



<https://singlecell.xena.net>



Welcome to the Xena's multi-omic
integration single cell portal

ENTER





Select an integration:

Name ▼	Donor ▼	Cells/Spot	Data types ▼
Metastatic melanoma HTAN Human ⓘ (Tirosh et. al. 2016)	4 8	64,000 400,000	10x Visium scRNAseq\scATACse
Human Squamous Cell Carcinoma (Ji et al Cell 2020, Chen et al BioRxiv 2022) ⓘ	2 10	64,000 400,000	10x Visium scRNAseq
Mouse spleen ⓘ (Govek et al Science Adv 2021) ⓘ (Goltsev et al Cell 2018) ⓘ	5 3	4,000 500,000	CITEseq CODEX
Single-cell transcriptomic analysis of mIHC images via antigen mapping (Govek et al Science Adv 2021) ⓘ	5	4,000	CITEseq
Deep Profiling of Mouse Splenic Architecture with CODEX Multiplexed Imaging (Goltsev et al Cell 2018) ⓘ	3	500,000	CODEX
Single-cell reconstruction of follicular remodeling in the human