODB – Annotation View



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# SODB – Comparison View



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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

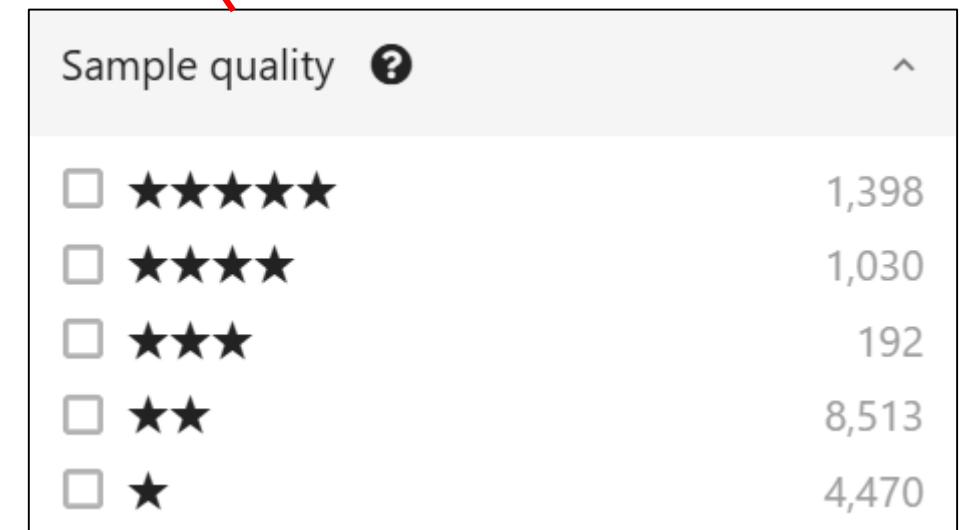
# STOmicsDB



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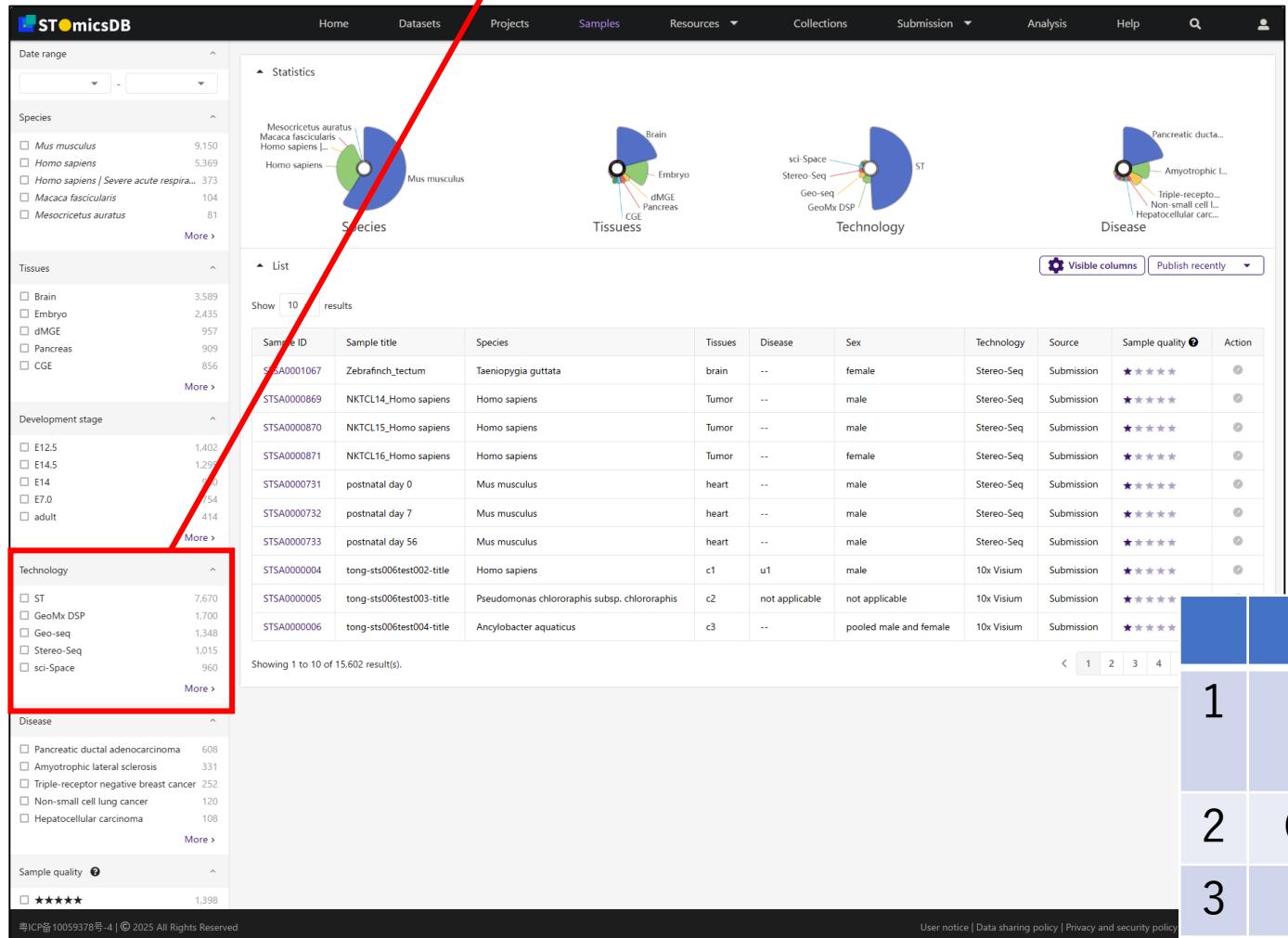
The screenshot shows the STOmicsDB homepage with a purple header. The top navigation bar includes links for Home, Datasets, Projects, Samples, Resources, Collections, Submission, Analysis, Help, and a search bar. Below the header, there's a large image of a 3D grid of blue dots representing spatial transcriptomics data. The main content area displays several statistics: 7,339 Publications, 362 Datasets, 17 Species, 128 Tissues, and 15,602 Samples. There are two main sections: 'Data Archive' and 'Data Visualization'. The 'Data Archive' section allows users to deposit sequencing data and expression data into the database, with 'Submit' and 'Example' buttons. The 'Data Visualization' section provides tools for visualizing expression data and presenting analysis results, also with 'Submit' and 'Example' buttons. At the bottom, there's a 'Species' section showing icons and names for Homo sapiens, Mus musculus, Danio rerio, Macaca fascicularis, and Rattus norvegicus, along with their respective dataset counts.

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



- 5★: spatial coordinates & images  
4★: spatial coordinates only  
3★: images only  
2★: lacks coordinates & images  
1★: not processed

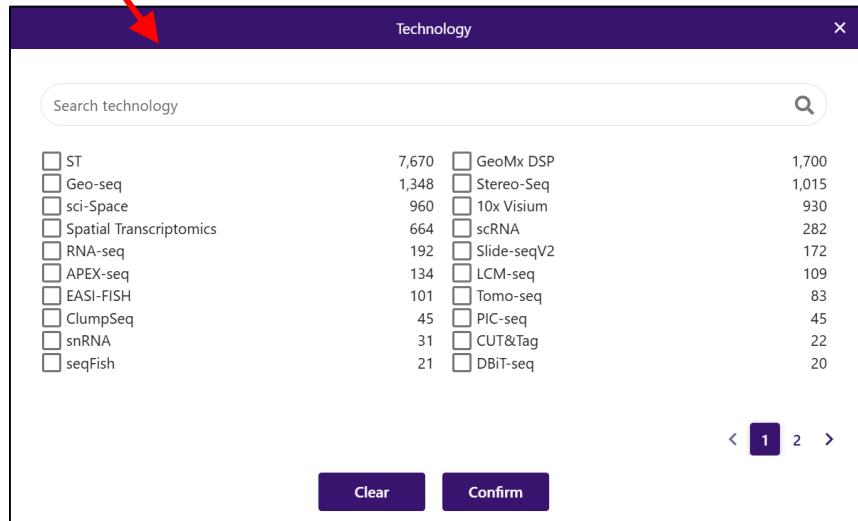
# STomicsDB – “Samples” page



The screenshot shows the 'Samples' page of the STomicsDB website. At the top, there are navigation tabs: Home, Datasets, Projects, Samples (selected), Resources, Collections, Submission, Analysis, and Help. Below the tabs are several filter sections:

- Species:** Includes filters for Mus musculus (9,150), Homo sapiens (5,369), and others like Macaca fascicularis, Homo sapiens Severe acute respiratory syndrome, Macaca fascicularis, and Mesocricetus auratus.
- Tissues:** Includes filters for Brain (3,589), Embryo (2,435), dMGE (957), Pancreas (909), and CGE (856).
- Development stage:** Includes filters for E12.5 (1,402), E14.5 (1,295), E14 (954), E7.0 (54), and adult (414).
- Technology:** A section highlighted with a red box, listing technologies like ST (7,670), GeoMx DSP (1,700), Geo-seq (1,348), Stereo-Seq (1,015), and sci-Space (960).
- Disease:** Includes filters for Pancreatic ductal adenocarcinoma (608), Amyotrophic lateral sclerosis (331), Triple-receptor negative breast cancer (252), Non-small cell lung cancer (120), and Hepatocellular carcinoma (108).
- Sample quality:** Includes a filter for ★★★★☆ (1,398).

Below the filters is a 'List' section showing 10 results from a total of 15,602. The columns include Sample ID, Sample title, Species, Tissues, Disease, Sex, Technology, Source, Sample quality, and Action. The first few rows show samples like STSA0001067 (Zebrafish\_tectum, Taenioptygia guttata) and STSA0000869 (NKTC14\_Homo sapiens, Homo sapiens). At the bottom, there are links for User notice, Data sharing policy, and Privacy and security policy.



A modal window titled 'Technology' is shown. It contains a search bar labeled 'Search technology' and a list of technologies with their counts:

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

At the bottom are 'Clear' and 'Confirm' buttons.

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

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

**STomicsDB**

Home Datasets Projects Samples Resources ▾ Collections Submission ▾ Analysis Help 🔎

Date range

Species

- Mus musculus** (house mouse) 3
- Ambystoma mexicanum* (axolotl) 0
- Arabidopsis thaliana* (thale-cress) 0
- Bos taurus* (cattle) 0
- Caenorhabditis elegans* (roundwo... 0

More >

Tissues

- Brain 3
- ACA 0
- ACP close to the hypothalamus 0
- ACP distant from the hypothalam... 0
- AI-CLA 0

More >

Technology

- Stereo-Seq 3
- 10x Visium 0
- 10x Visium,MERFISH 0
- 10x Visium,Spatial Transcriptomic... 0
- 10x Visium,scATAC,scRNA 0

More >

Dataset quality

- ★★★★★ 0
- ★★★★ 1

List (3) Table Relevance (0)

1 SAW: An efficient and accurate data analysis workflow for Stereo-seq spatial transcriptomics (ID: STDS0000234)

The basic analysis steps of spatial transcriptomics involves obtaining gene expression information from both space and cells. This process requires a set of tools to be completed, and existing tools face performance...

Chun Gong, Shengkang Li, Leying Wang, Fuxiang Zhao, Shuangshang Fang, Dong Yuan, Zijian Zhao, Qiqi He,...

2023-09-07 0 2,906 276 **Mus musculus** Spots: 2,343 Stereo-Seq

2 ABSTA : Amniotes Brain Spatiotemporal Transcriptomic Atlas (ID: STDS0000241)

The evolution of amniotes introduced the emergence of intricate brain organization, particularly in the telencephalon, but its genoarchitectonic identity and evolutionary trajectory remain unclear. By construct...

Zhenkun Zhuang, Fubaoqian Huang, Kuo Liao, Youning Lin, Duoyuan Chen, Hong Wang, Jinfeng Huang, Che...

2024-04-17 0 2,092 611 **Mus musculus** Spots: 89,060 Stereo-Seq

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

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...

Mengnan Cheng, Liang Wu, Chuanyu Liu, Longqi Liu

2022-02-16 0 8,422 451 **Mus musculus** Spots: 120,000 PMID: 35656552

All results loaded.

**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 8,503 452 Spots: 120,000 Genes: 27,330 PMID: 35656552

Summary Visualization Data Related Sample

Catalog

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, Ventrie, 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

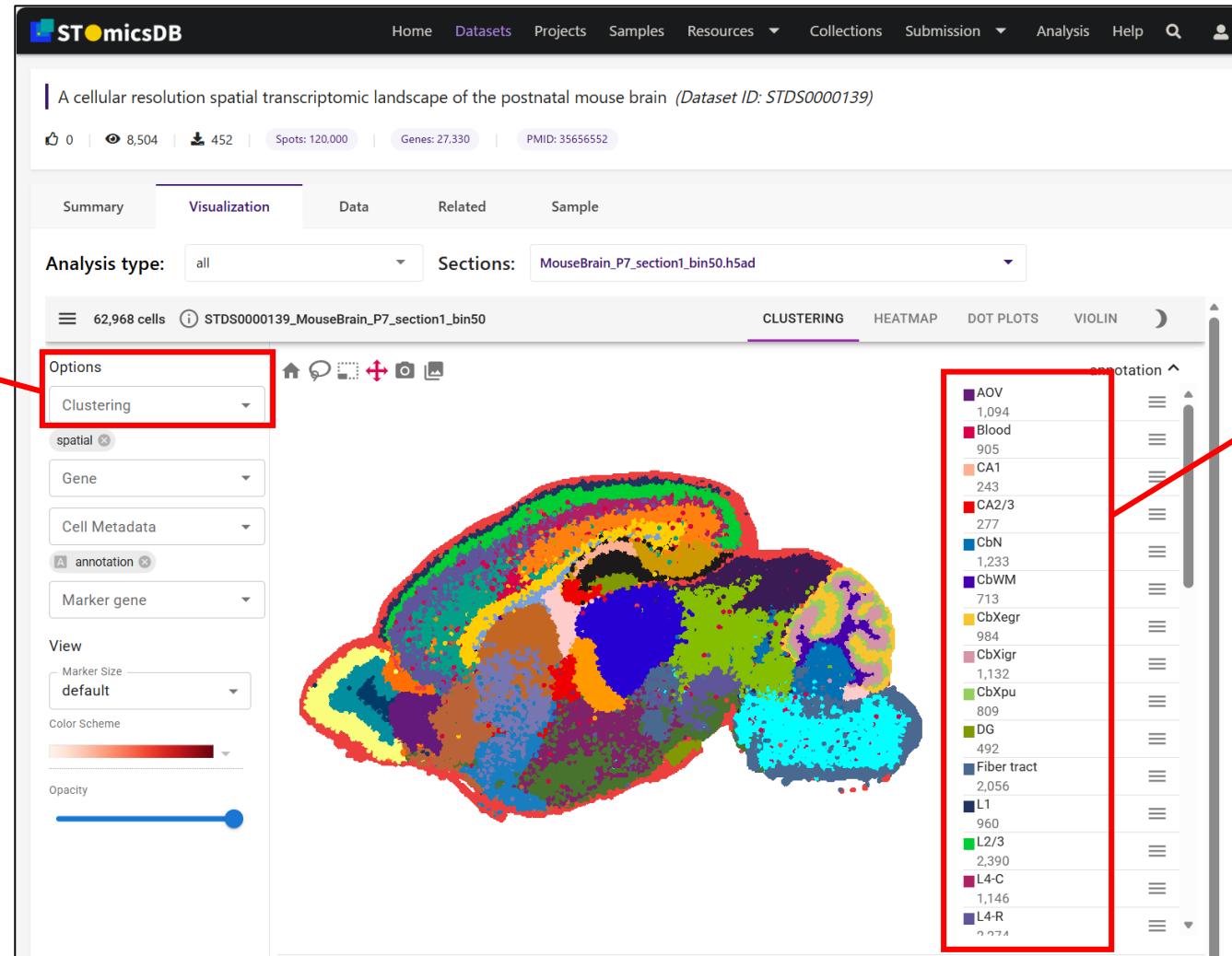
CNGB Project: CNP0002646  
Publication: A Cellular Resolution Spatial Transcriptomic Landscape of the Medial Structures in Postnatal Mouse Brain

How to cite

Cite database of STomicsDB:

# STOmicsDB – Visualization (1)

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



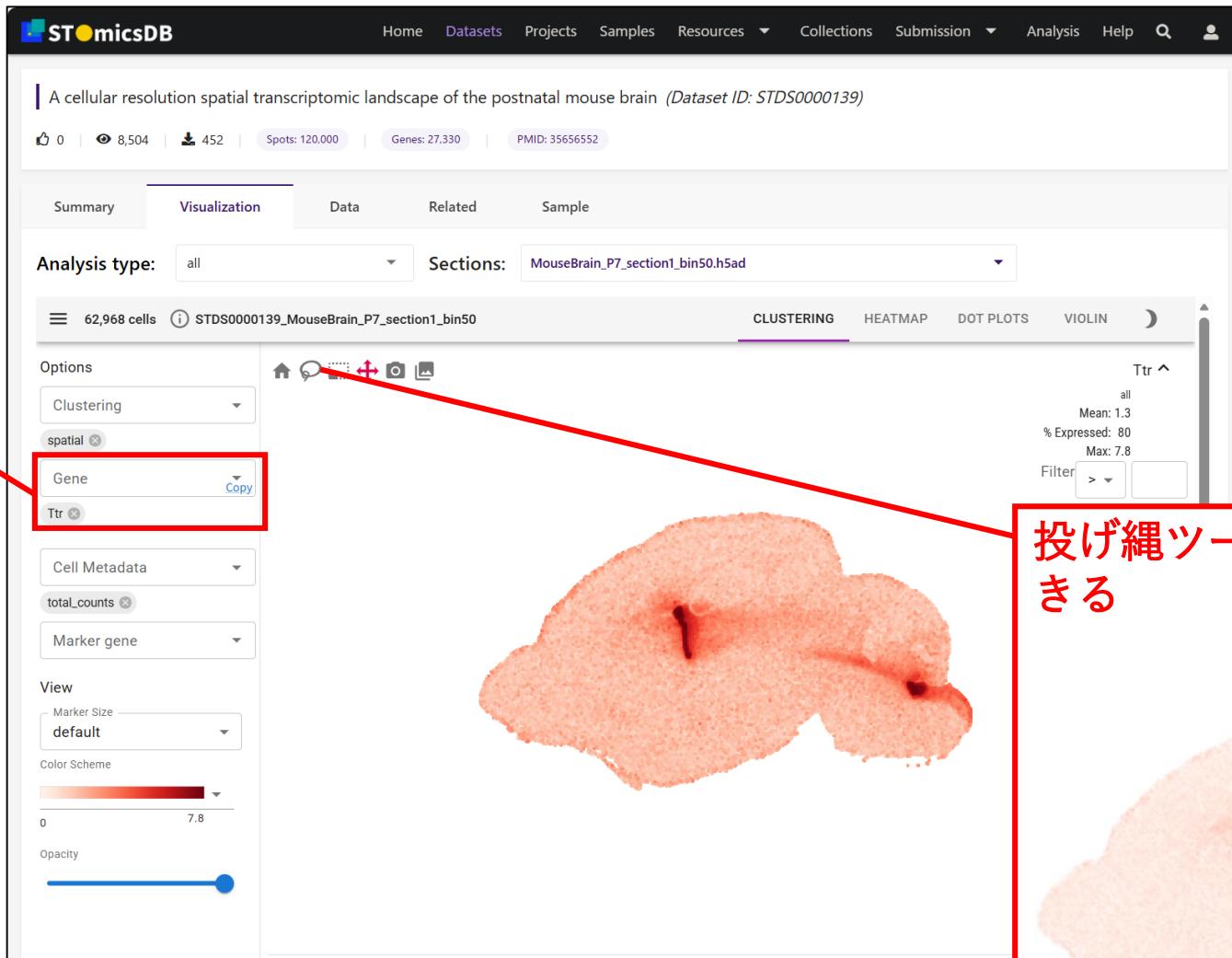
Here:  
細胞種や組織のアノテーション

# STOmicsDB – Visualization (2)

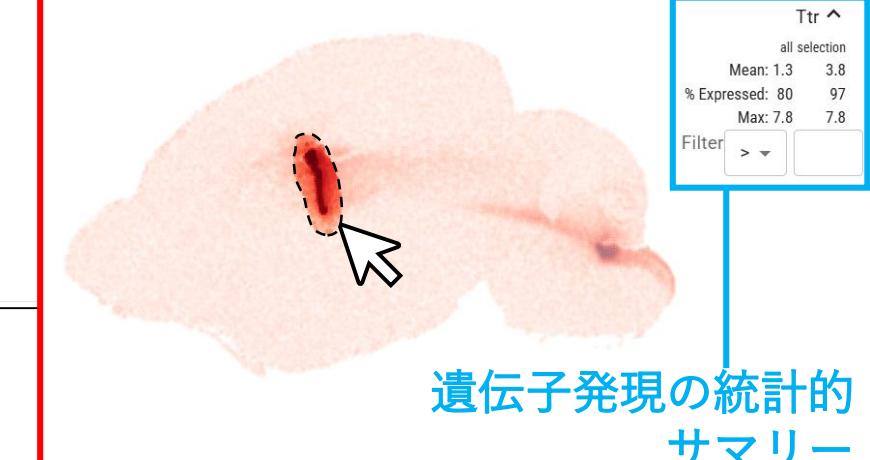


32

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



# STOmicsDB – Data



33

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
MouseBrain_P7_section1_bin50.h5ad	h5ad	processed	P7_section1_Bin50	3.0G	
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.  
 \*processse.h5ad: AnnData format, with analysis results generated by STOmicsDB.

Summary Visualization Data Related Sample

Related type Related ID Related link Related title

CNSA project CNP0002646 <https://db.cngb.org/search/project/CNP0002646/>

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).

h5ad 形式でダウンロード可能

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 (185.6GB)</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 (189.5GB)</a>

# STOmicsDB – Visium example

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

Date range

Species

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

Tissues

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

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 BioVIT Asterand Homo sapiens Tissue Specimens (BioVIT):

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 BioVIT: ASTERAND (Westbury, NY). Raw sequencing data (FASTQ and BAM files) are not included.

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 BioVIT 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 BioVIT 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 BioVIT Asterand Homo sapiens Tissue Specimens (BioVIT):

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

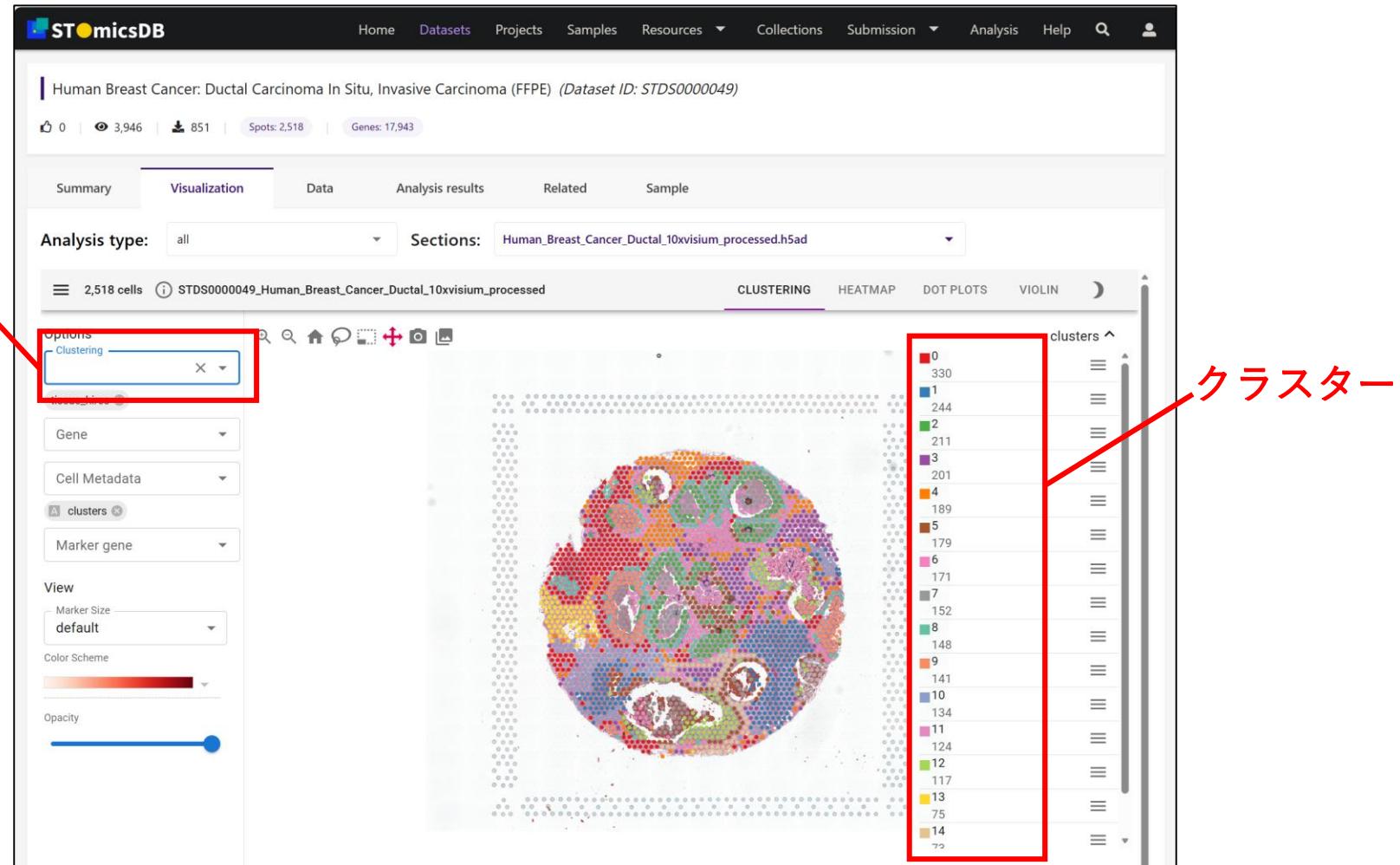
Contributors No results.

Accessions 10x visium data: 10x GENOMICS

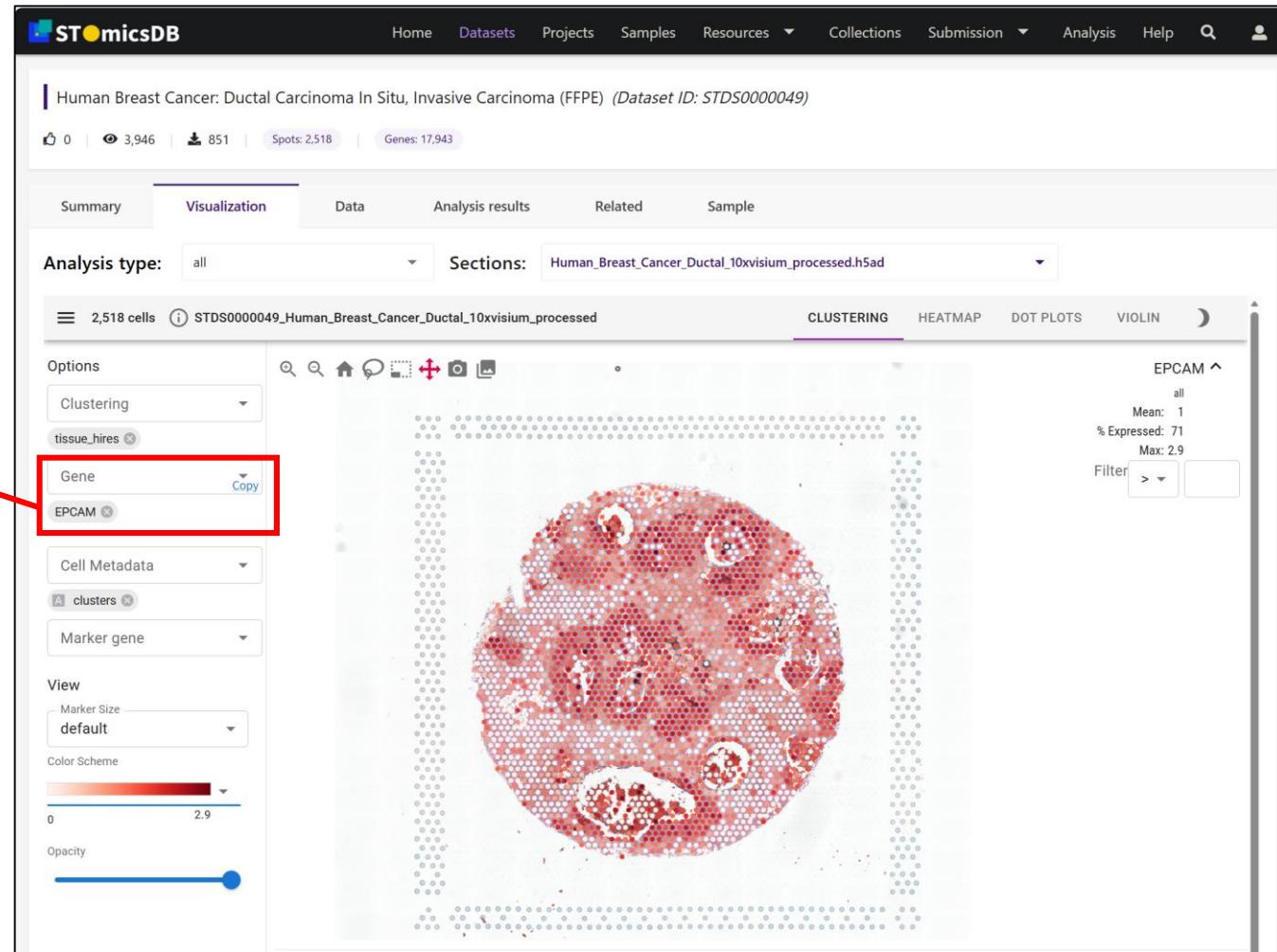
How to cite

- 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. 52,1 (2024): D1053-D1061. doi: 10.1093/nar/gkad933
  - [2] xxxxx. 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)



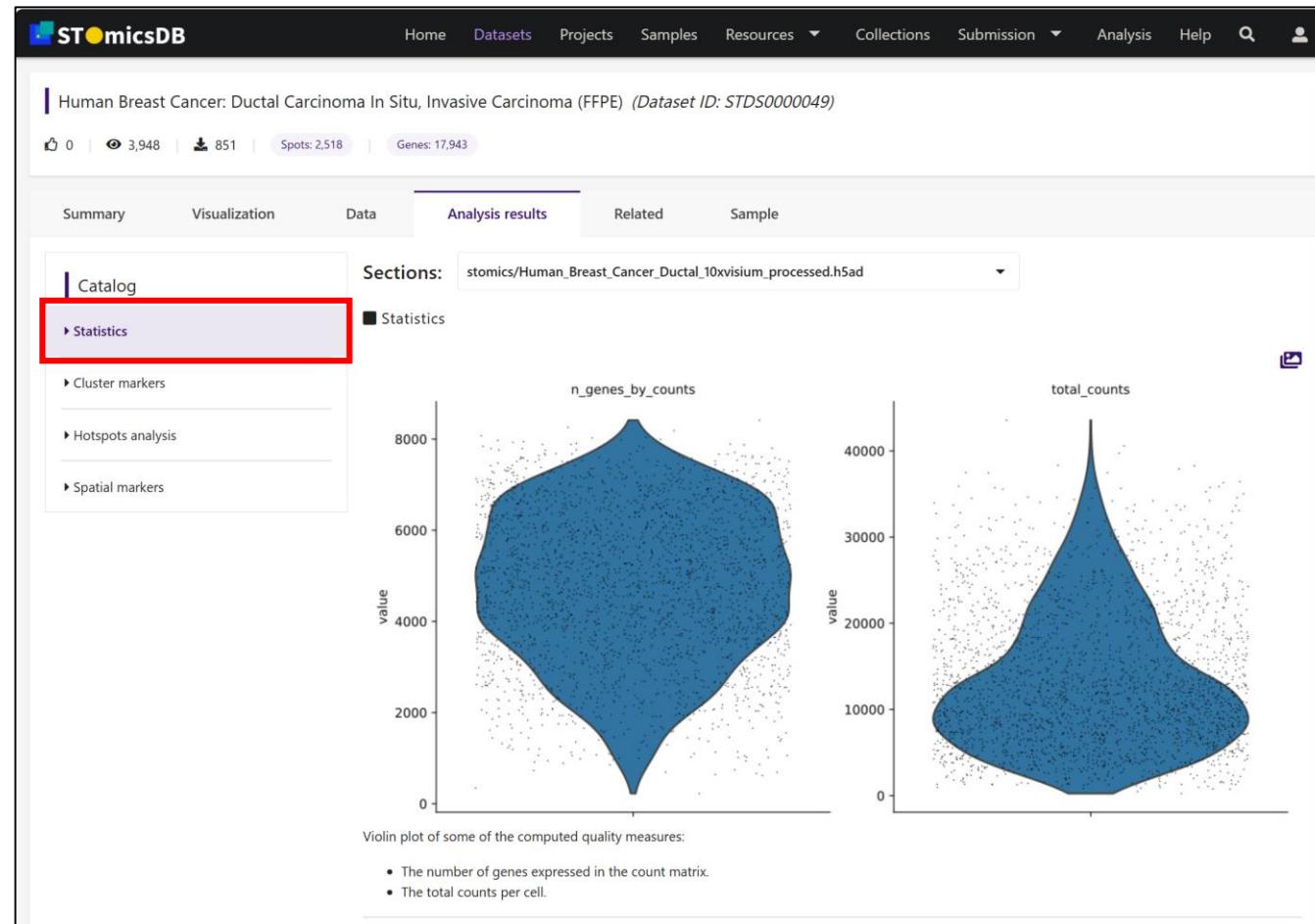
# STOmicsDB – Visualization (Visium) (2)



# STOmicsDB – Analysis results (Visium) (1)



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)



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

The marker genes of each cluster were calculated by `scipy.stats.rank_genes_groups` with the "wilcoxon" method. If the original annotation information of dataset is available, we use the original one, if not, we get the annotation information through `scipy.stats.ttest_leiden`.

Heatmap of the expression of the top 10 marker genes (bottom) for each cluster (right).

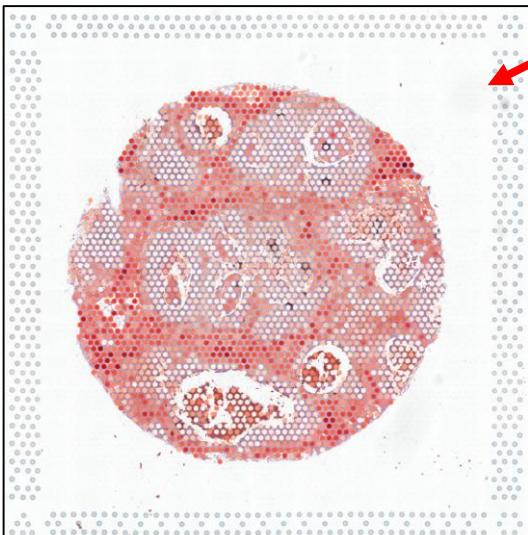
Top 100 gene expression markers for each cluster.

Show 10 results

Gene name	p_val_adj ⓘ	p-value ⓘ	LogFoldChanges ⓘ	Cluster ⓘ
SFRP4	3.7113010735301077e-82	6.659187516235072e-78	2.2289662	0
MMP2	1.6442420183301429e-72	1.4751317267448876e-68	1.7148831	0
CCDC80	4.067168867740835e-70	2.432573699795794e-66	1.8558598	0
DCN	2.022245523762502e-69	9.071287858217643e-66	1.6184675	0
CTSK	9.844439621362846e-68	3.532775602522271e-64	1.5896567	0
C1R	8.361668897965531e-66	2.5005570839365922e-62	1.3780049	0
C3	5.3817431885650745e-65	1.3794945433203305e-61	1.493301	0
COL6A3	6.447541554250786e-65	1.446102976349023e-61	1.5188199	0
SFRP2	8.244238046739091e-65	1.6436262585848837e-61	1.6295322	0
JCHAIN	1.0164968712612627e-61	1.8239003361040836e-58	1.9364282	0

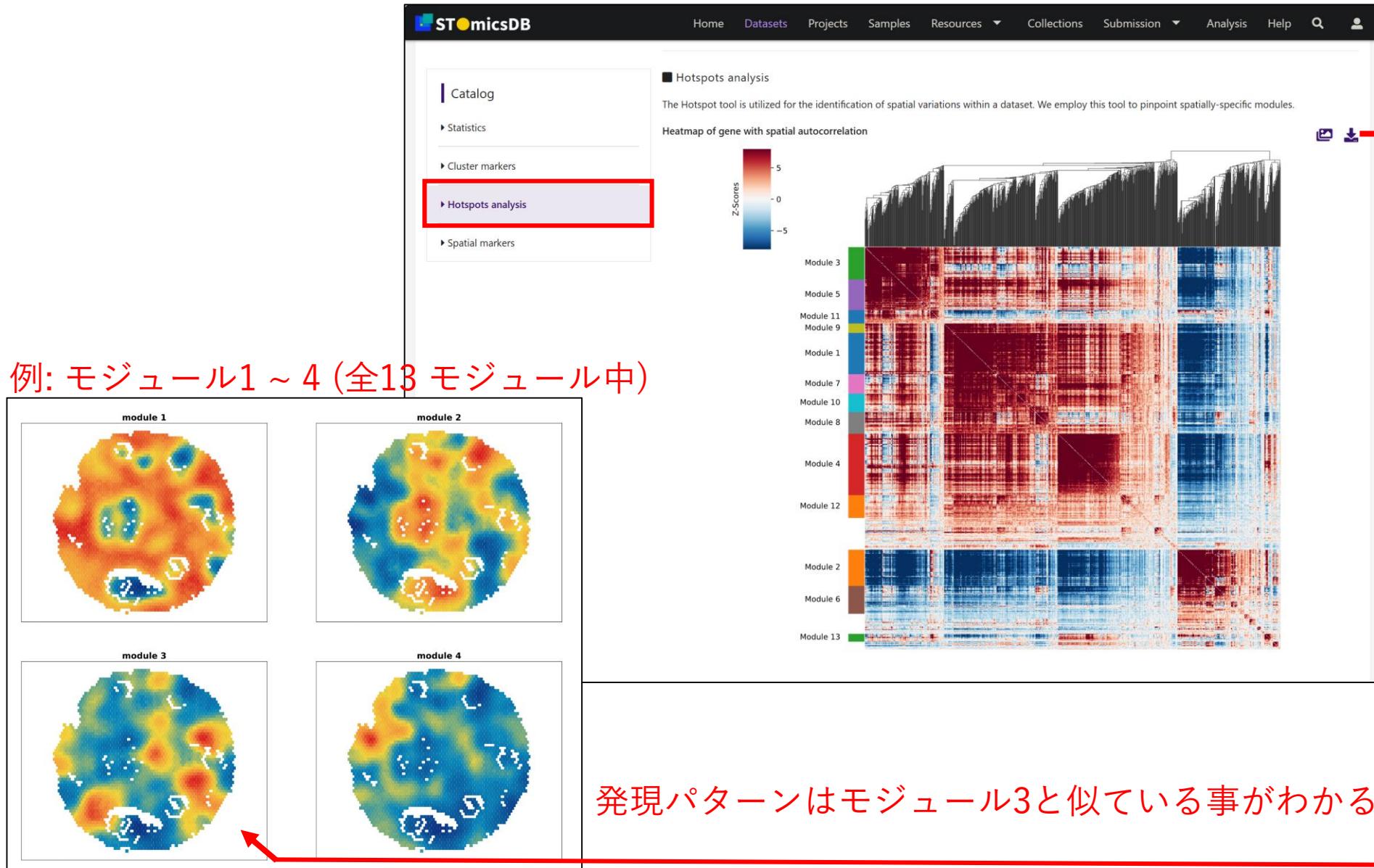
Showing 1 to 10 of 1,600 result(s). < 1 2 3 4 5 6 ... >

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



The figure shows the STOmicsDB interface for Hotspots analysis. On the left, a sidebar lists 'Catalog' options: Statistics, Cluster markers, Hotspots analysis (highlighted with a red box), and Spatial markers. The main area displays a heatmap titled 'Hotspots analysis' with a color scale from -5 (blue) to 5 (red). Below the heatmap, a legend identifies 13 modules: Module 3 (green), Module 5 (purple), Module 11 (yellow), Module 9 (light green), Module 1 (dark blue), Module 7 (pink), Module 10 (cyan), Module 8 (orange), Module 4 (brown), Module 12 (light orange), Module 2 (dark brown), Module 6 (dark green), and Module 13 (dark grey). To the right of the heatmap is a download icon with the text 'ダウンロード (約1000個の遺伝子リスト)'. A red arrow points to this text. Below the heatmap, a note says '例としてmodule3に属するAPOC1を見てみると' (Let's look at APOC1 belonging to module 3). A red arrow points down to a circular heatmap for 'module 3' on the left. Another red arrow points to the text 'APOP1発現パターン' (APOC1 expression pattern) below a circular heatmap on the right. A red arrow also points to the text '発現パターンはモジュール3と似ている事がわかる' (It can be seen that the expression pattern is similar to module 3).

例: モジュール1～4 (全13 モジュール中)

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

APOP1発現パターン

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 – Analysis results (Visium) (4)

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-seq (e.g. Spatial Transcriptomics), or *in situ* gene expression measurements (e.g. SeqFISH or MERFISH).

Show 10 results

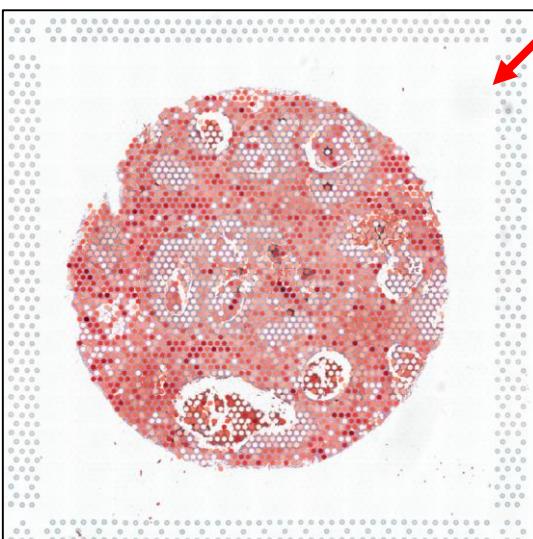
Gene name	p-value	q-value	I	Max_delta	Max_ll	Max_mu_hat	Max_s2_t
A2M	0.0	0.0	482.88131414...	1.9383192508...	-2651.484957...	1.1800456542...	0.2713584
AAMP	0.0	0.0	482.88131414...	4.3509832352...	-2186.378124...	0.7667497270...	0.0938177
AARD	0.0	0.0	881.20428215...	8.0508302370...	-583.0216138...	0.1407644310...	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). ◀ 1 2 3 4 5 6 ... ▶

Download (17651 genes)

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



SOAR Data Browser Gene & Cell Analysis Drug Discovery Download Help ▾

**Spatial transcriptOomics Analysis Resource**

- SOAR is a comprehensive database of 3,461 spatial transcriptomics samples with spatial coordinates from 13 species across 42 tissue types.
- Use SOAR to evaluate the spatial variability of genes in different tissues, assess possible cell-cell interactions, perform drug discovery, and visualize the spatial gene expression of 3,461 samples with spatial coordinates.
- Our fast and easy to use analytic and visualization framework aims to support your research needs!

Type to select a gene

**Data Sources**

- GEO (Gene Expression Omnibus)
- Single Cell PORTAL
- Other public data collections and atlases

**Data Curation**

- 3,461 samples with spatial coordinates
- 13 species, 42 tissue types
- 19 spatial transcriptomics technologies

**Data Processing**

- Quality control
- Normalization and transformation
- Dimensionality reduction
- Cell typing (deconvolution/annotation)

**Data Exploration and Analysis**

- Spatial visualization (CD4 heatmap)
- Spatial variability (Gpx3, Cops5)
- Cell-cell interaction (CCl via CXCL16-CXCR6)
- DGE analysis (Log2FC, -log(p))
- Drug discovery (PPI, Drug perturbation)

**Data Browser**

3,461 samples with coordinates | Different filters available

Technology, Organ, Number of Spots, Disease/Condition

**Gene & Cell Analysis**

Evaluate spatial variability | Assess cell-cell interaction

Species, Tissue Type, Number of Genes, Research Topic

**Drug Discovery**

Assess protein-protein interaction | Evaluate drug perturbation

**Download**

3,461 post-quality-control samples from 42 tissue types

123 Cancer Datasets, 109 Brain Datasets, 21 Embryonic Datasets, And so many more!

- 3,461 サンプル
- 13 種
- 19 テクノロジー

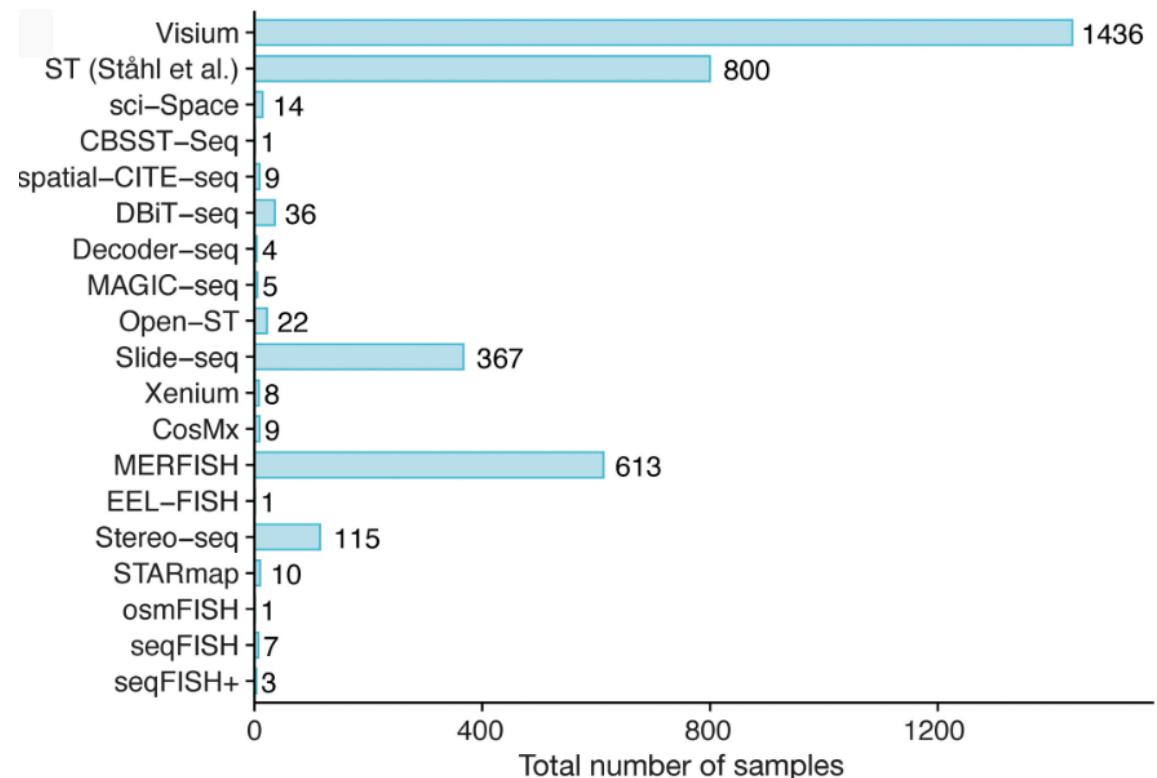


Figure from Li *et al.*, Scientific Advances, 2025

# SOAR – Data Browser (Visium) (1)



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**Data Browser**

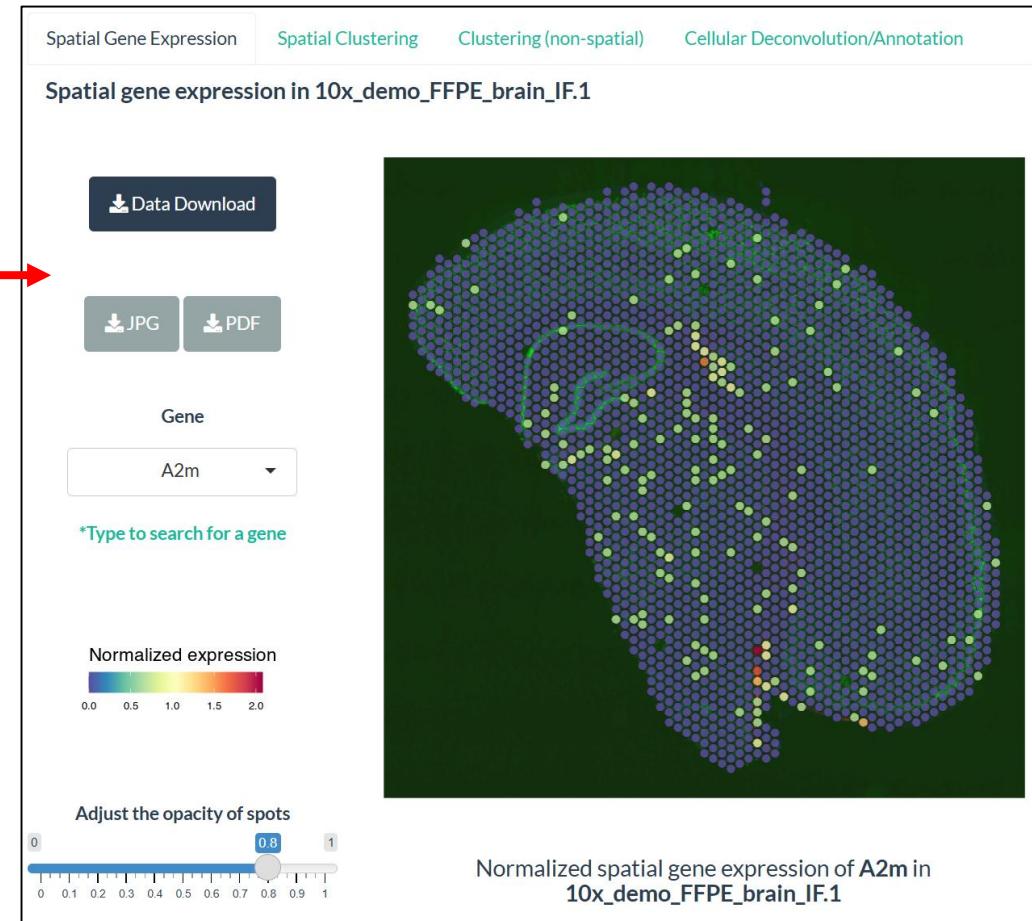
- Click on a **Sample number** to visualize spatial gene expression and view its spatial variability analysis results
- The datasets are categorized into different research topics (the **Topic** column), and sample-wise conditions are recorded in the **Condition** column

Show 100 entries

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

Showing 1 to 10 of 3,461 entries

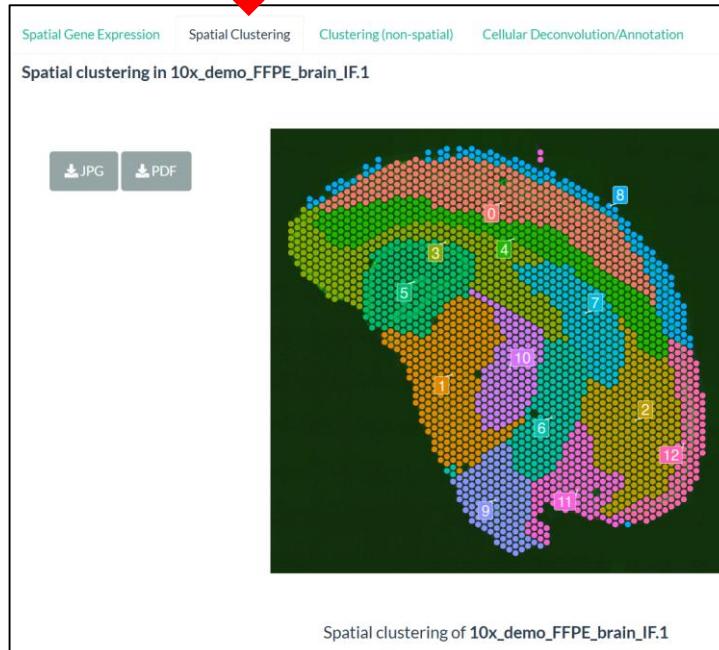
Previous [1](#) [2](#) [3](#) [4](#) [5](#) ... [347](#) Next



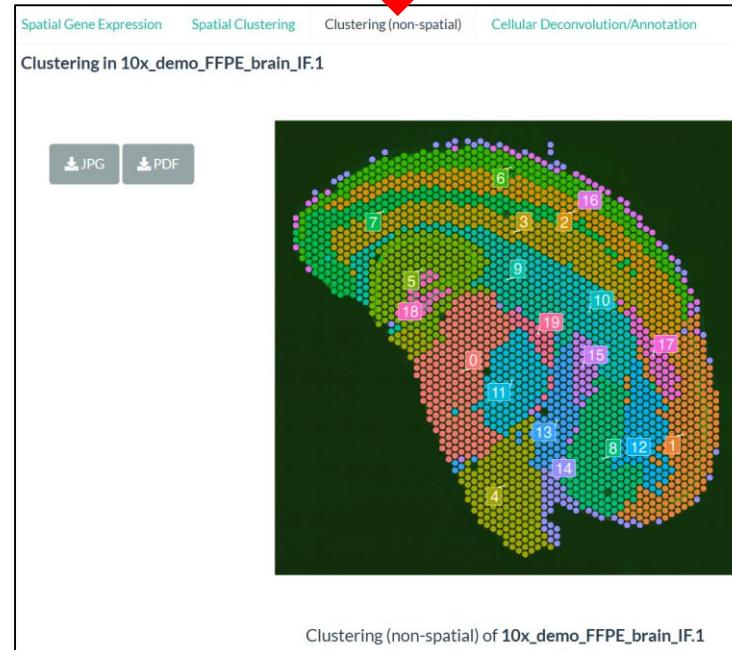
# SOAR – Data Browser (Visium) (2)



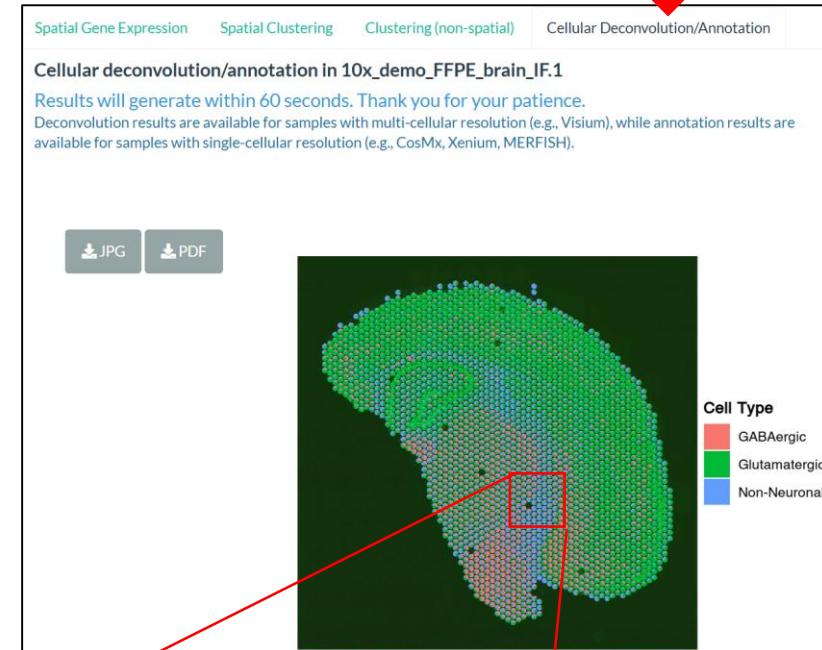
STAGATEを用いた  
spatial domains



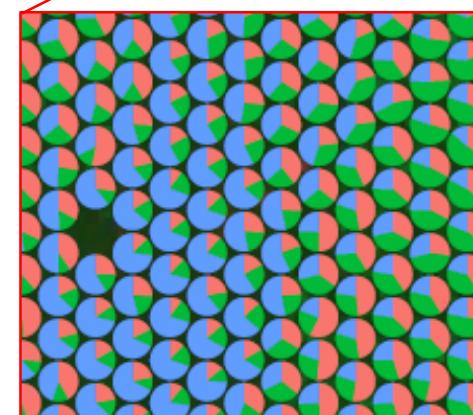
遺伝子発現のみに基づく  
クラスタリング



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)



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

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

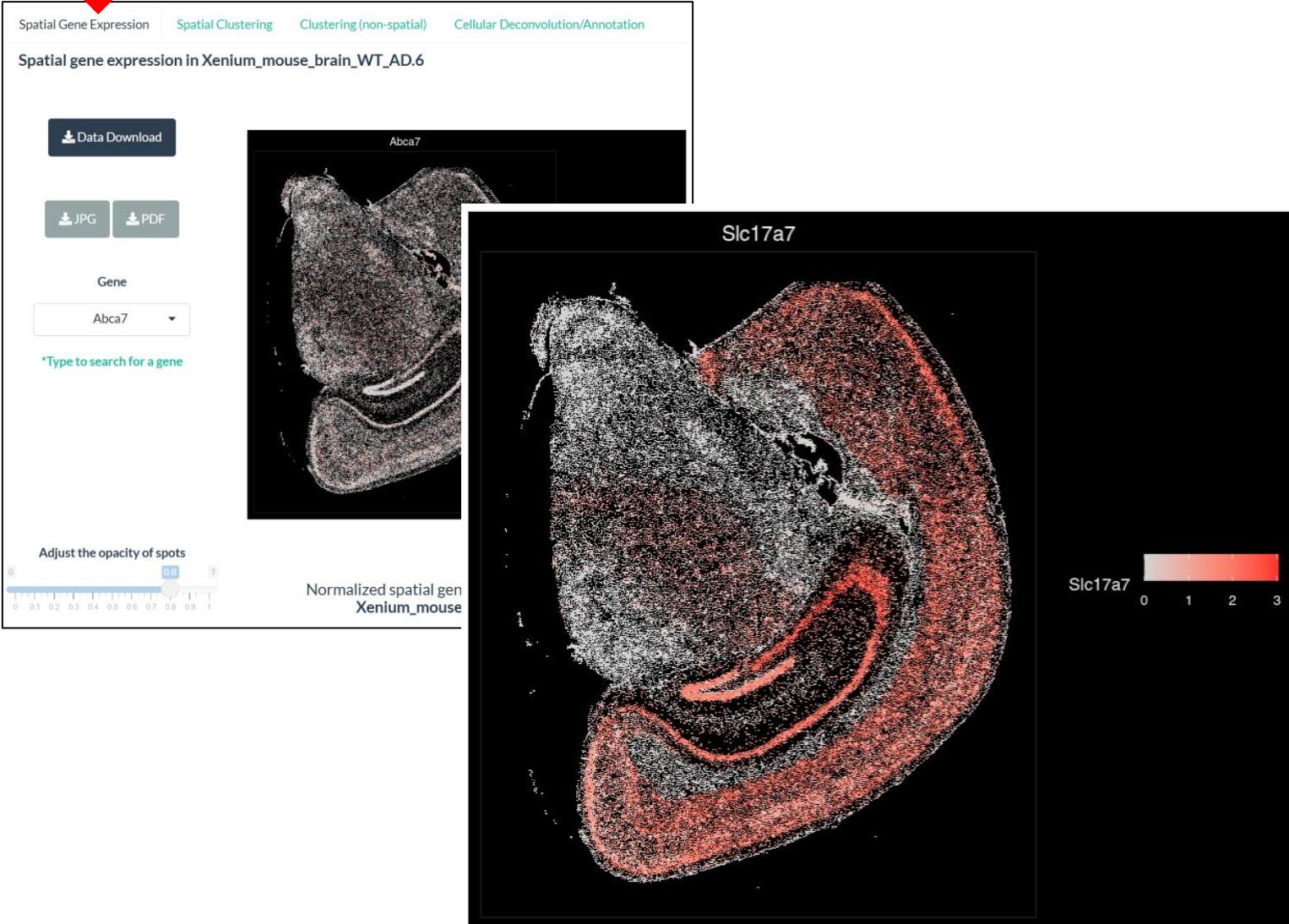
SOAR にはXeniumが  
8サンプルを集められている

このマウスの脳サンプルをクリックすると

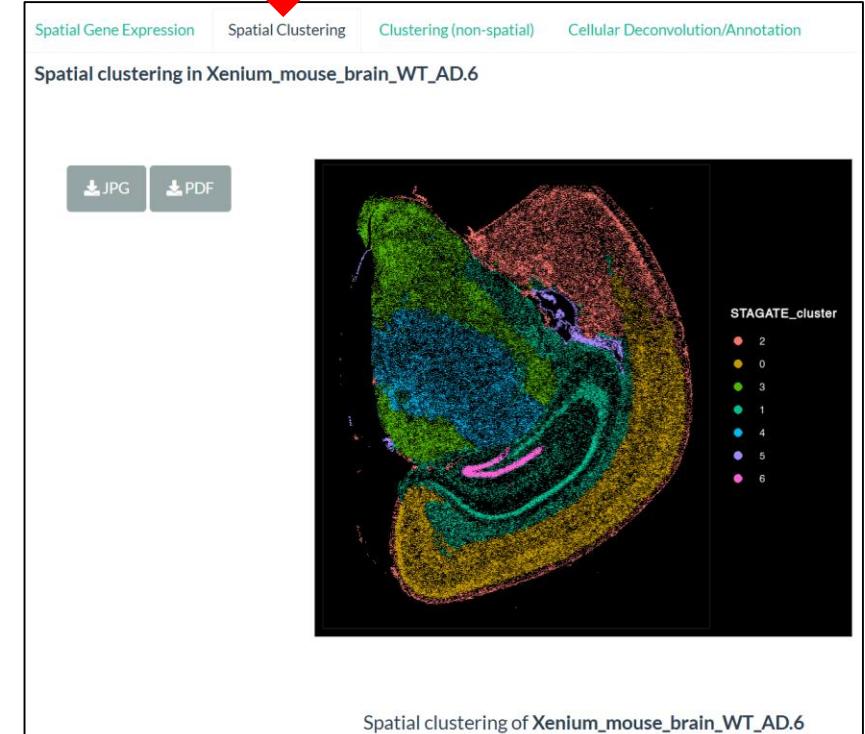
# SOAR – Data Browser (Xenium) (2)



## 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скриプトミクスデータ解析
  - Visium example
  - Xenium example
- 既存の空間トランскри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

# ワークフロー

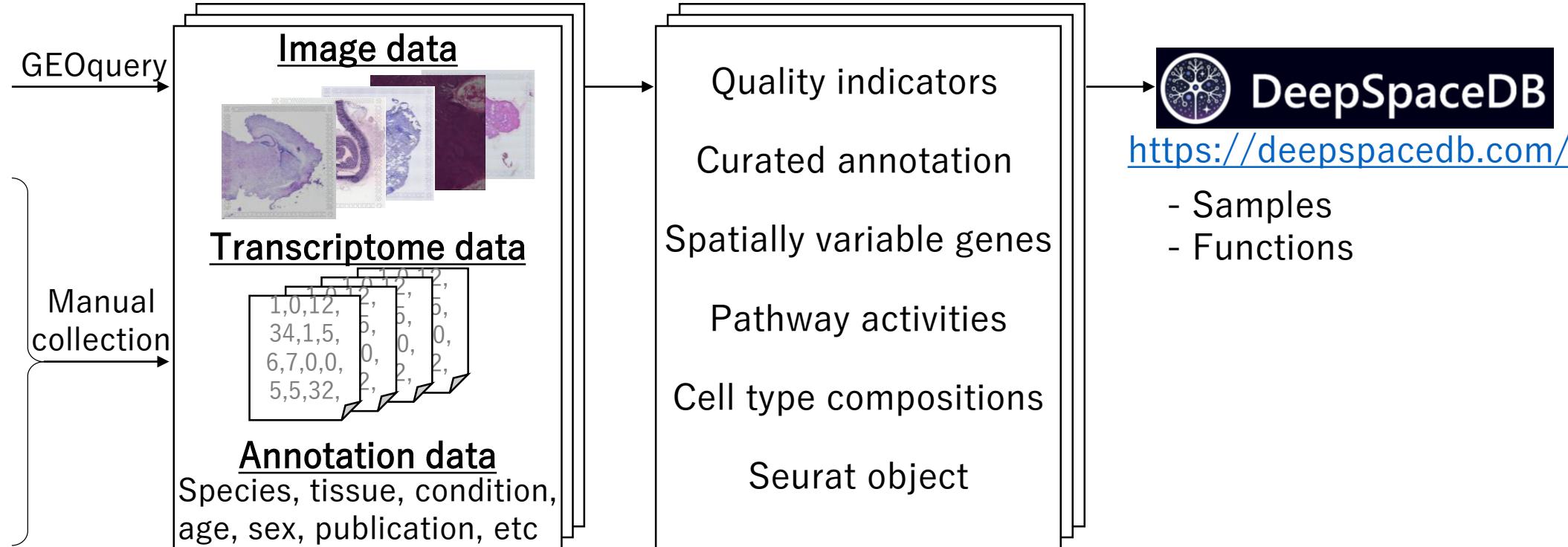


## Data Sources



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

## Raw Data      Processed Data      Database



# アノテーションデータの収集例

 NCBI

 Gene Expression Omnibus

HOME | SEARCH | SITE MAP | GEO Publications | FAQ | MIAME | Email GEO | Not logged in | Login

NCBI > GEO > Accession Display

Scope: Self Format: HTML Amount: Quick GEO accession: GSE225766 Go

**Series GSE225766** Query DataSets for GSE225766

Status	Public on Jun 16, 2023
Title	A cellular and molecular spatial atlas of dystrophic muscle
Organism	<u>Mus musculus</u>
Experiment type	Expression profiling by high throughput sequencing Other
Summary	Asynchronous 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 design	Gene 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. <i>Proc Natl Acad Sci U S A</i> 2023 Jul 18;120(29):e2221249120. PMID: <u>37410813</u>
Submission date	Feb 21, 2023
Last update date	Sep 18, 2023
Contact name	Michael Stec
Organization name	Regeneron Pharmaceuticals
Street address	777 Old Saw Mill River Rd
City	Tarrytown
State/province	NY
ZIP/Postal code	10591
Country	USA
Platforms (1)	GPL19057 Illumina NextSeq 500 (Mus musculus)
Samples (11)	GSM7055901 WT1 GSM7055902 WT2 GSM7055903 MDX1 GSM7055904 MDX2 GSM7055905 WT3 GSM7055906 MDX3 GSM7055907 MDX4

**Sample GSM7055907** Query DataSets for GSM7055907

Status	Public on Jun 16, 2023
Title	MDX4
Sample type	SRA
Source name	Gastrocnemius
Organism	<u>Mus musculus</u>
Characteristics	tissue: <u>Gastrocnemius</u> genotype: <u>MDX</u>
Extracted molecule	polyA RNA
Extraction protocol	10x Genomics Visium Spatial Gene Expression for Fresh Frozen Tissue v1.0
Library strategy	RNA-Seq
Library source	transcriptomic
Library selection	cDNA
Instrument model	Illumina NextSeq 500
Data processing	Spaceranger 1.3.0 Assembly: mm10
Submission date	Feb 21, 2023
Last update date	Sep 18, 2023
Contact name	Michael Stec
Organization name	Regeneron Pharmaceuticals
Street address	777 Old Saw Mill River Rd
City	Tarrytown
State/province	NY
ZIP/Postal code	10591
Country	USA
Platform ID	GPL19057
Series (1)	GSE225766 A cellular and molecular spatial atlas of dystrophic muscle
Relations	RinSample SAMNRR407466

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

# アノテーション及びオントロジー



# UBERON anatomy ontology

# Human disease ontology

**muscular dystrophy**

[http://purl.obolibrary.org/obo/DOID\\_9884](http://purl.obolibrary.org/obo/DOID_9884)  Copy

A myopathy is characterized by progressive skeletal muscle weakness degeneration. ⓘ

Also appears in [BAO](#)

Search DOID...

Exact match  Include obsolete terms  Include imported terms

-  Tree
-  Graph

- └ disease (11,597)
  - └ disease of anatomical entity (8,755)
    - └ musculoskeletal system disease (1,266)
      - └ muscular disease (330)
        - └ muscle tissue disease (260)
          - └ myopathy (232)
            - └ muscular dystrophy (106)

## データビューの一例 (sample DSID000466)

DeepSpace ID	DSID000466
Sample ID	GSM7055907
Series ID	GSE225766
Platform	Visium V1
Organism	mouse
Organ	<a href="#">skeletal musculature</a>
Organ Detailed	<a href="#">gastrocnemius</a>
Condition	<a href="#">muscle tissue disease</a>
Condition Detailed	<a href="#">muscular dystrophy</a>
Sex	male

- 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

# 総サンプル数 ヒト及びマウス

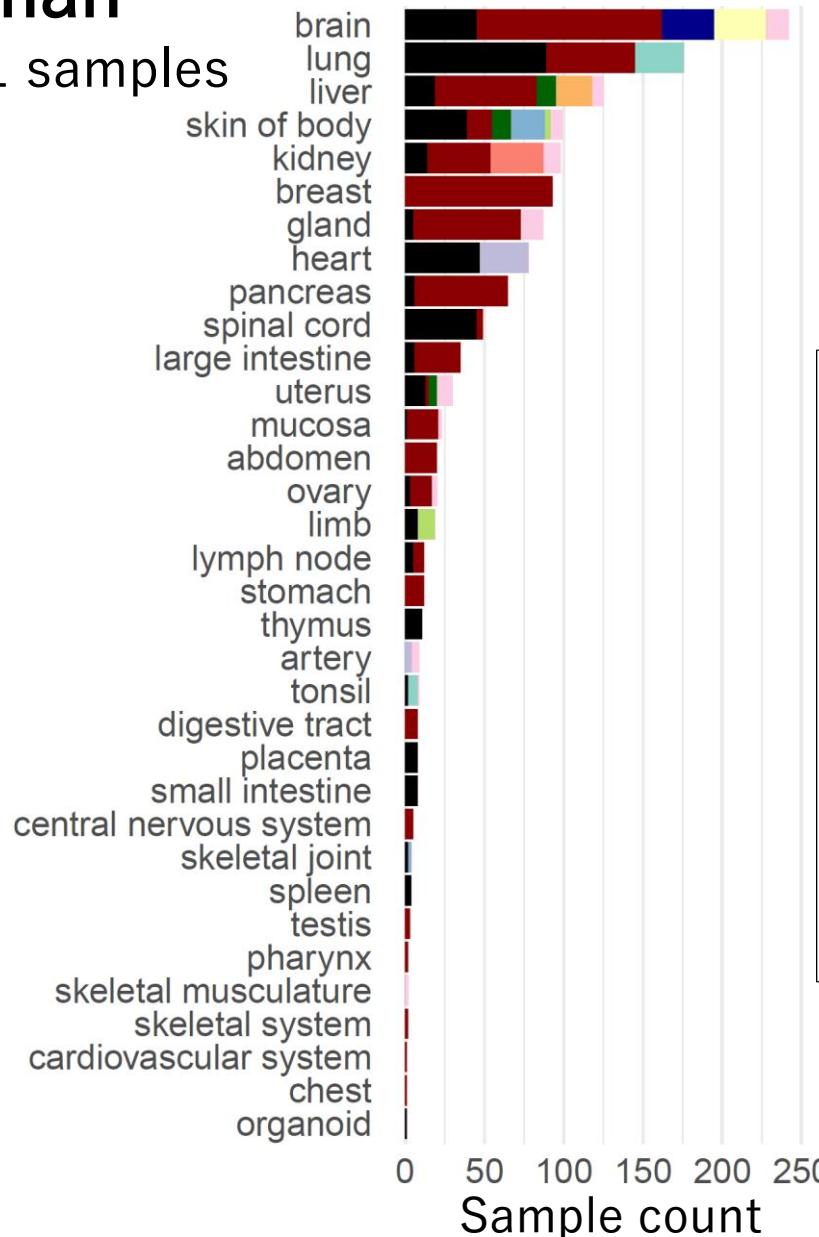
(version 1.1)



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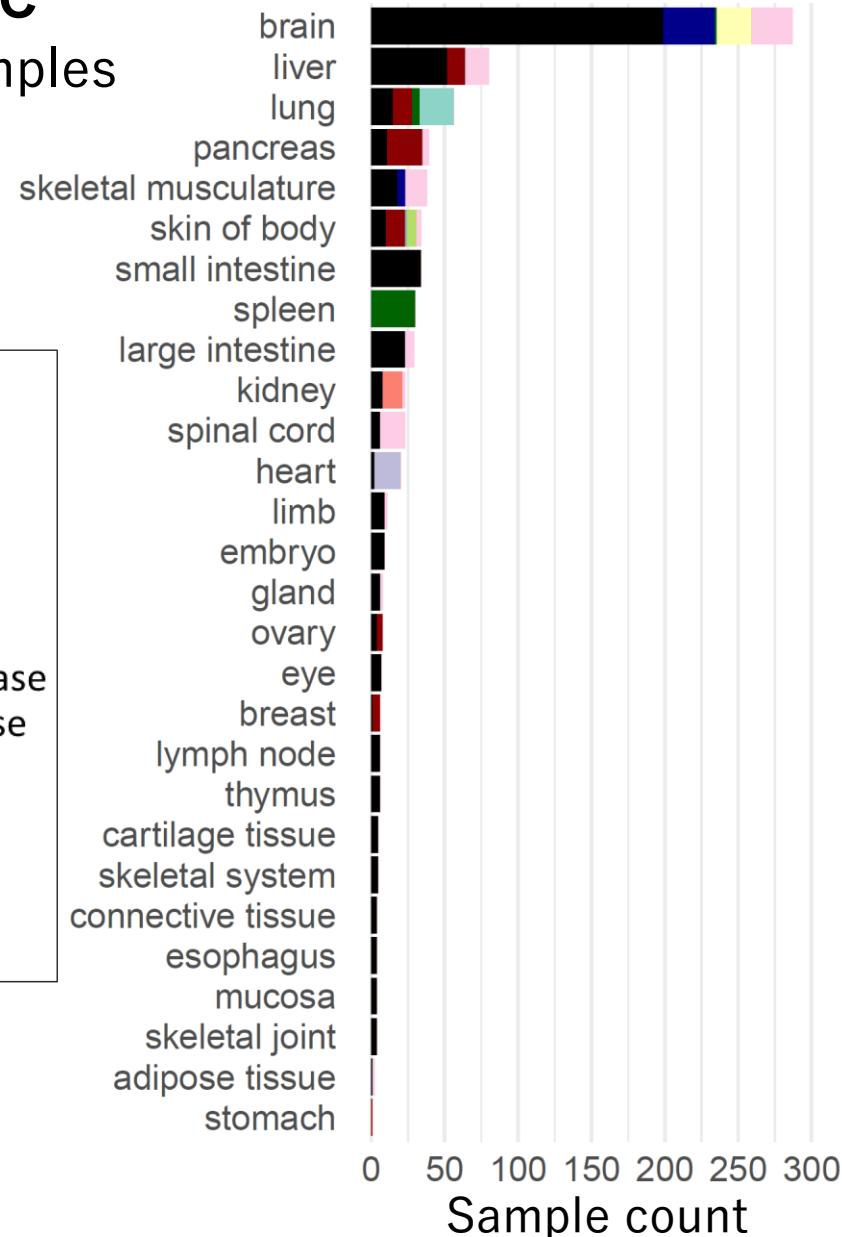
## Human

1,361 samples



## Mouse

783 samples



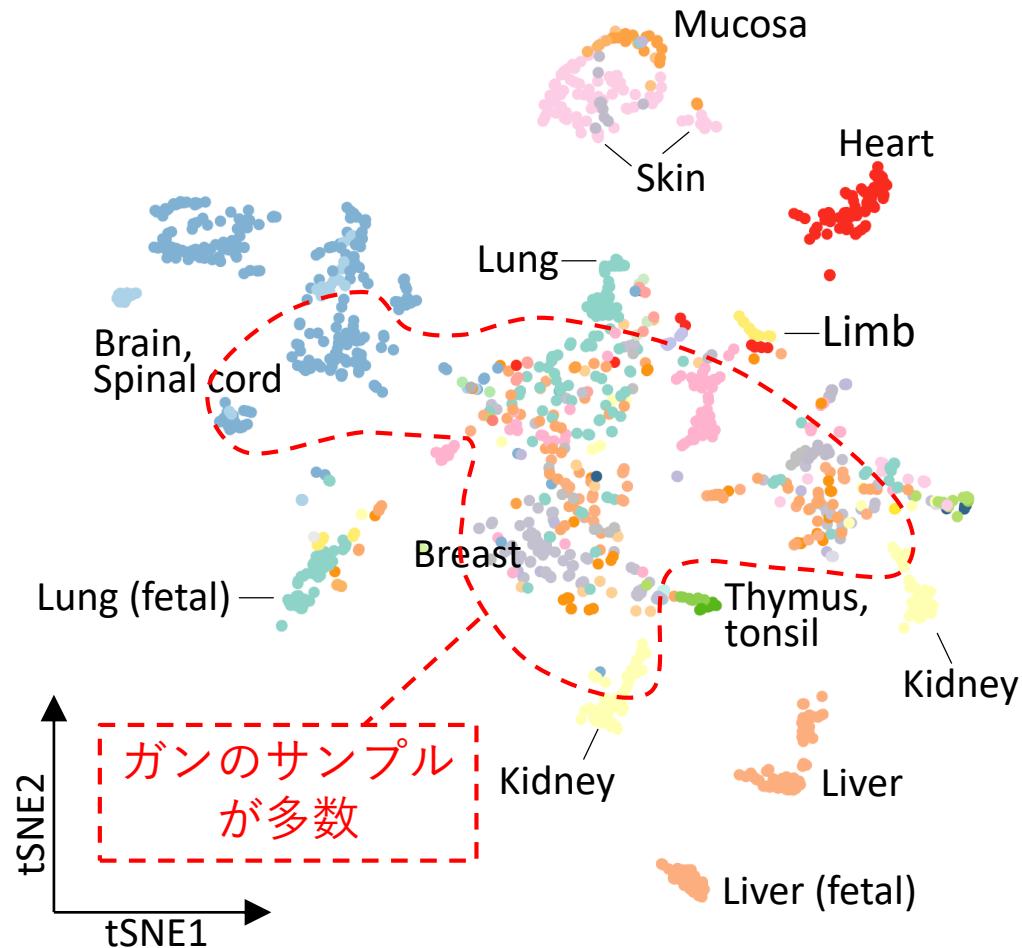
Sample count

Sample count

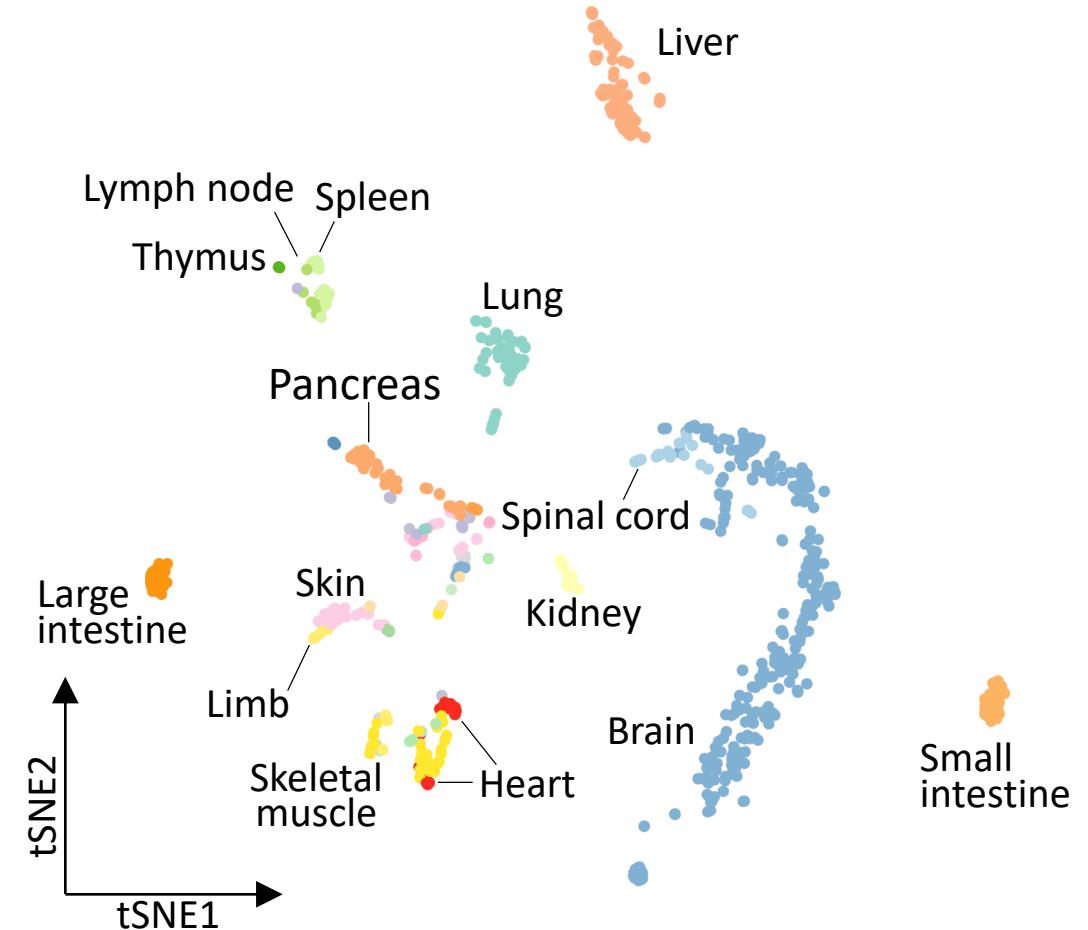
# データの生物学的一貫性

- 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

1 2 3 4 5 6

## 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:

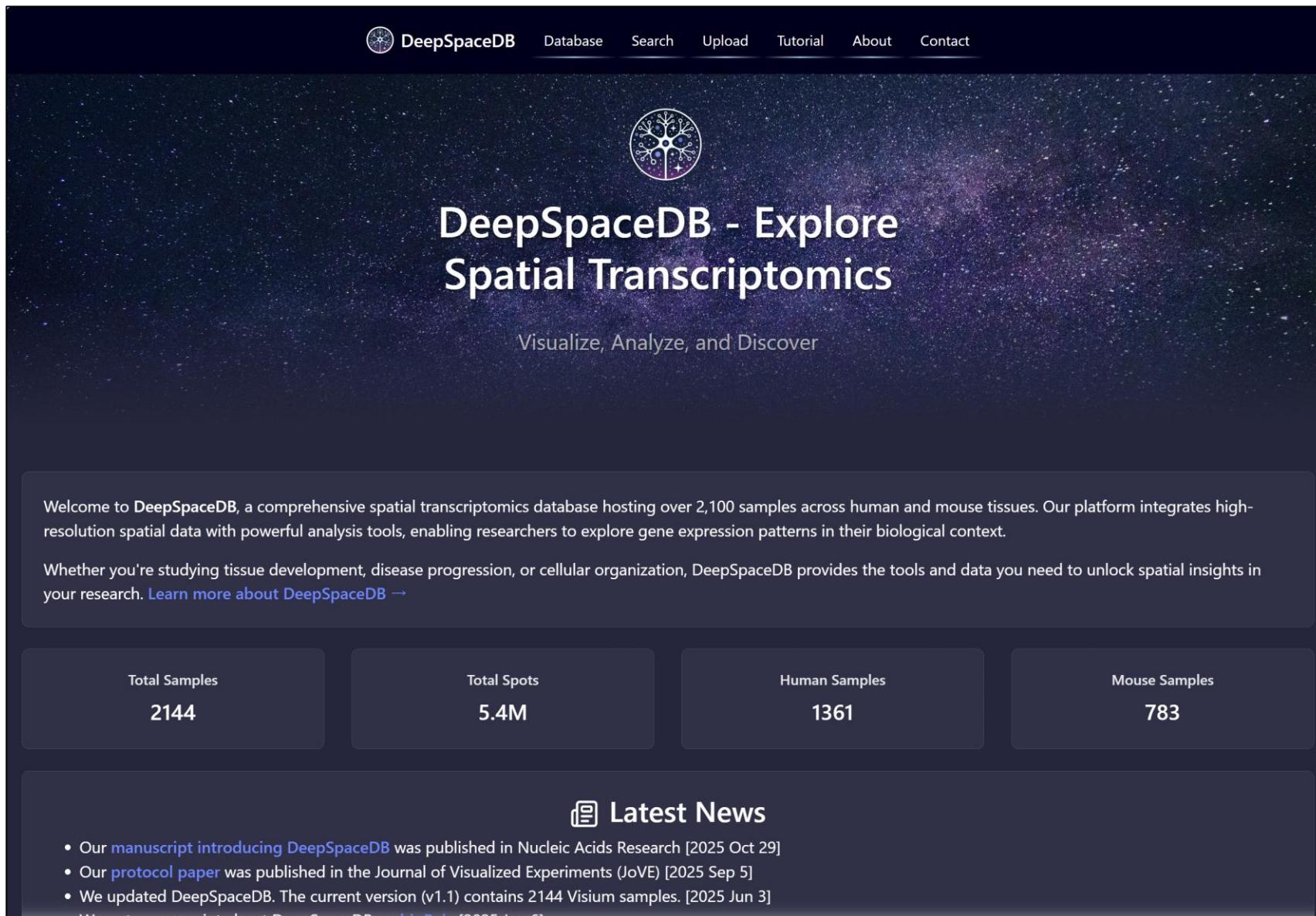
ビデオとFAQs

## 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



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

- 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.

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- A short article about DeepSpaceDB was published in [客觀日本 \(Simplified Chinese and Traditional Chinese\)](#) [2024 Dec 13]
- A short article about DeepSpaceDB was published in [JST News \(Japanese\)](#) [2024 Dec 2]

# DeepSpaceDB – Database tab (1)

各種フィルター

キーワード検索 (and)

サンプルテーブル

現在選んでいる  
サンプルのサマリー

The screenshot shows the DeepSpaceDB interface. On the left, a sidebar titled 'Filters' contains dropdown menus for Organism, Organ, Detailed Organ, Condition, Detailed Condition, Sex, Source, and Platform. A red box highlights this sidebar with the label '各種フィルター'. In the center, a search bar with placeholder text 'Search terms...' has a red box around it with the label 'キーワード検索 (and)'. Below the search bar is a table titled 'Sample Table' with columns: DS ID, Organism, Condition, Organ, Source, PMID, Date Published, and two download icons. The table lists 10 entries from DSID000001 to DSID000010. A red box highlights this table with the label 'サンプルテーブル'. On the right, a 'Preview' section shows a thumbnail image of a histology slide and a detailed table for the selected sample (DSID000001). The preview table includes columns: DeepSpace ID, Organism, Processed Organ, Condition, Condition Detailed, and Details. A red box highlights this preview area with the label '現在選んでいるサンプルのサマリー'.

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

# DeepSpaceDB – Database tab (2)

フィルターにてヒト乳がんを選択した例

The screenshot shows the DeepSpaceDB interface with the following components:

- Filters Panel:** On the left, it lists various filters under categories like Organism, Organ, Condition, Sex, Source, and Platform. The "Organism" section has "human (1361)" checked. The "Condition" section has "breast (99)" checked. The "Source" section has "GEO" selected.
- Search Results Table:** The main area displays a table of 93 results from 2,144 total entries. The columns include DS ID, Organism, Condition, Organ, Source, PMID, Date Published, and two download icons. A red box highlights the star icon in the first row's DS ID column, indicating a pathology expert annotation. The table footer shows pagination and entry selection controls.
- Preview Panel:** On the right, it shows a histological image of a breast tissue sample and a detailed preview table for the selected sample (DSID000600). The preview table includes fields for DeepSpace ID, Organism, Processed Organ, Condition, Condition Detailed, and Details. A red box highlights the "Sample Page" button.

Annotations in Japanese:

- Red boxes highlight the "human (1361)" checkbox in the Organism filter, the "breast (99)" checkbox in the Condition filter, the "GEO" source in the Source filter, the star icon in the DS ID column of the first result, and the "Sample Page" button in the Preview panel.
- A yellow star icon with the text "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" (A star indicates an annotation by a pathology specialist) is located at the bottom left.
- A red arrow points from the "Sample Page" button to the text "選んだサンプルへのリンク" (Link to the selected sample).
- A red arrow points from the bottom center to the text "ページスクロール" (Page scroll).

# DeepSpaceDB – Sample page (1)



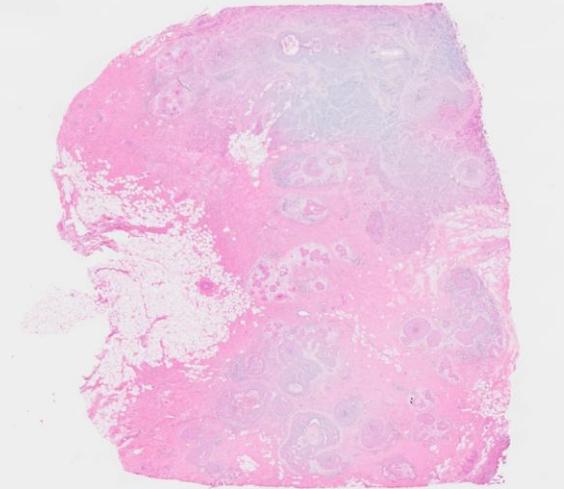
様々な情報を見  
ることが出来る

DeepSpaceDB Database Search Upload Tutorial About Contact

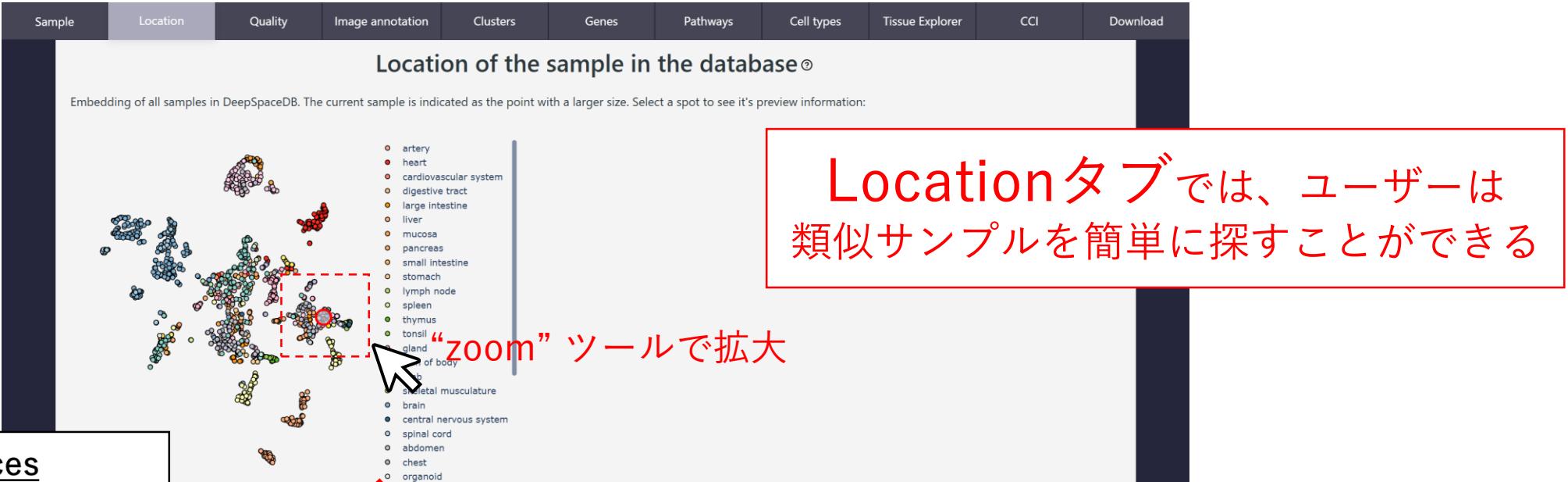
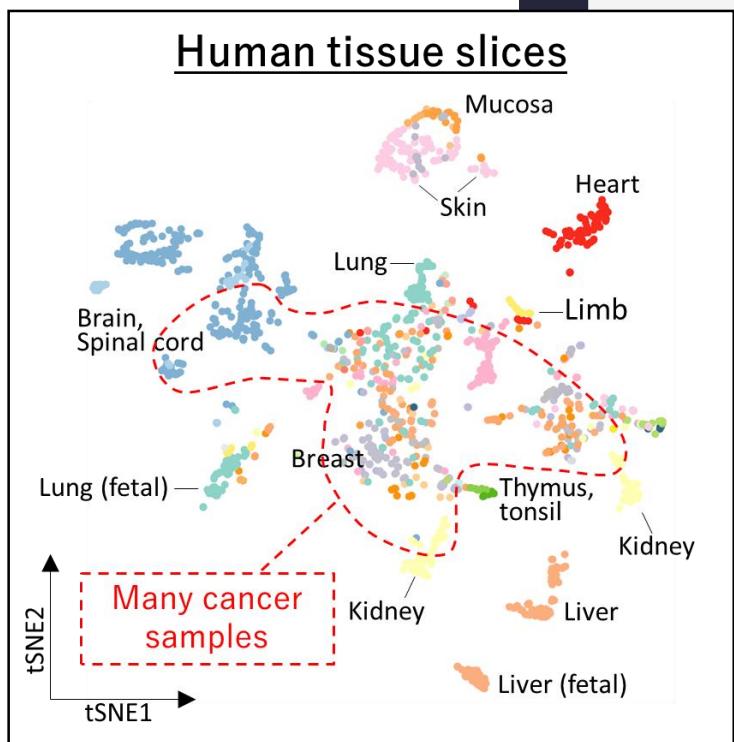
Sample Location Quality Image annotation Clusters Genes Pathways Cell types Tissue Explorer CCI Download

Metadata of DSID000600

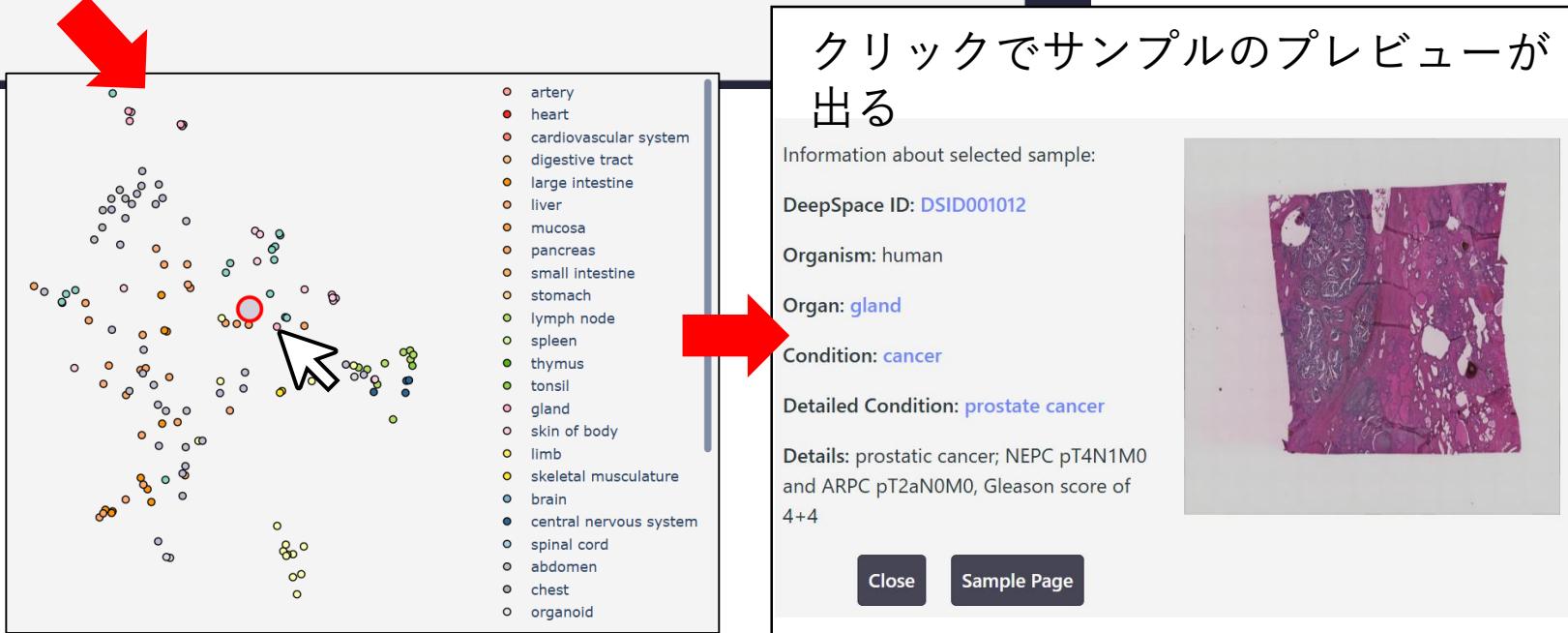
DeepSpace ID	DSID000600
Sample ID	GSM7782699
Series ID	GSE243275
Platform	Visium V2
Organism	human
Organ	breast
Organ Detailed	--
Condition	cancer
Condition Detailed	breast cancer
Sex	--
Age or Stage	--
Post Mortem	--
Ethnicity or Strain	--
Description	--
Source	GEO
Source URL	<a href="#">GSE243275</a>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



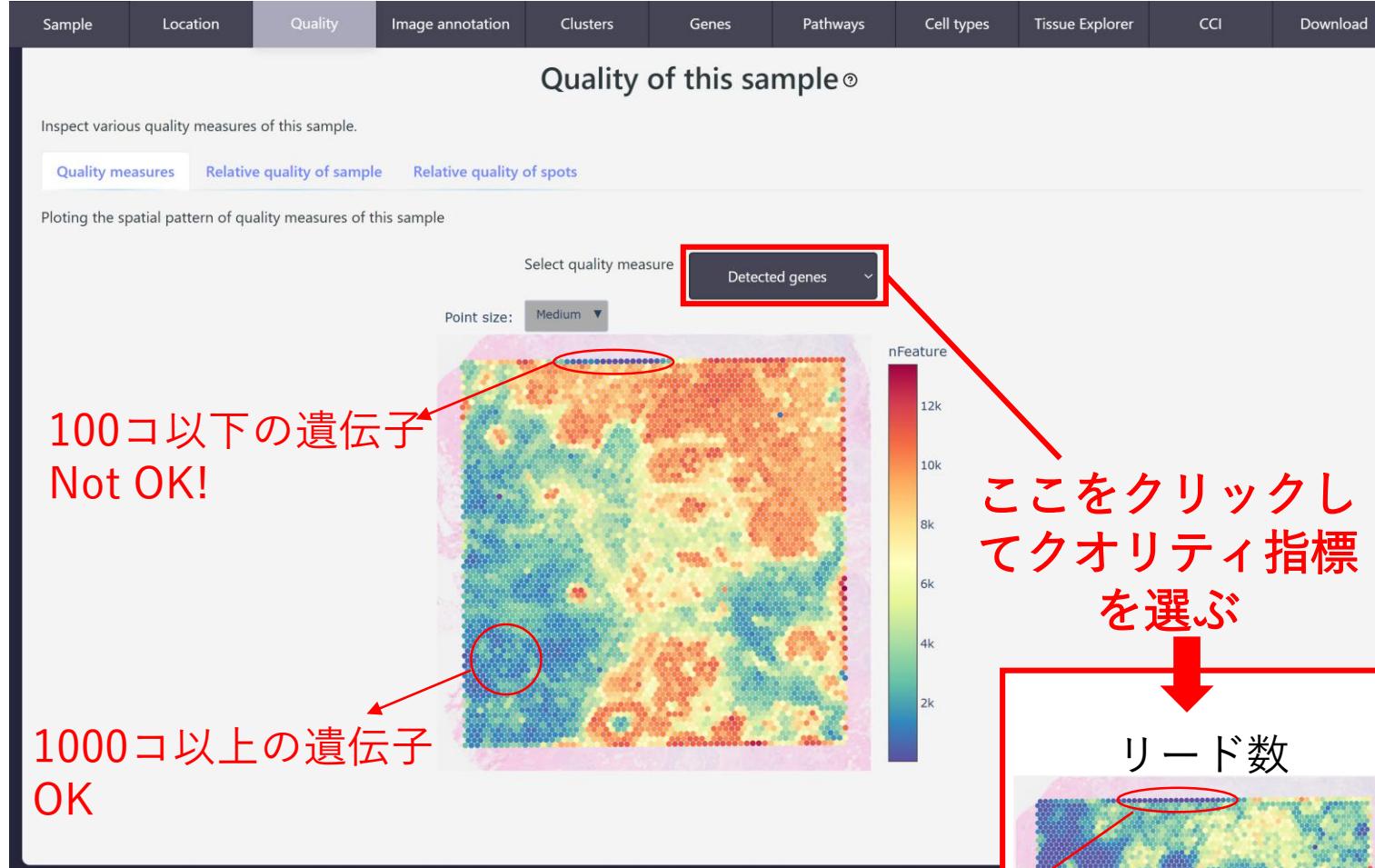
# DeepSpaceDB – Sample page (2)



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



# DeepSpaceDB – Sample page (3)



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。

# DeepSpaceDB – Sample page (4)



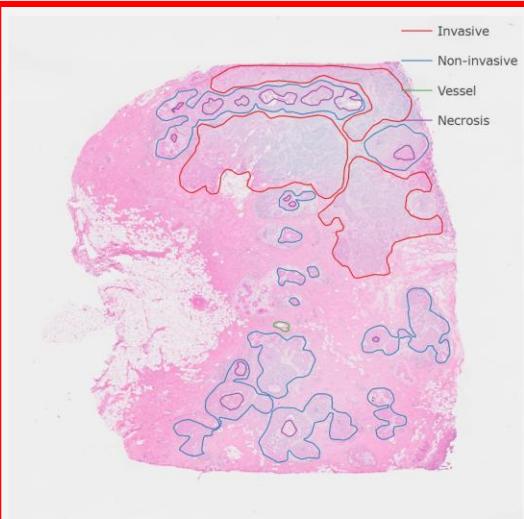
60

Sample Location Quality Clusters Genes Pathways Cell types Tissue Explorer CCI Download

Image annotation®

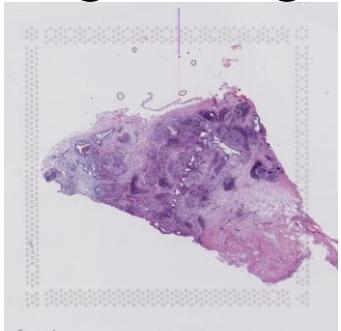
Show LLM annotation

Annotation by a human expert is on the right:

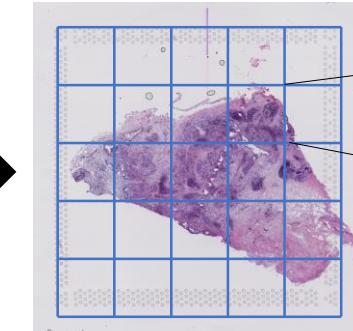


LLM（大規模言語モデル）ベースのアノテーション

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'.*

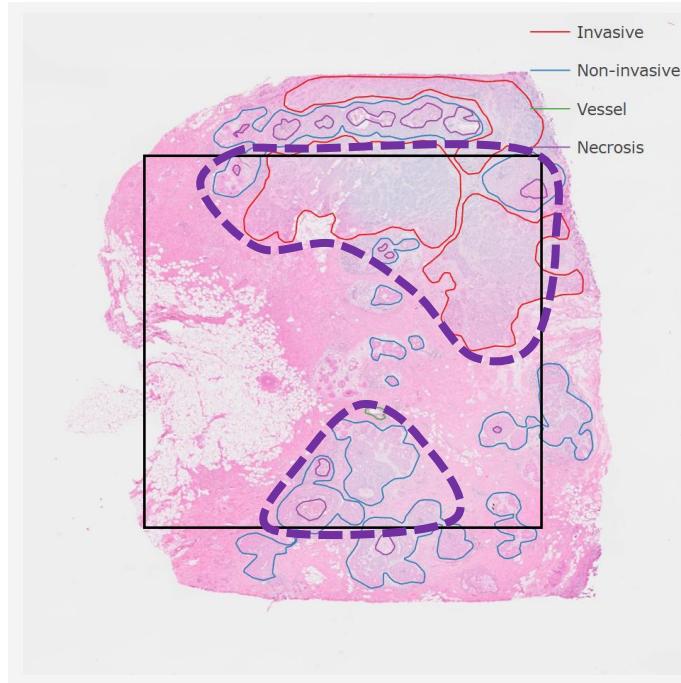


LLMベースのアノテーションは  
注意が必要

返答を収集

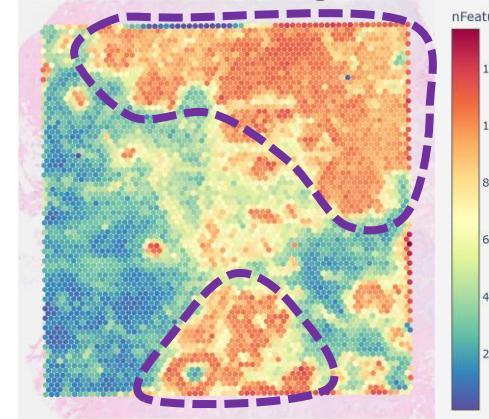
# DeepSpaceDB – Sample page (5)

Image annotation

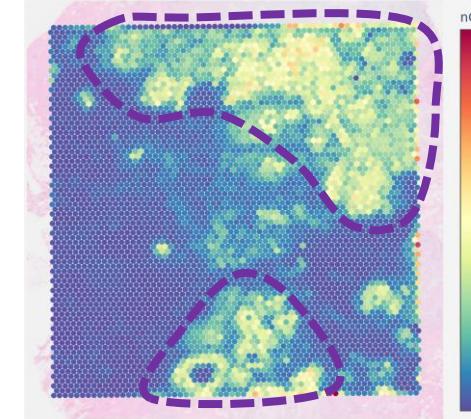


クオリティ指標

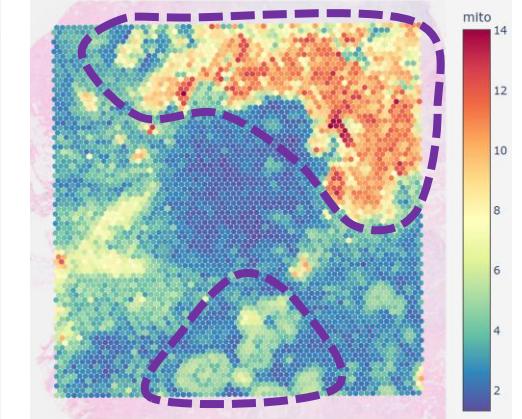
Detected genes



Read count



% mitochondrial reads

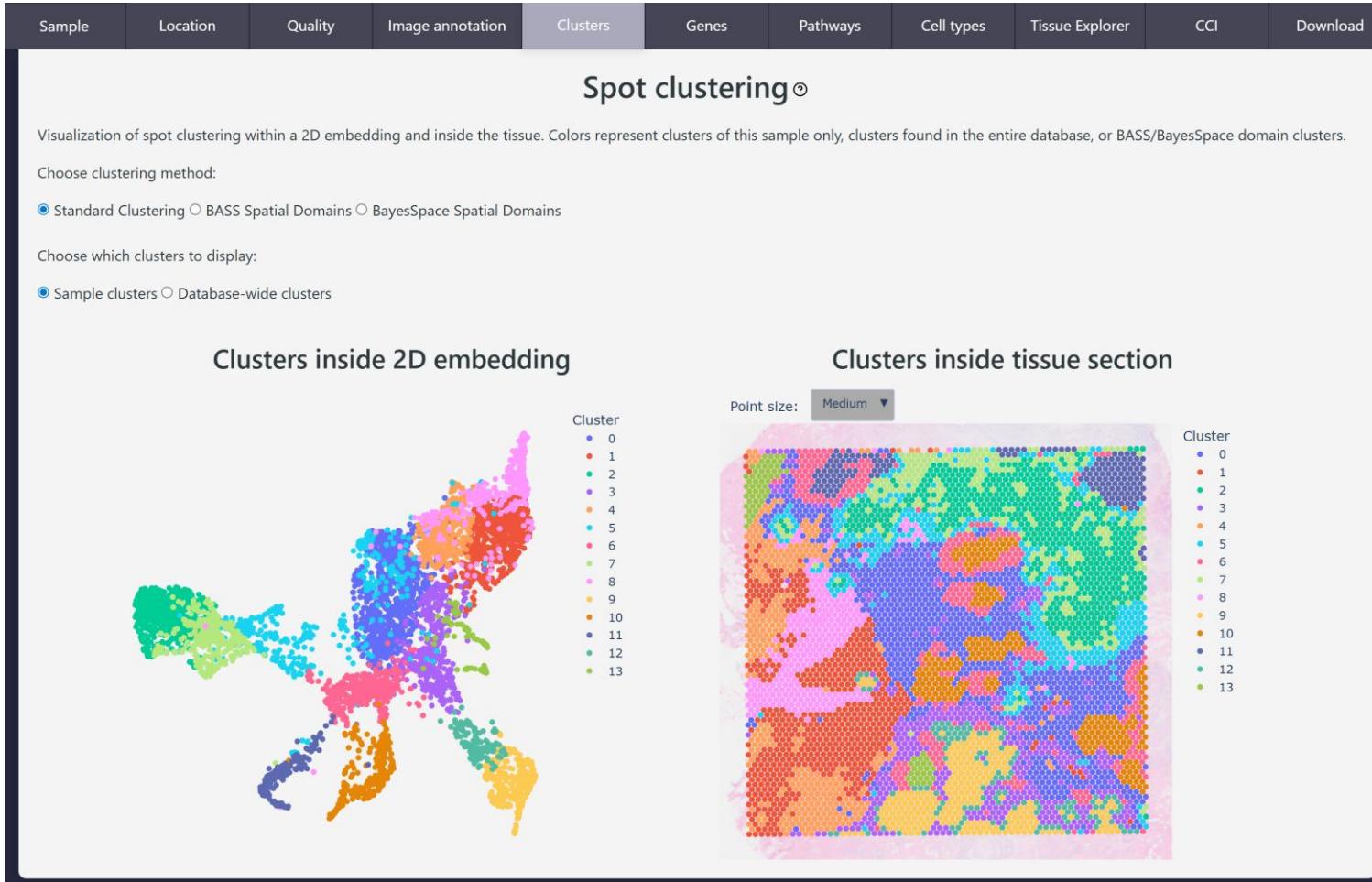


浸潤性、非浸潤性に関わらずガン組織は発現遺伝子数やリード数が多く、ミトコンドリア由来リード数も多いことが分かる。

# DeepSpaceDB – Sample page (6)

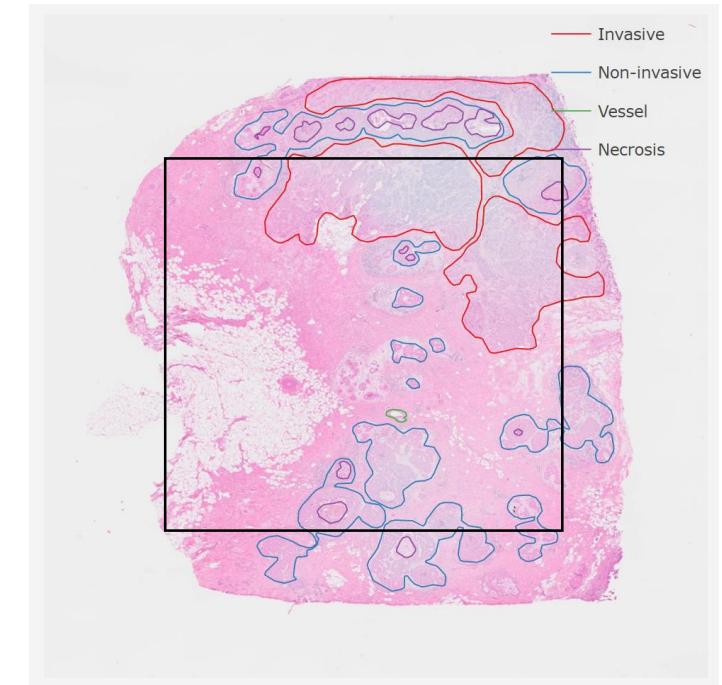


62



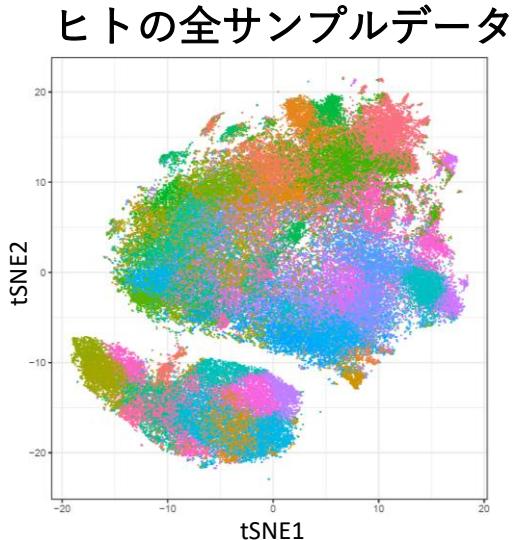
## Clustersタブ

### Image annotation

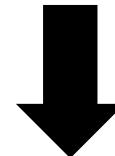


- サンプルのスポットは遺伝子発現パターンの類似性によりクラスタリングされる
- クラスターは生物学的特性をしばしば反映している（細胞種やガン組織など）

# データベースワイドのクラスターアノテーション



これらのクラスターは  
何を意味しているのか?

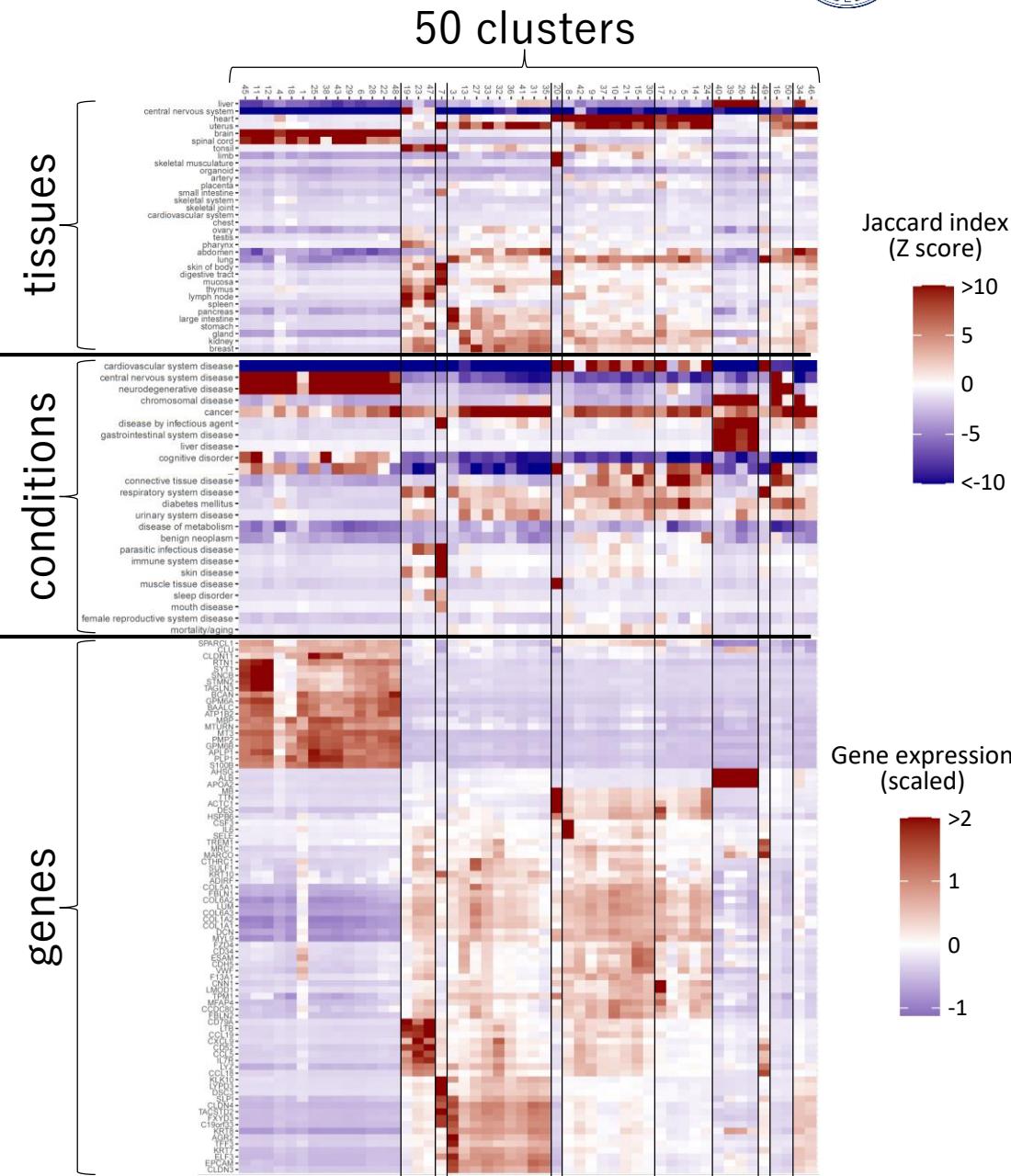


スポットクラスターの  
アノテーション  
(神経、ガン、上皮細胞など)

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?

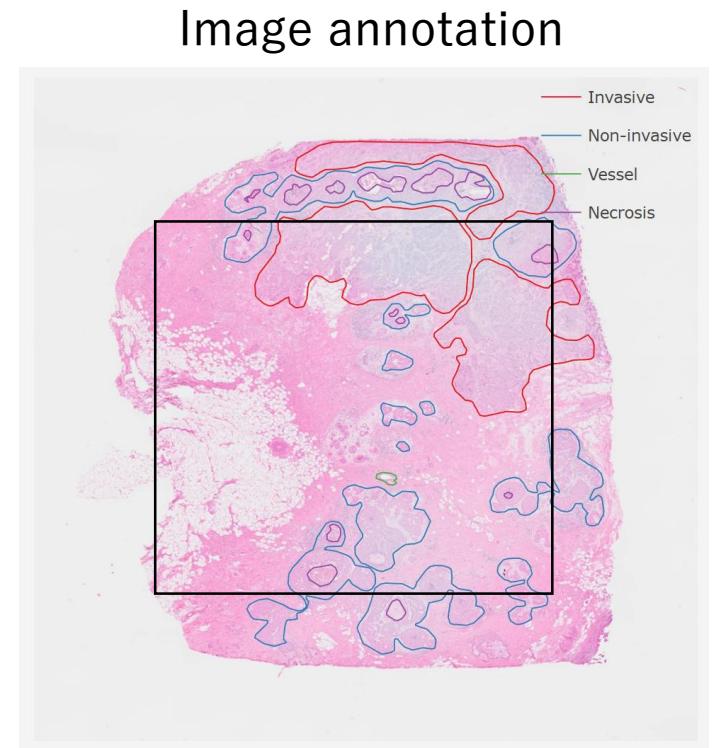
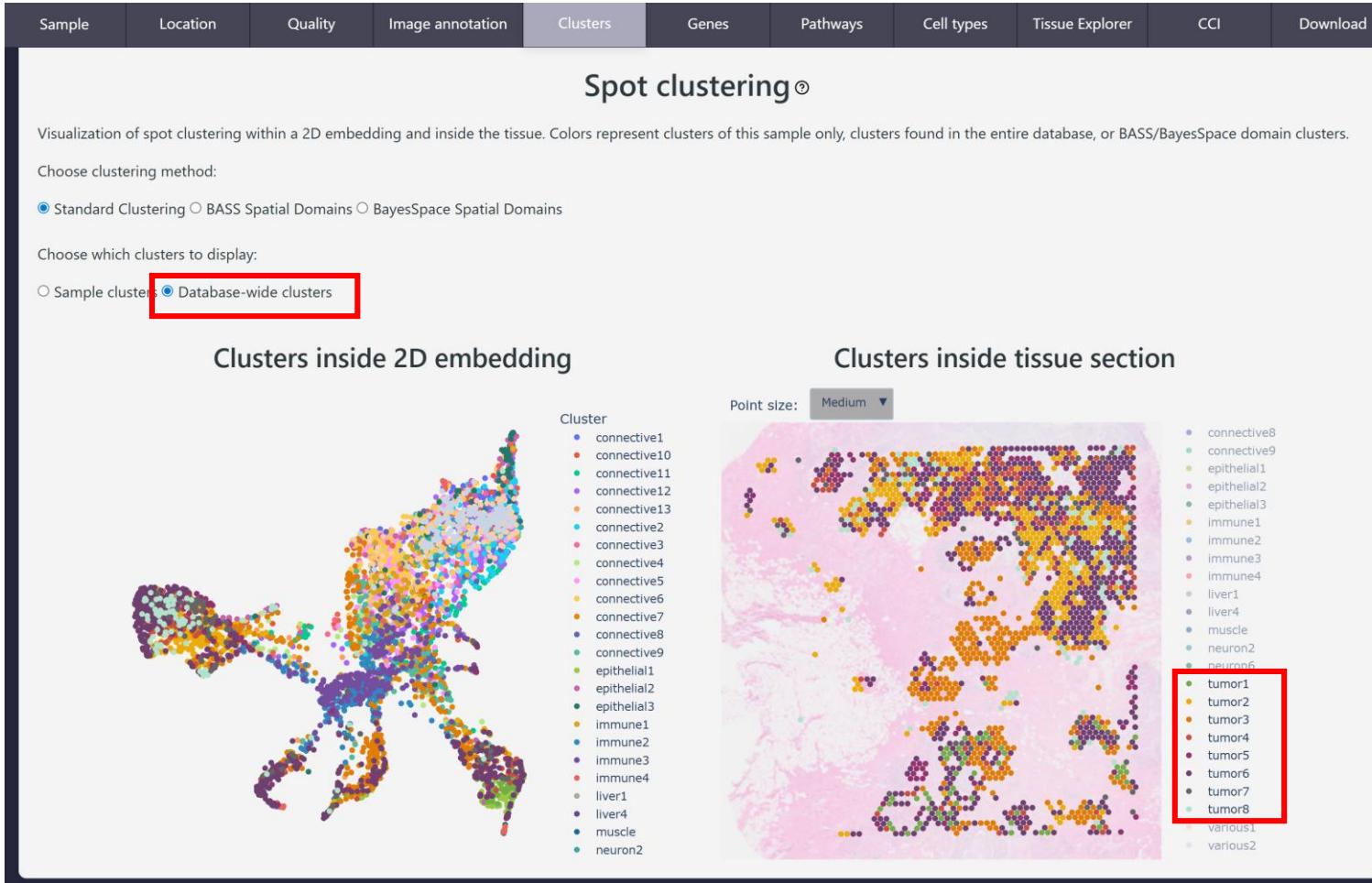
それぞれのクラスターの  
マーカー遺伝子は?



# DeepSpaceDB – Sample page (7)



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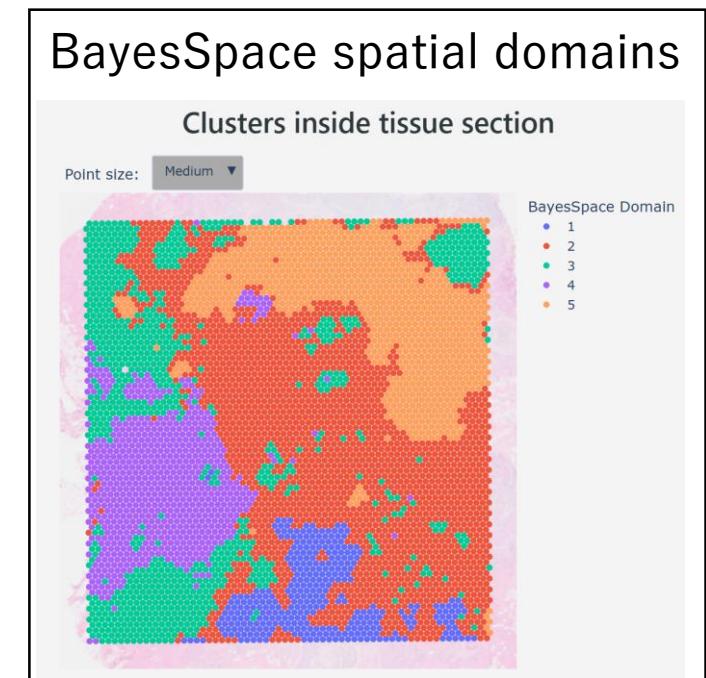
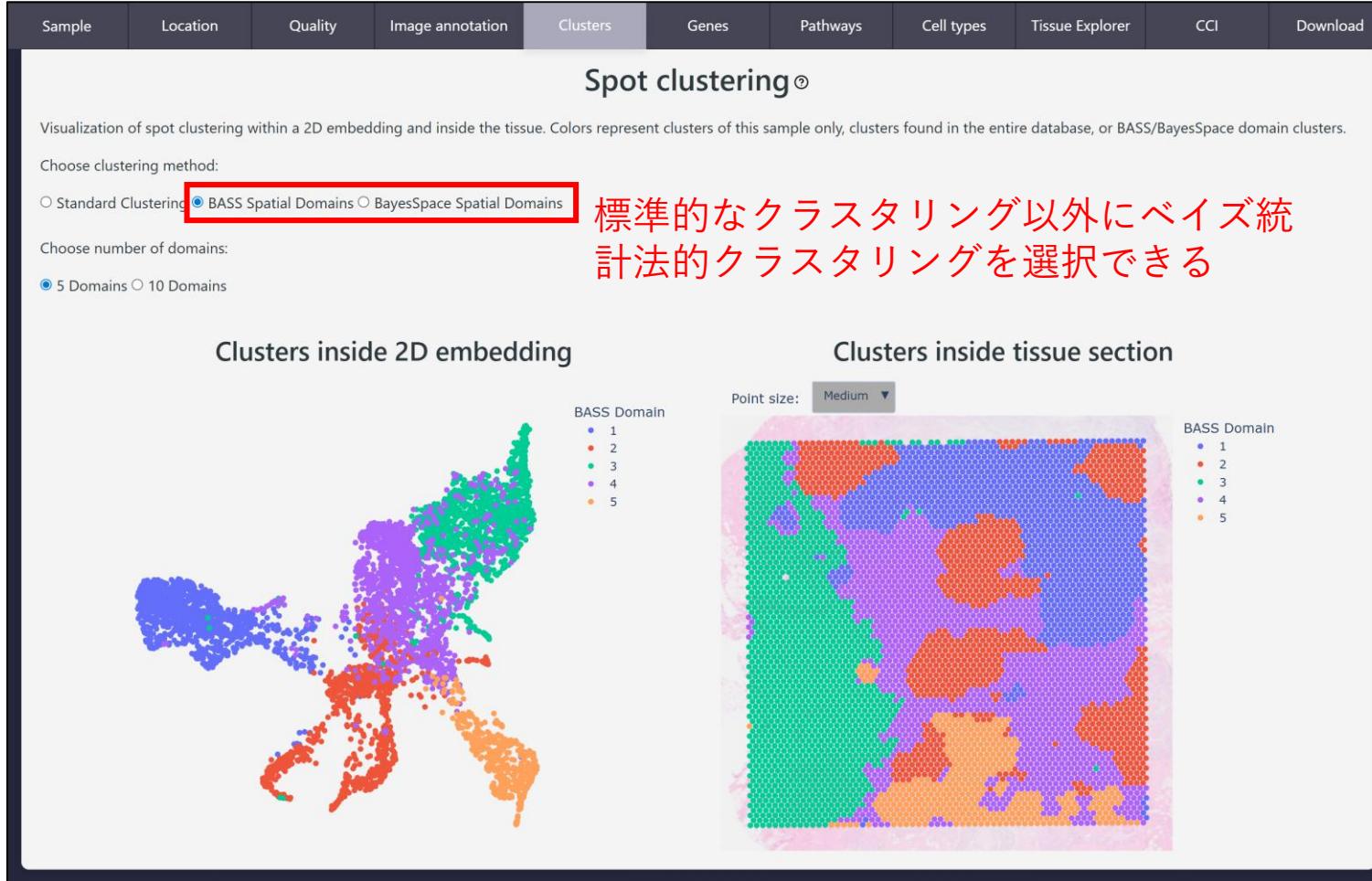


- データベースワイドのクラスターは Visium サンプルの組織構造を解釈する際に有益である。
- ここではtumorクラスター(1から8)がサンプルのガン組織上に局在する

# DeepSpaceDB – Sample page (8)



65

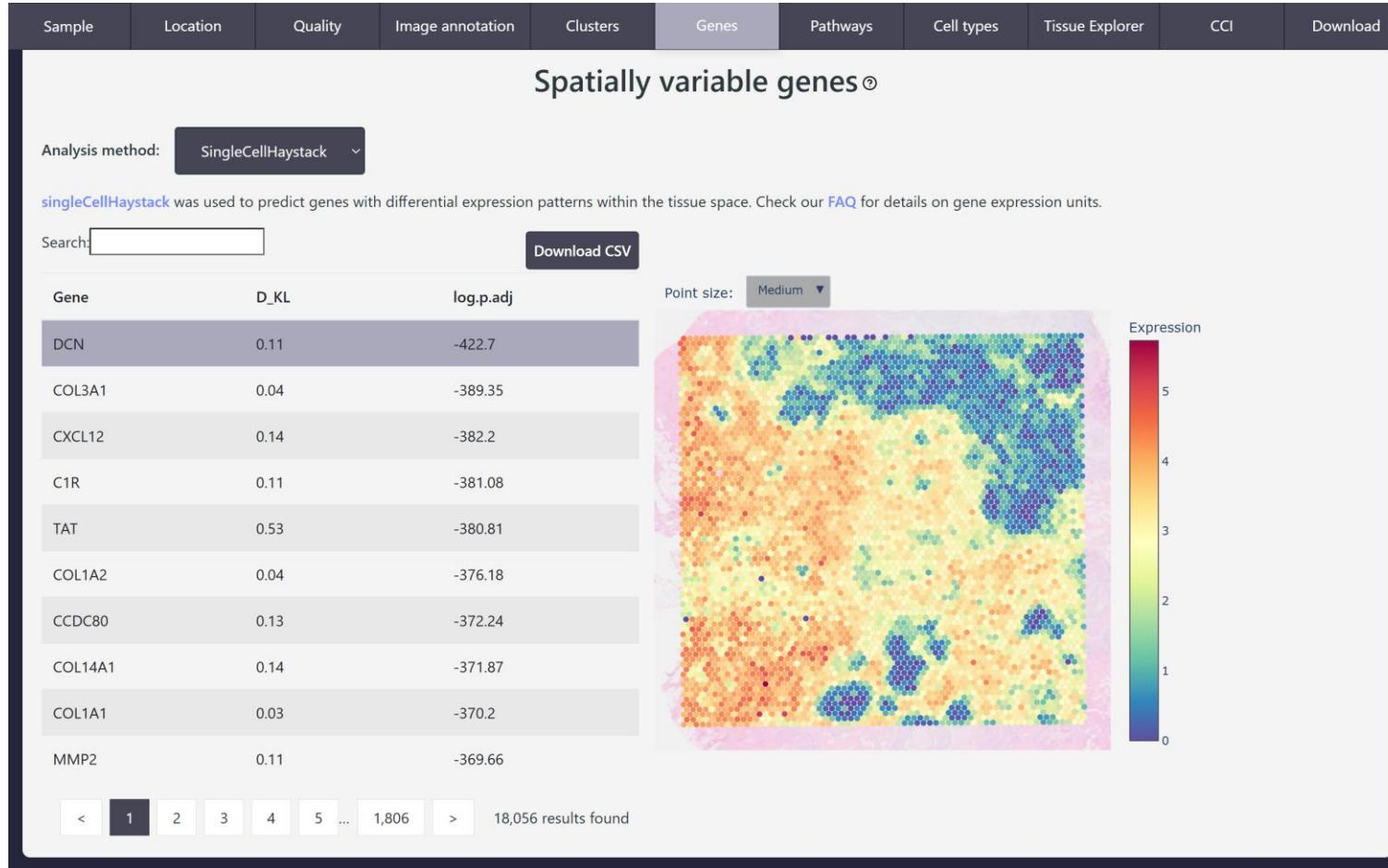


- **Spatial domains** は遺伝子発現情報に加えて空間情報を用いてクラスタリングを行う。
- DeepSpaceDB はBASS や BayesSpaceを用いたクラスタリングを提供している
- 解析から得られたドメインは生物学的特性をしばしば表している
- **当ウェビナー後半 酒井俊輔博士の講演**

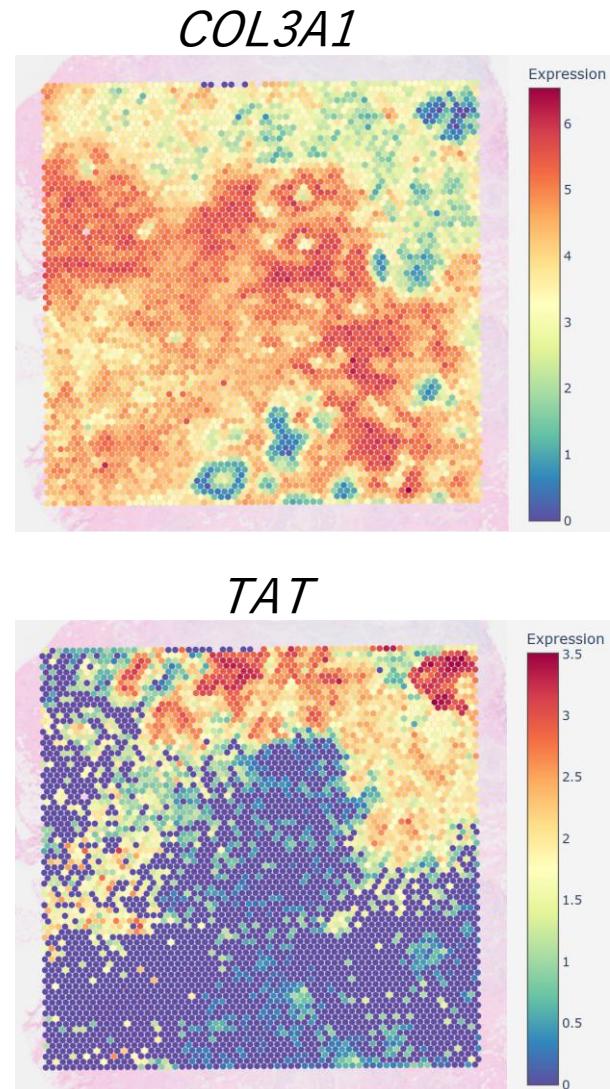
# DeepSpaceDB – Sample page (9)



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- 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



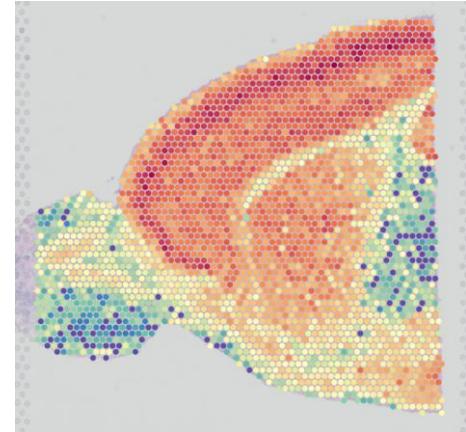
# singleCellHaystack 方法論

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



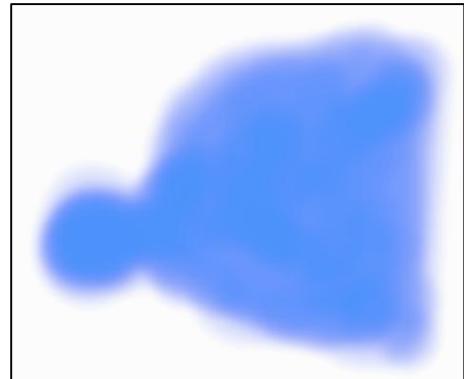
high  
low

SVGではない

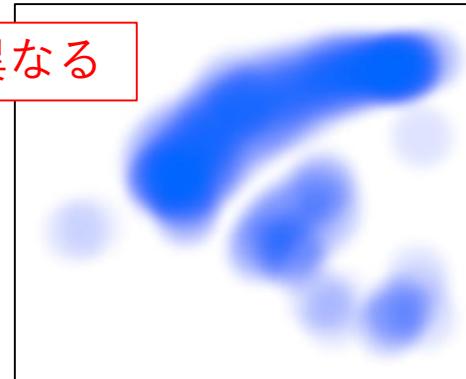


high  
low

偏りのない基準分布

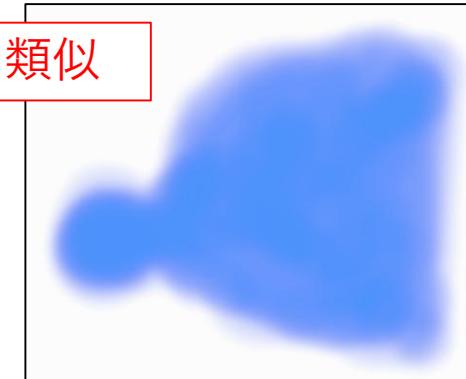


基準と異なる

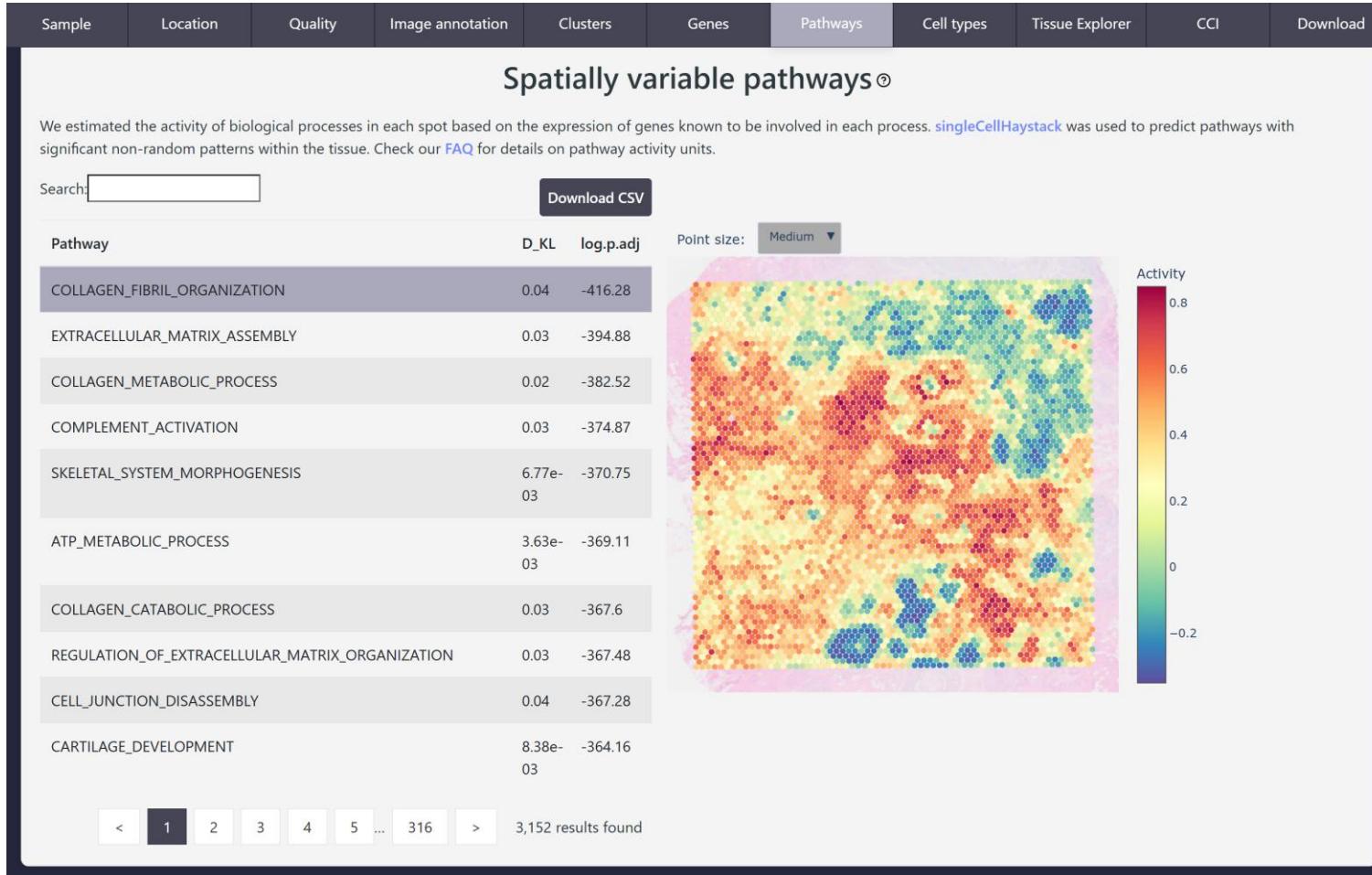


個々の遺伝子発現の分布

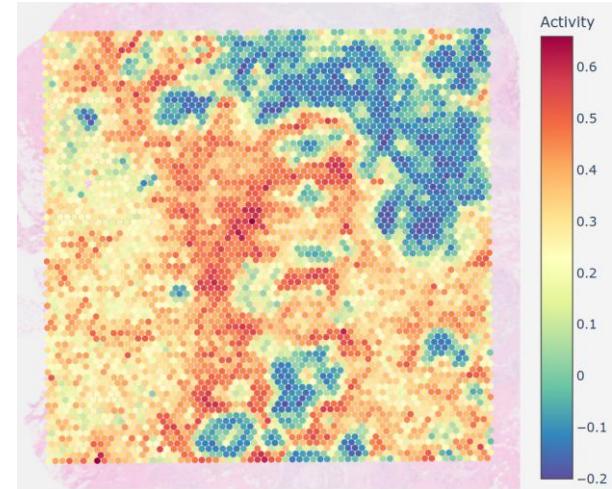
基準に類似



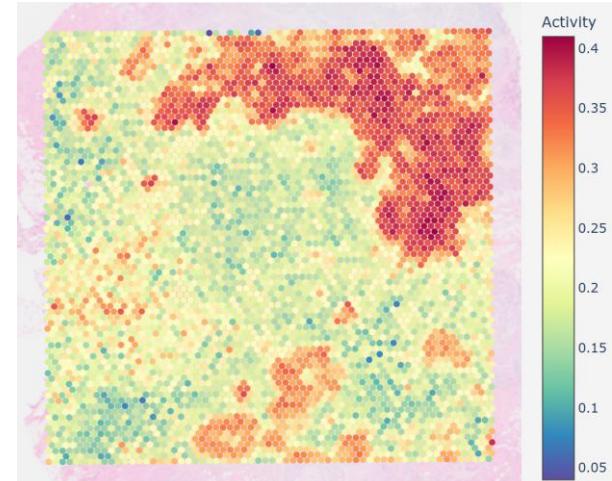
# DeepSpaceDB – Sample page (10)



補体活性化

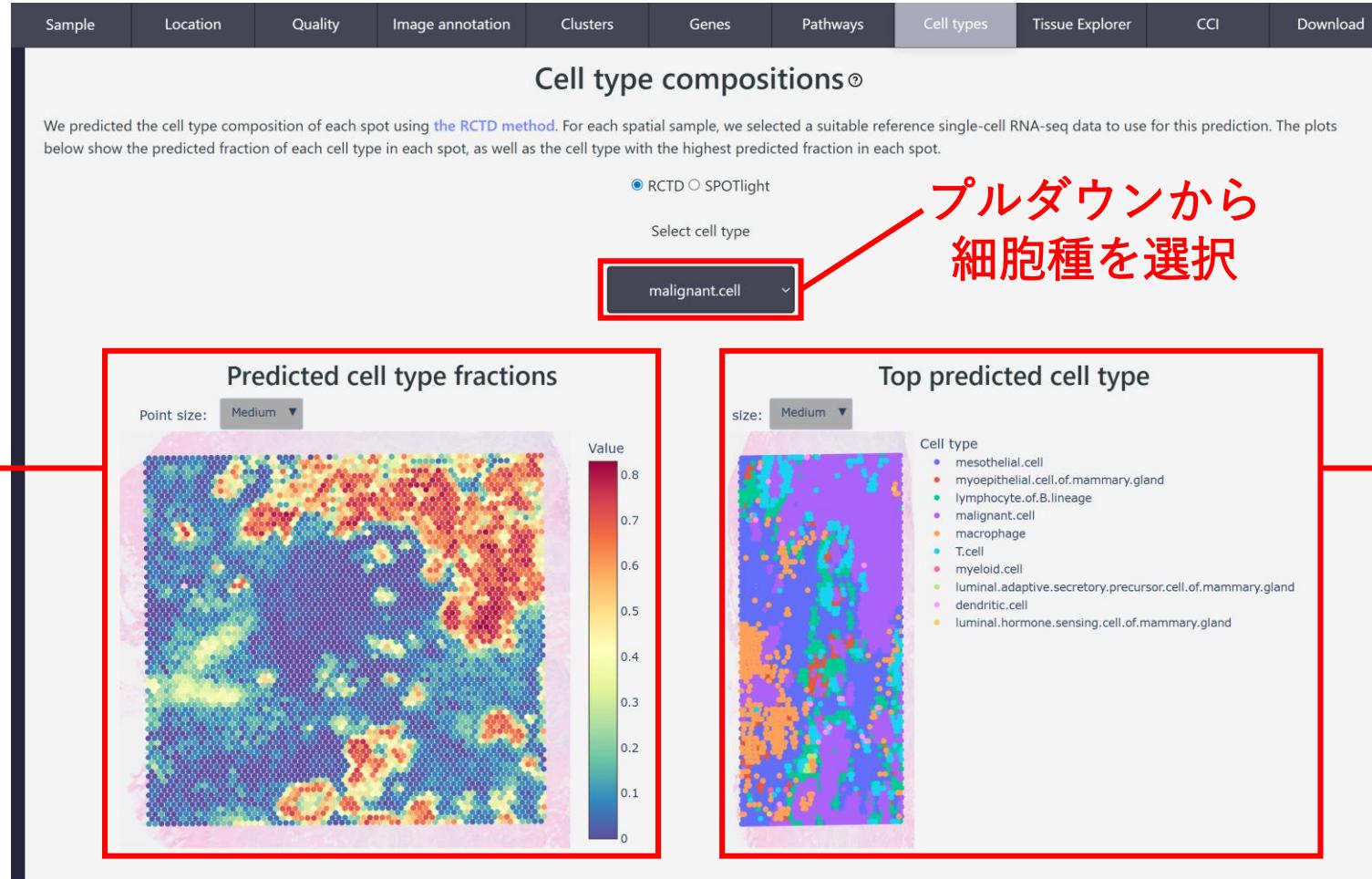


ATP 代謝プロセス



- 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)



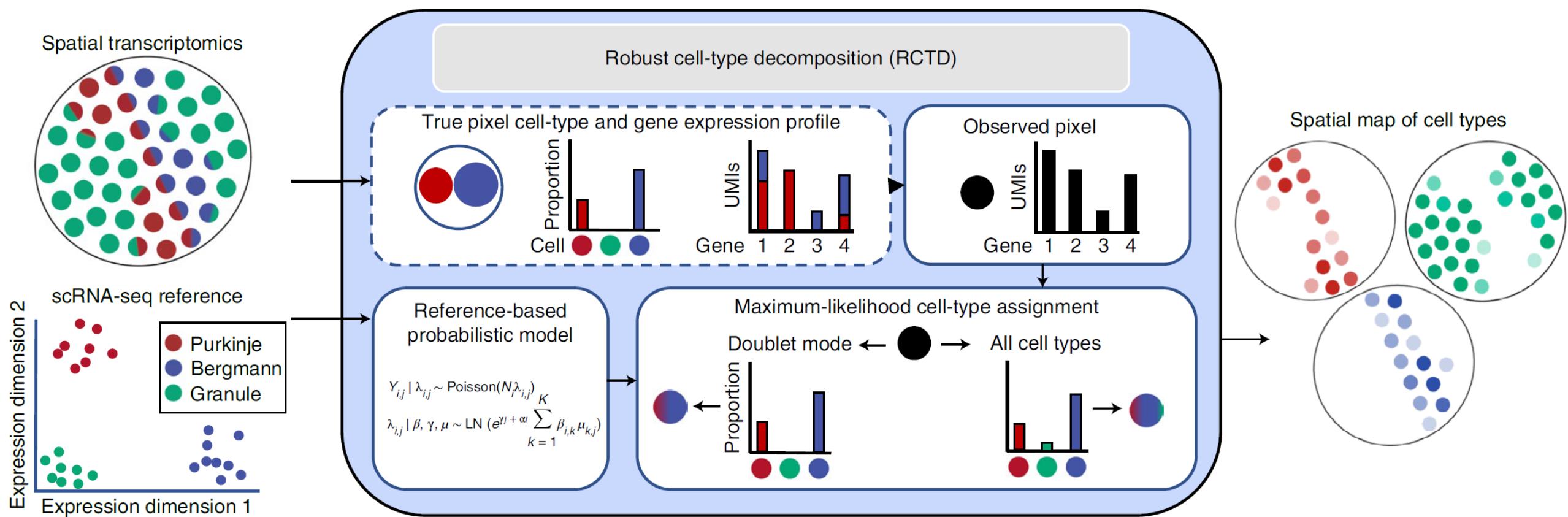
スポットごとの  
malignant cells(悪性細胞)である確率  
が表現されている

プルダウンから  
細胞種を選択

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

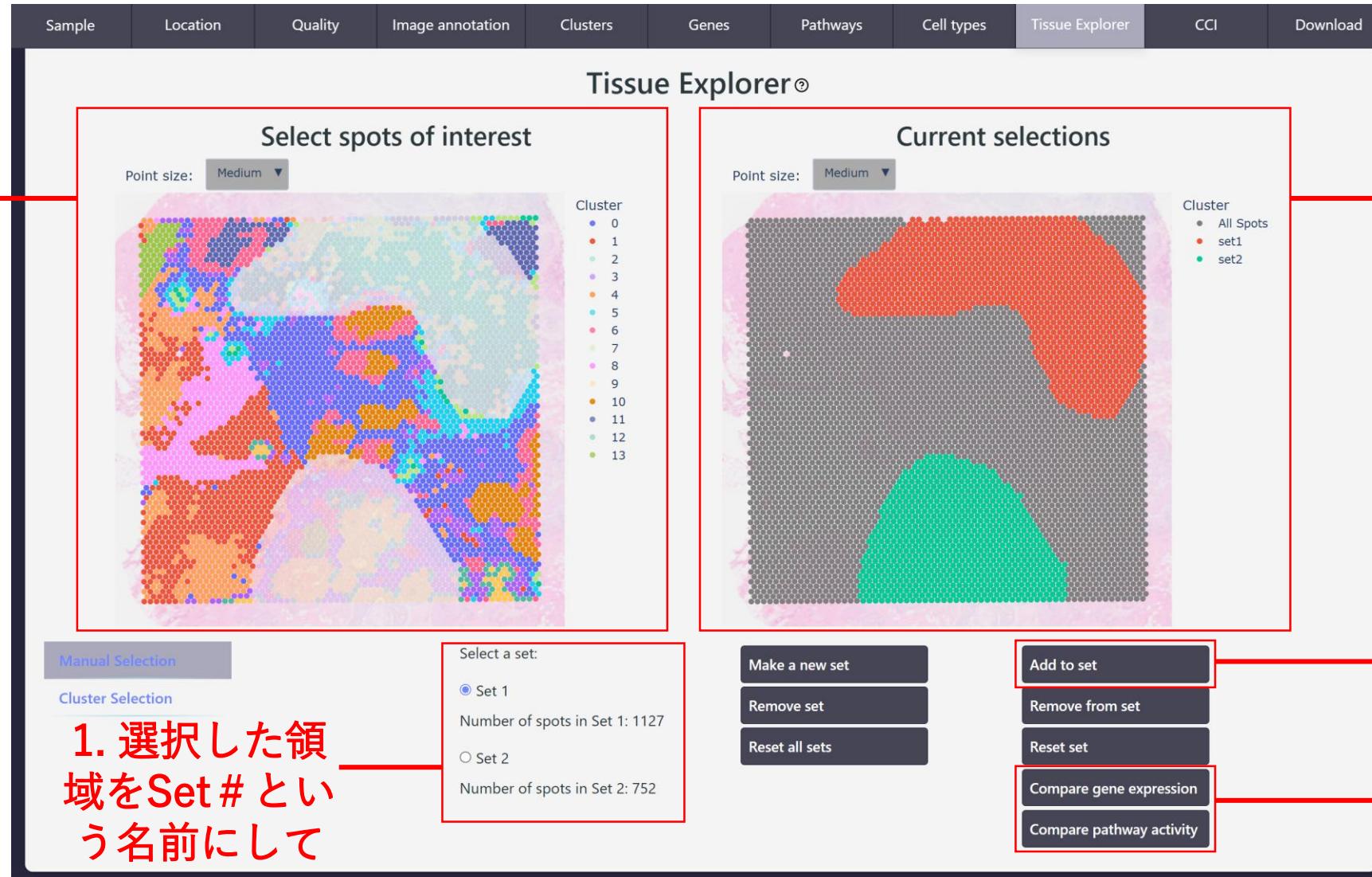
# RCTD 方法論



- 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)

“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



# 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

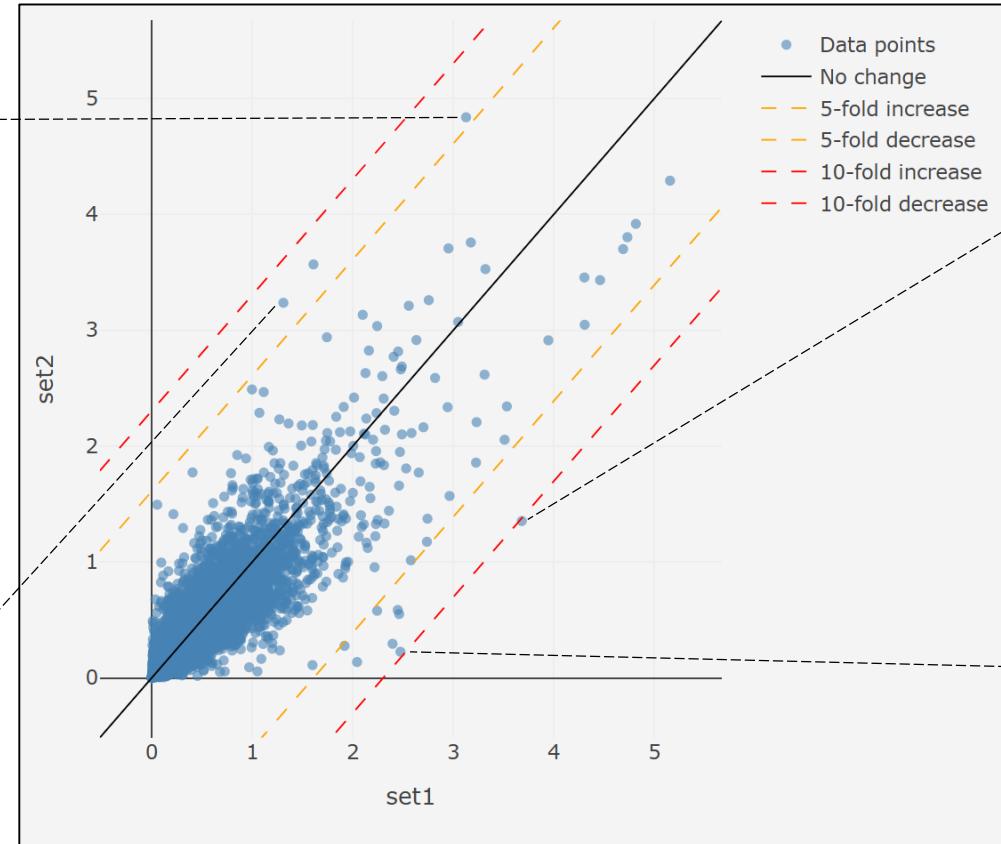
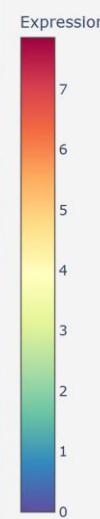
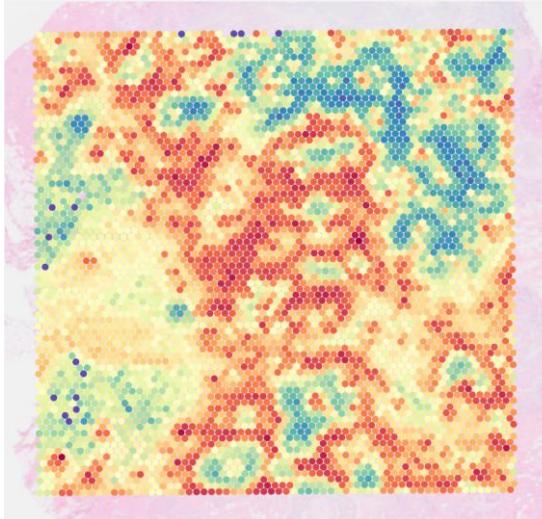
遺伝子発現テーブル:  
- 選択領域それぞれ  
の平均値  
- 発現の差  
- P-value (t-test)  
- Adjusted p-value



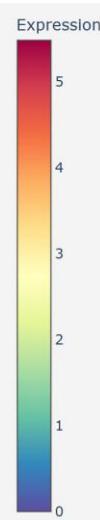
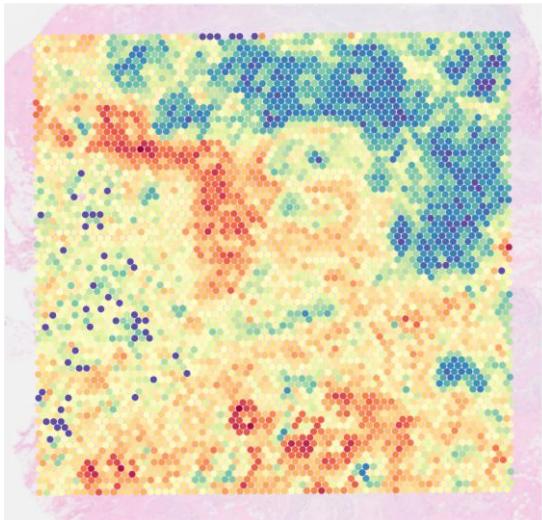
# DeepSpaceDB – Sample page (14)

比較で得た結果は“Genes” タブで確認することができる

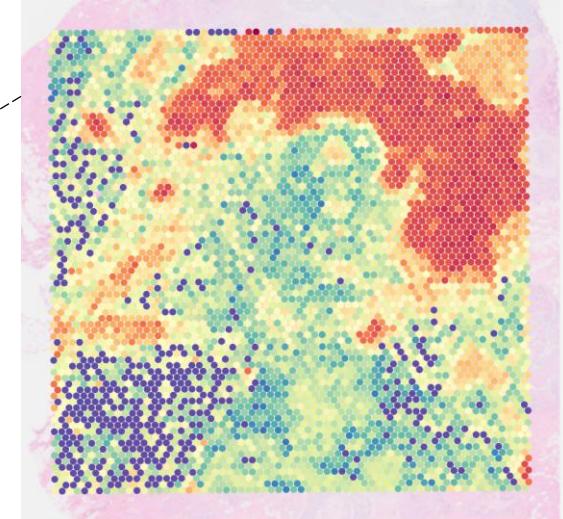
*IGKC*



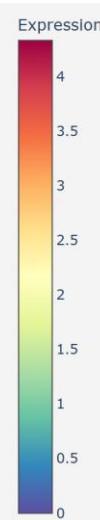
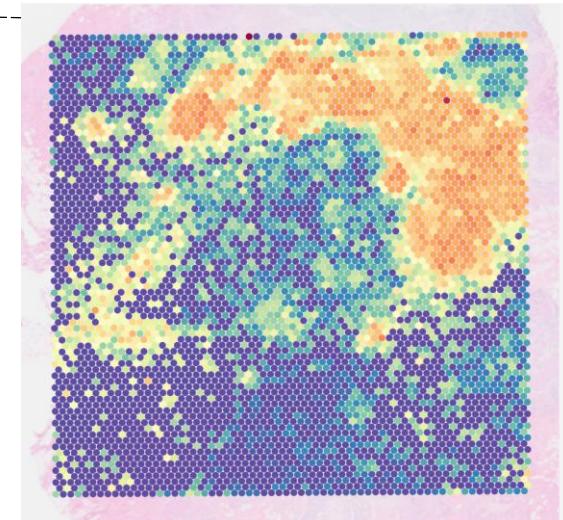
*MGP*



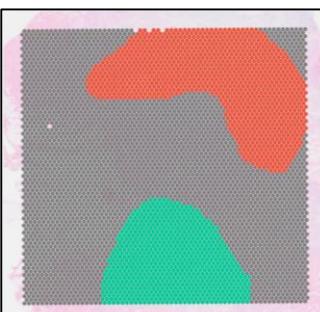
*DCAF7*



*CDH2*



マウス操作で選んだ領域→



# DeepSpaceDB – Sample page (15)



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## 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

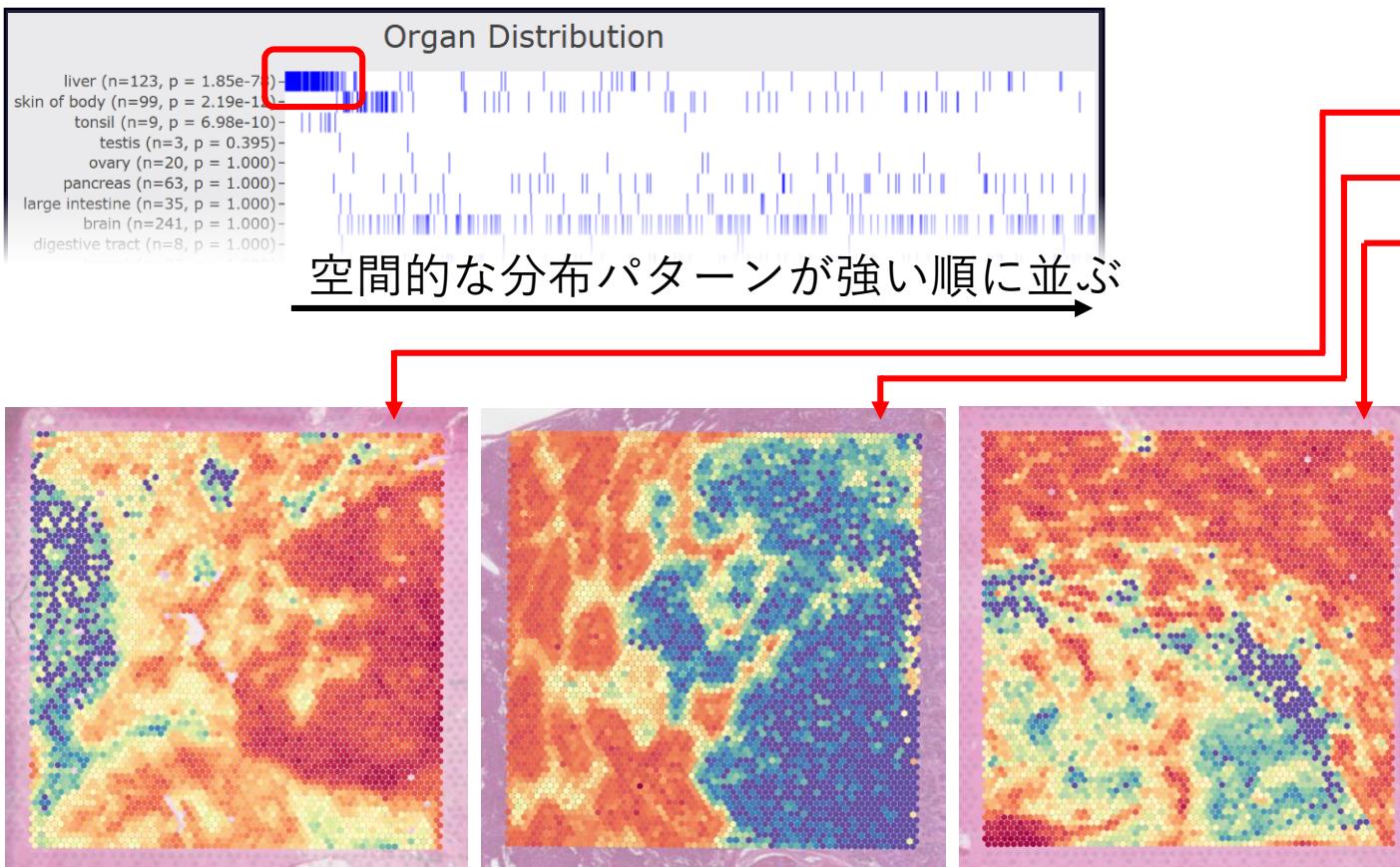
# Search tool: データベース全体から検索

DeepSpaceDB Database **Search** Upload Tutorial About Contact

Gene and Pathway Search

Human Gene CYP2E1

検索したい遺伝子やパスウェイを入力



- ・ 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
DSID001919	liver	cancer	GEO	39900120	-536.15
DSID001370	liver	cancer	GEO	--	-487.46
DSID001917	liver	cancer	GEO	39900120	-415.15
DSID000838	liver	cancer	GEO	36652202	-365.63
DSID001916	liver	cancer	GEO	39900120	-355.89
DSID001913	liver	cancer	GEO	39900120	-346.59
DSID001912	liver	cancer	GEO	39900120	-336.28
DSID001914	liver	cancer	GEO	39900120	-322.7
DSID001918	liver	cancer	GEO	39900120	-306.73
DSID001915	liver	cancer	GEO	39900120	-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でご安心下さい



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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: Select Image Resolution: Load example:

Enter a label for this job Human Mouse High Low Load Example Data

Advanced Settings

Barcodes File Features File Matrix File

Select Barcodes File Select Features File Select Matrix File

Upload your barcodes file (.tsv.gz) Upload your features file (.tsv.gz) Upload your matrix file (.mtx.gz)

Image File Scalefactors File Tissue Position File

Select Image File Select Scalefactors File Select Tissue Position File

Upload your tissue image file (.png) Upload your scalefactors file (json) Upload your tissue position file (.csv)

I'm not a robot reCAPTCHA Privacy - Terms

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	

Compare Download Data

解析結果を表示

プロセシングステータス

アップロードオプション

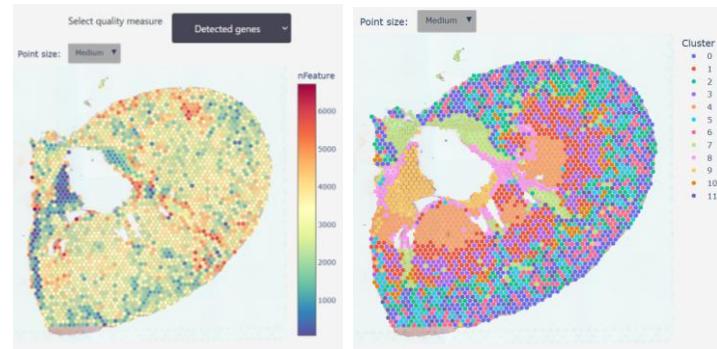
アップロードするファイルを選ぶ

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

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

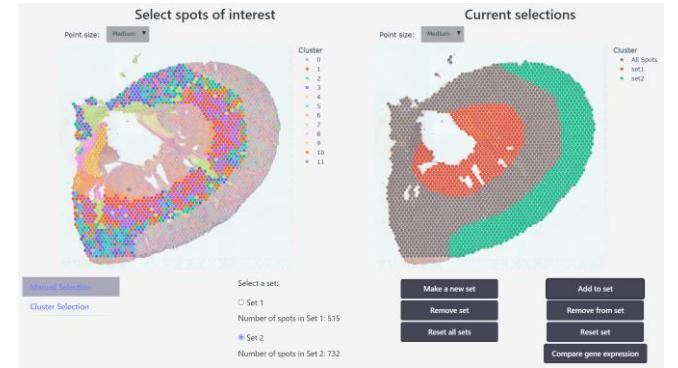
Quality Clustering



Spatially variable genes



Tissue explorer tool

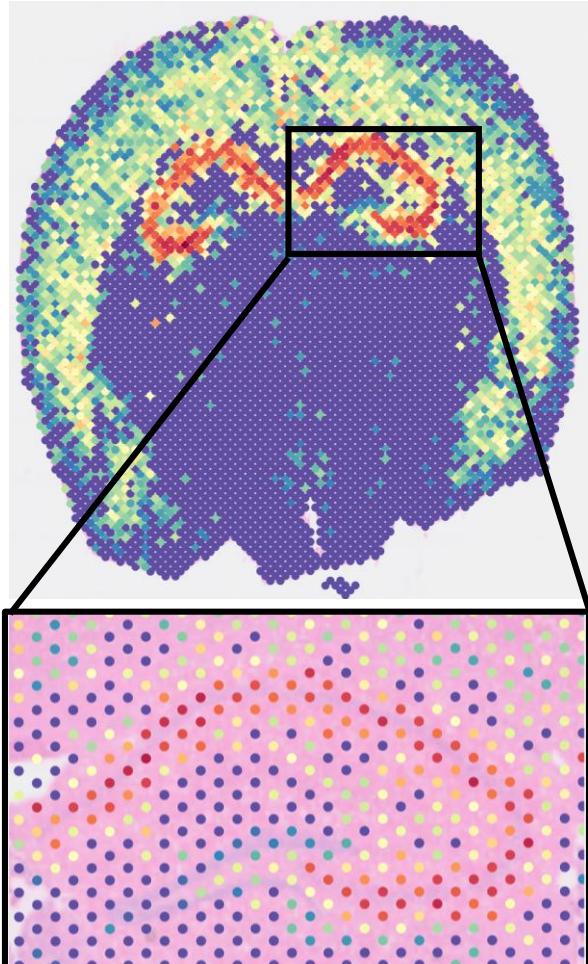


- Rを使った空間トランскриプトミクスデータ解析
  - Visium example
  - Xenium example
- 既存の空間トランскриプトミクスデータベースの紹介
- DeepSpaceDBの紹介
  - Visium interface
  - Xenium interface
- まとめ

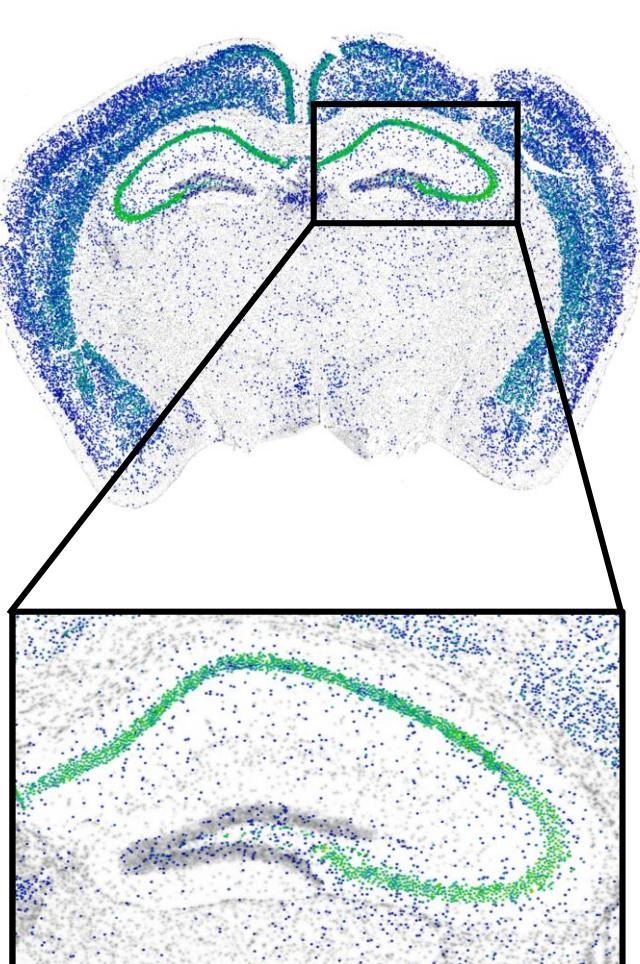
# VisiumとXeniumの比較例

*Neurod6*

Visium

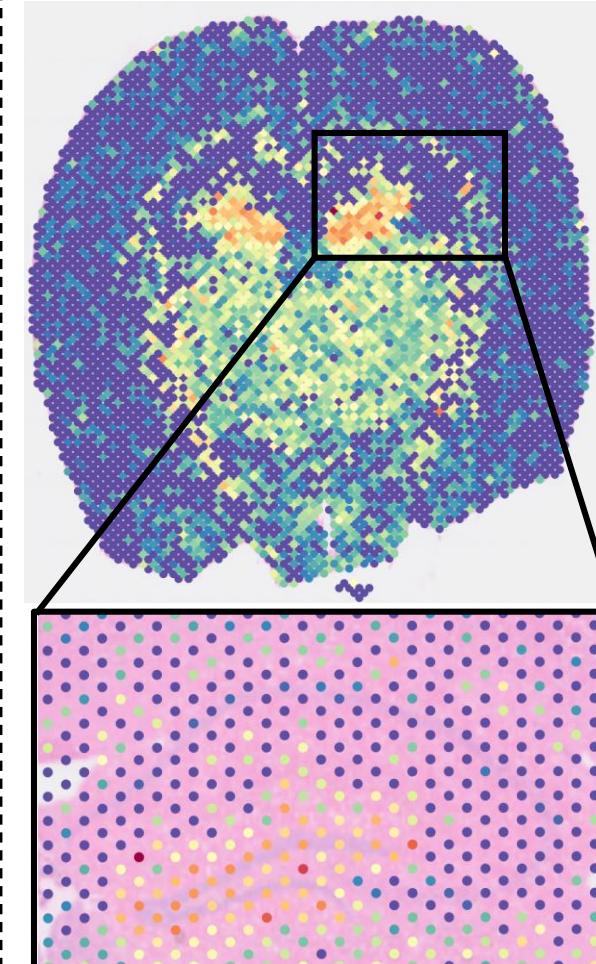


Xenium

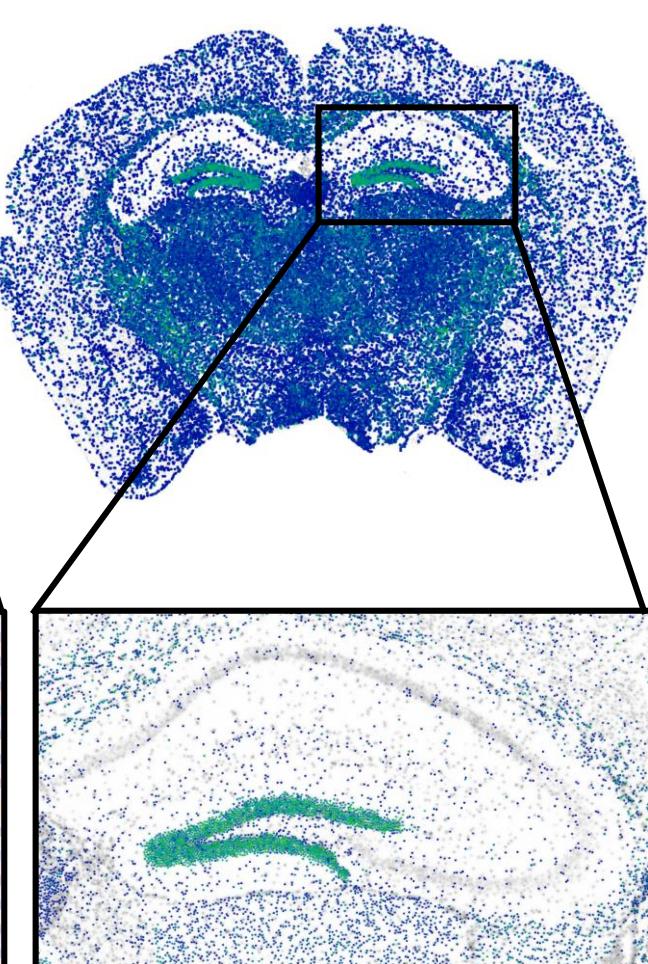


*Prox1*

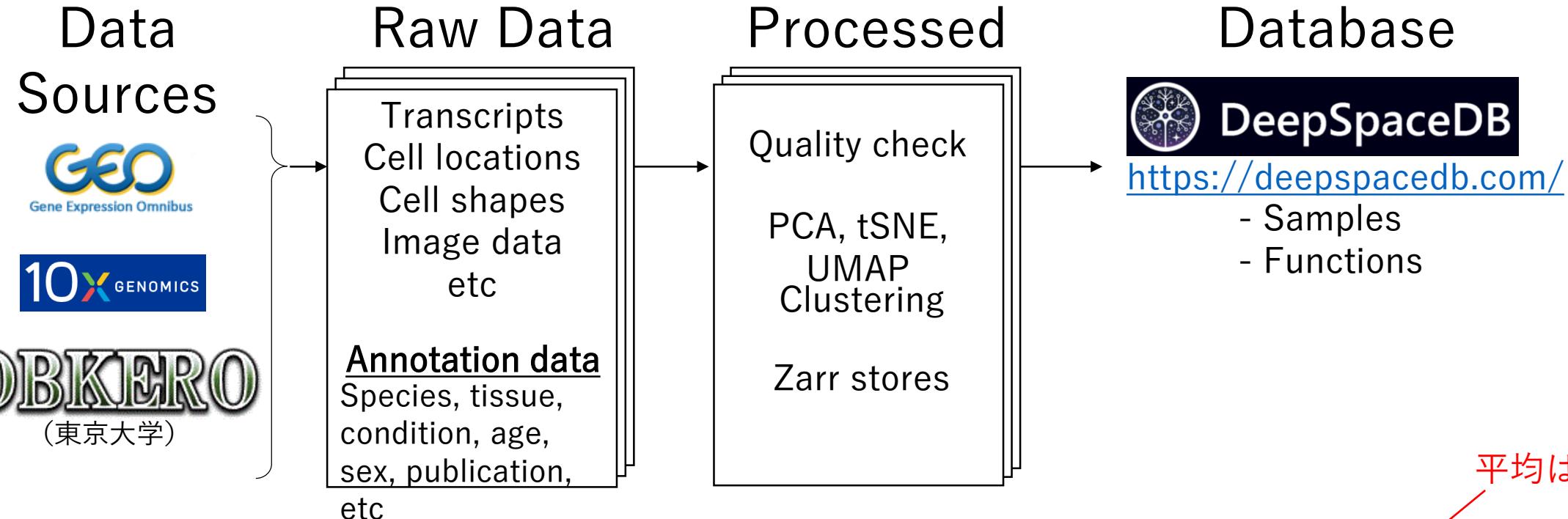
Visium



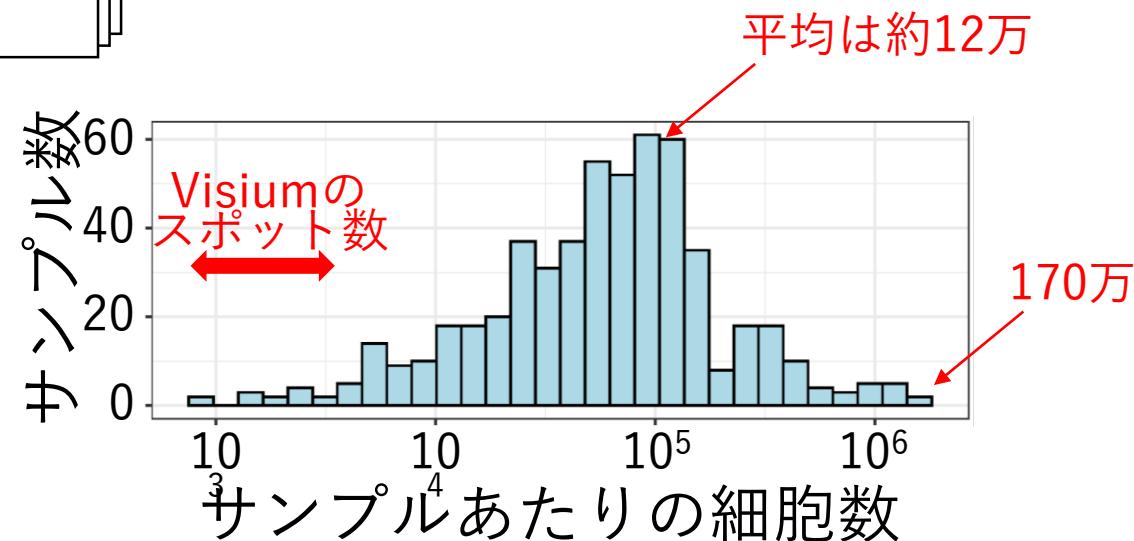
Xenium



# Xeniumのワークフロー



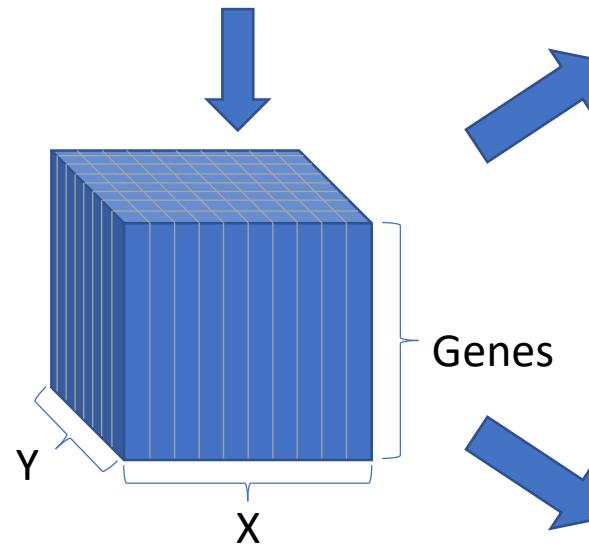
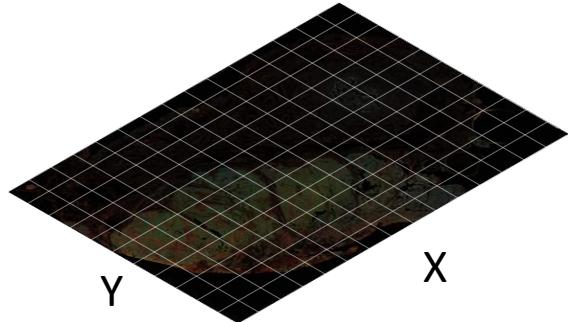
- Xeniumサンプル約600件を処理済み
- 高速アクセス実現のための工夫が必要



# 目的ごとに最適化されたフォーマットを採用

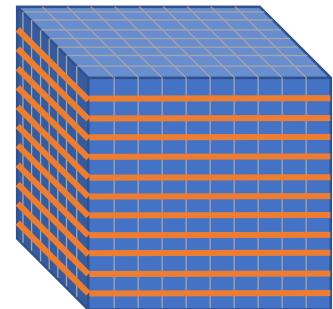


Xenium sample

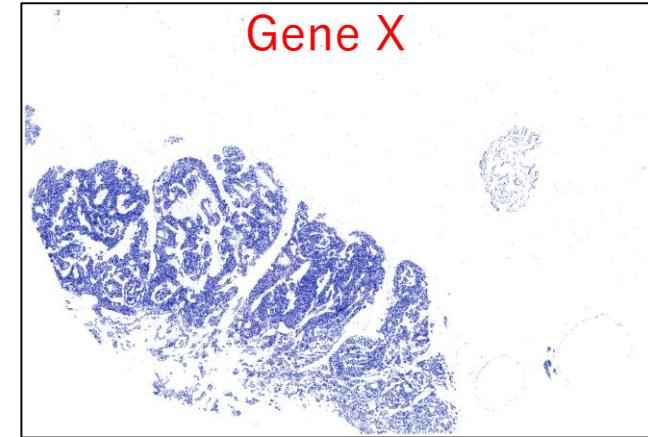


1つの遺伝子の可視化 -> その遺伝子の情報のみ読み込む

Zarr store #1



Gene X

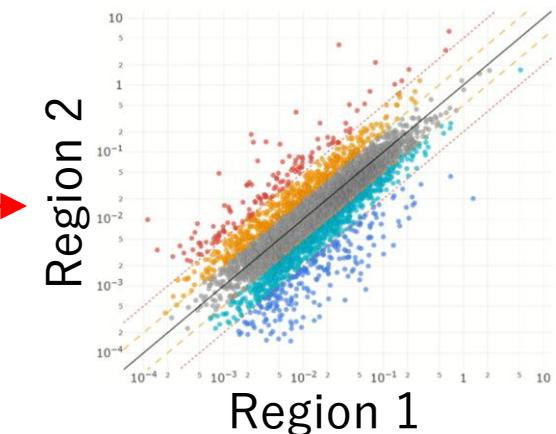
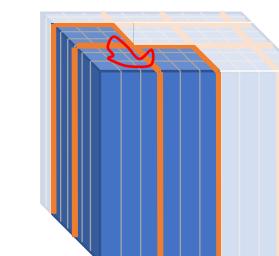
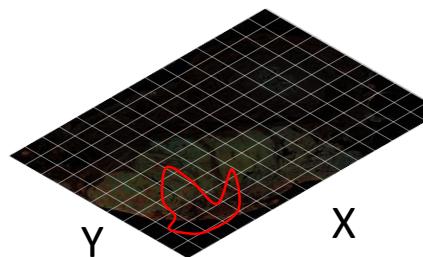
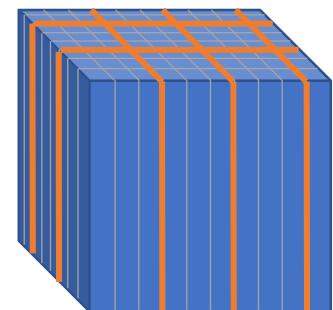


Gene X

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)



DeepSpaceDB Database Search Upload Tutorial About Contact

Plot Export Customize

Sample Information

DeepSpace ID	DSIDX00085
Sample ID	10X_Xenium_Prime_Ova
Series ID	10X_website
Organism	human
Organ	ovary
Organ Detailed	--
Condition	cancer
Condition Detailed	ovarian cancer
Sex	female
Age or Stage	--

Gene List

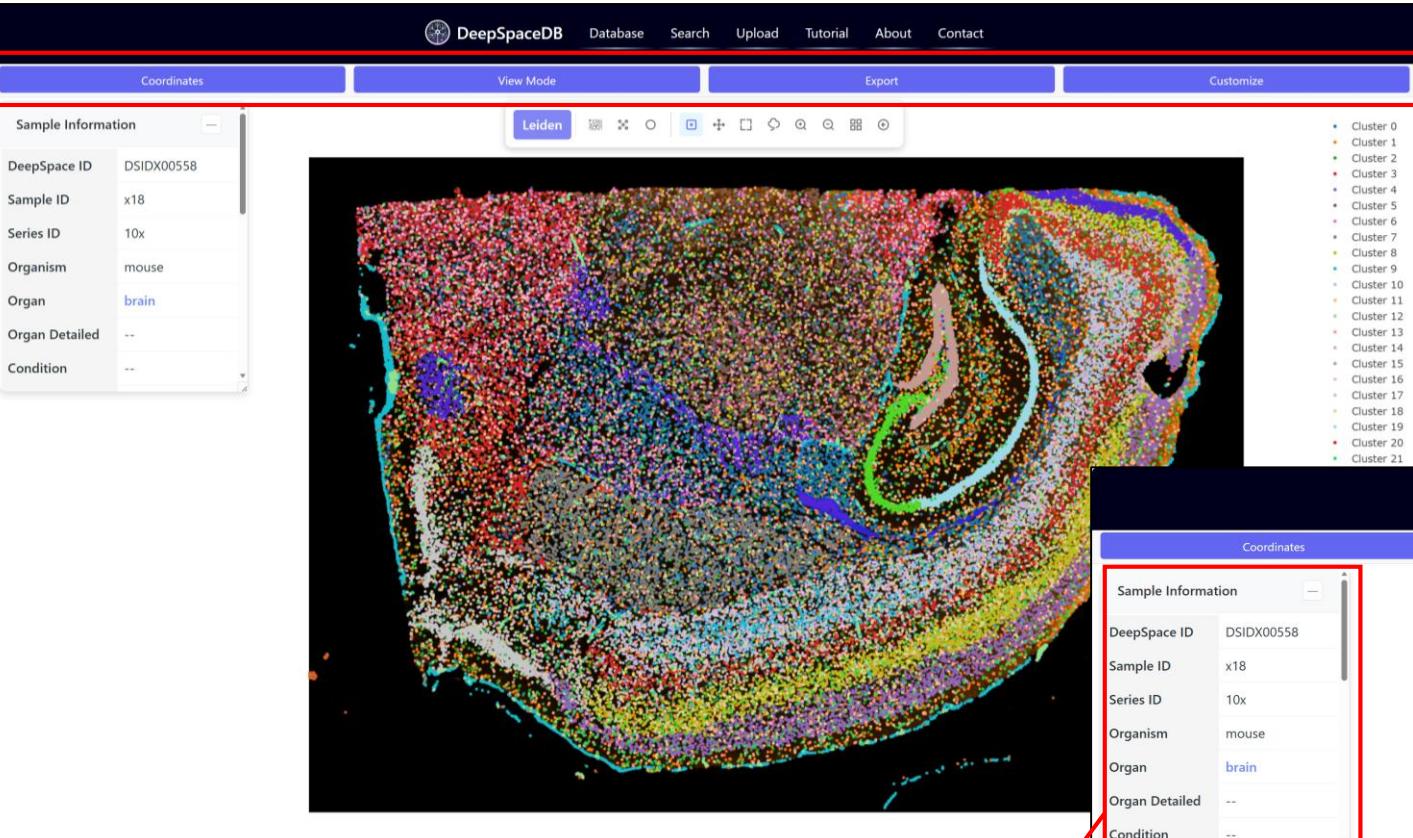
Multi-Gene Mode (up to 5)

epcam

EPCAM

Selected Gene

# Xenium interface (1)

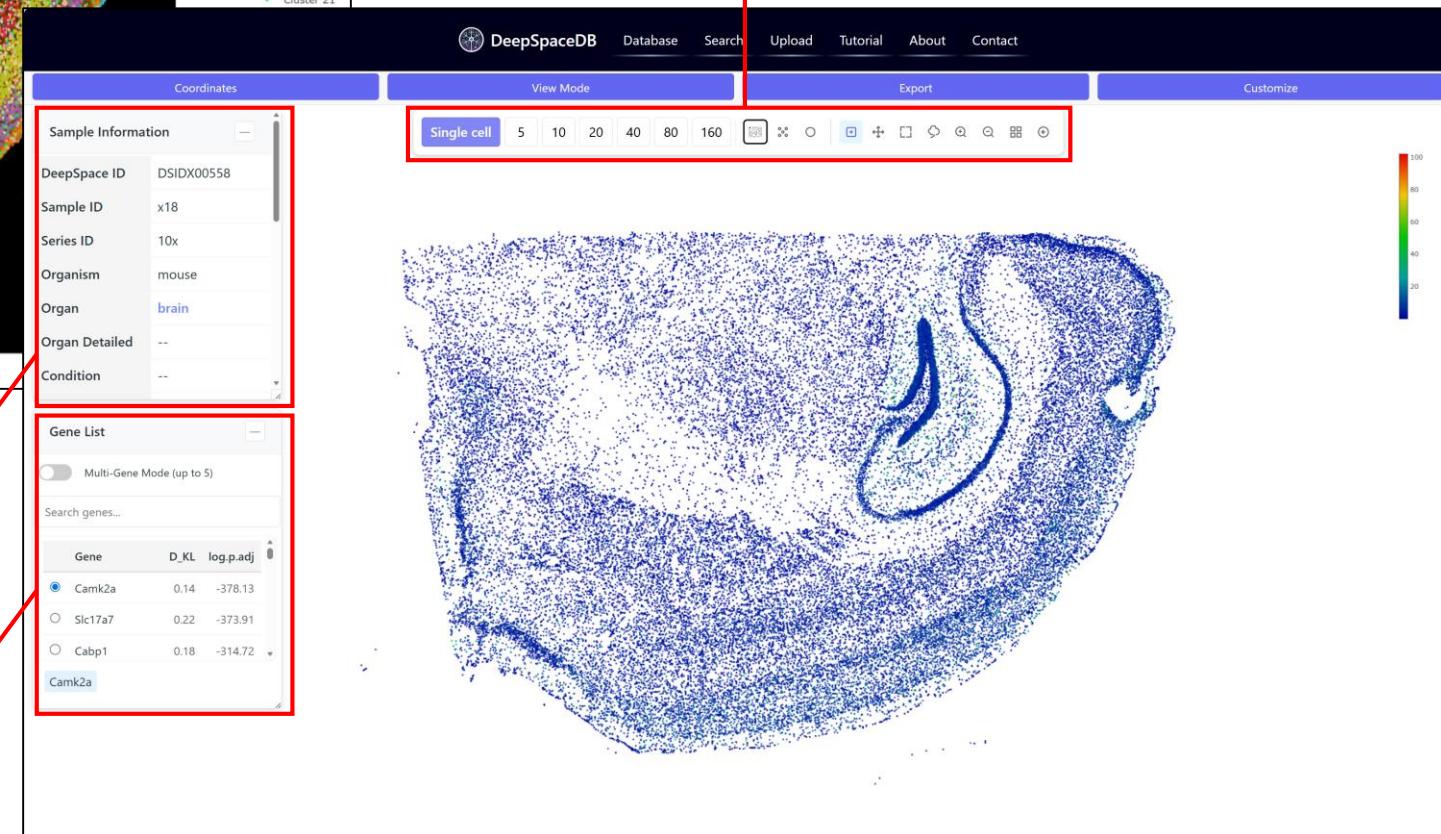


メニュー:

- 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)

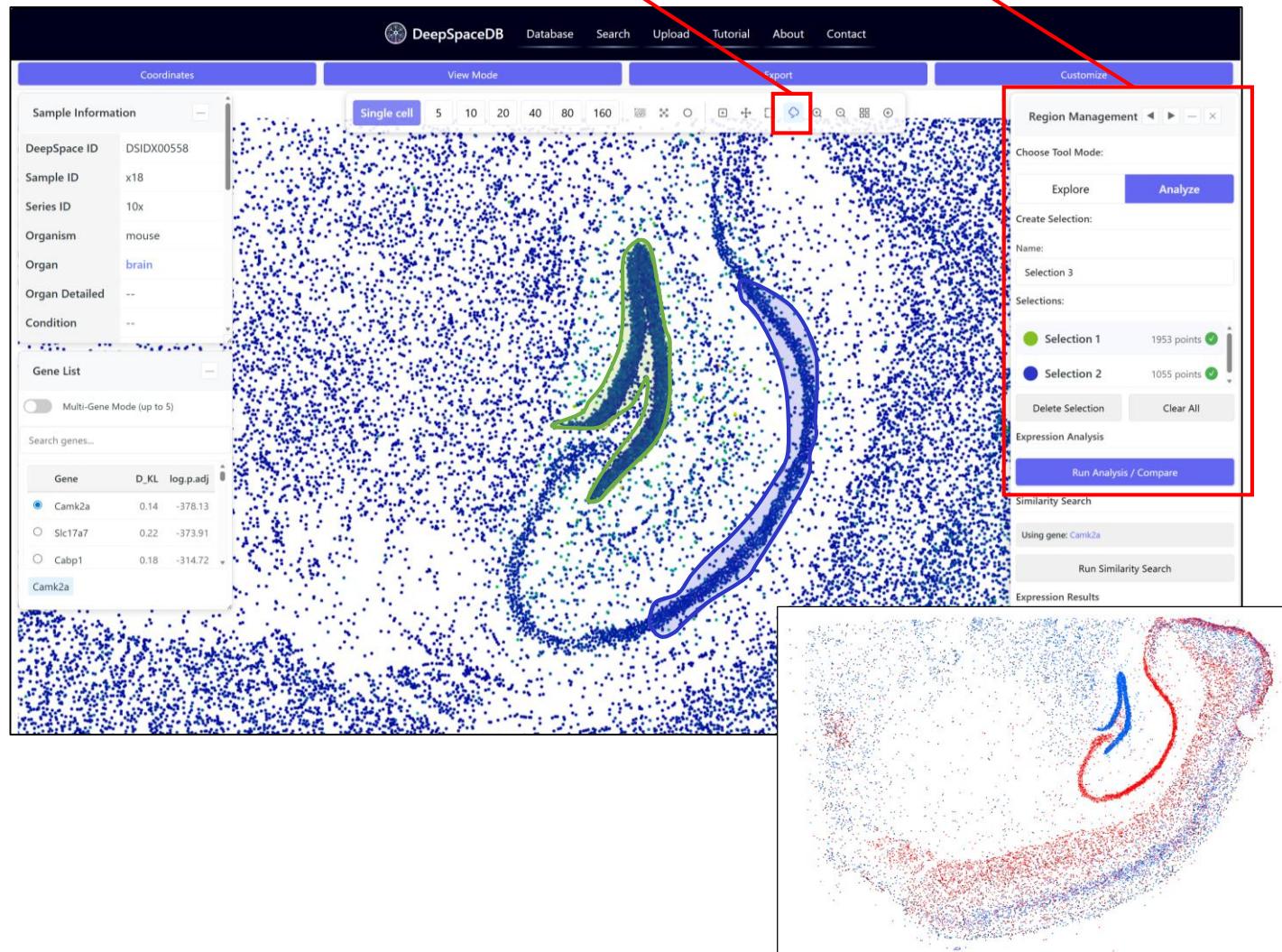


アノテーションデータ

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

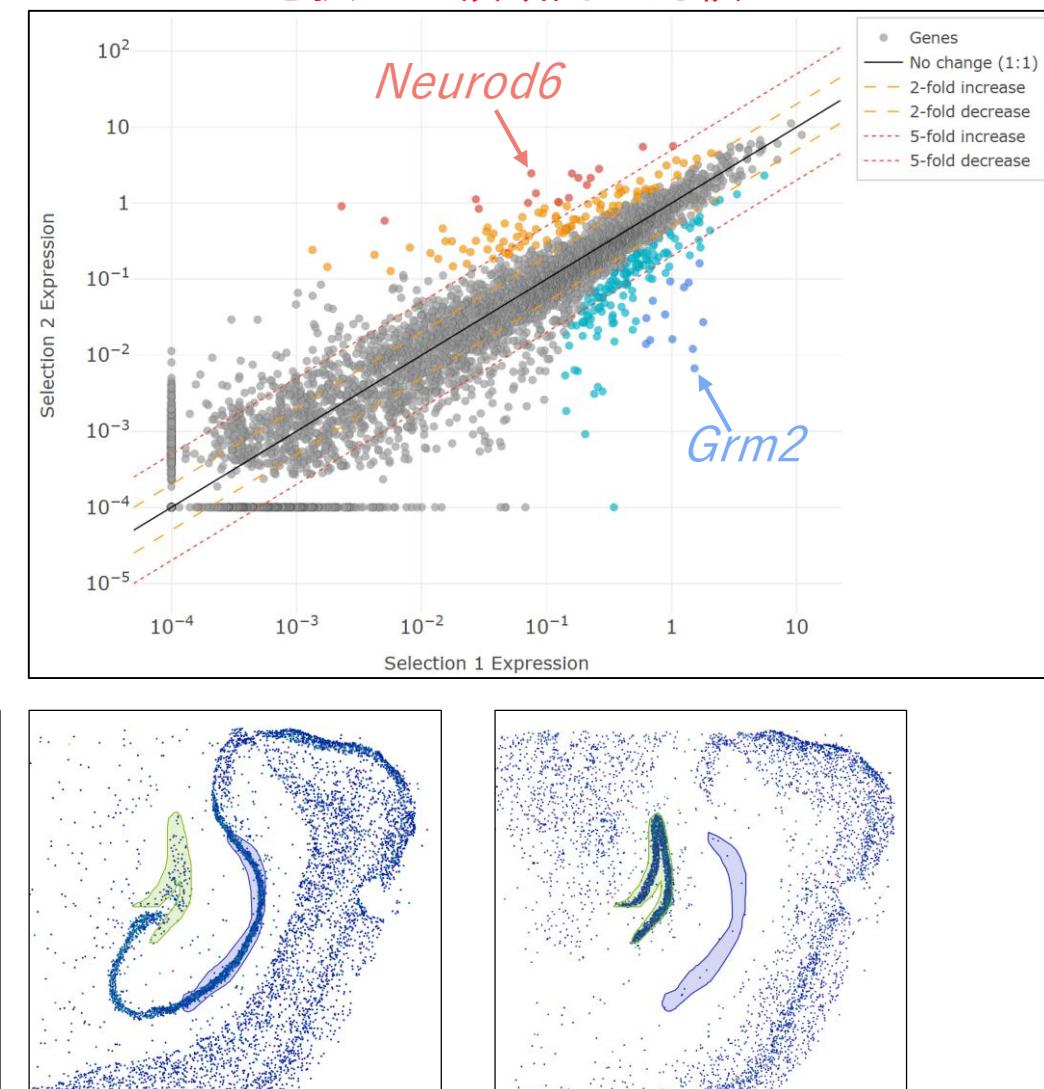
# Xenium interface (2)

ユーザーは興味のある領域を自由に選択できる



複数の遺伝子発現プロット  
*Neurod6* *Grm2*

選択した領域間の比較



*Neurod6* *Grm2*

- Rを使った空間トランскриプトミクスデータ解析
  - Visium example
  - Xenium example
- 既存の空間トランскри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

# 謝辞



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## Our team

- Vladyslav HONCHARUK
- Afeefa ZAINAB
- TAKEMOTO Keiko
- Hongyi ZHAO



一緒に研究する仲間を募集しています。  
学生の皆さん、大歓迎です。

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- Diego DIEZ (Osaka Univ)



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AMED Grant Number JP24gm2010003

# DeepSpaceDBのまとめ

- ・空間トランск립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](#)

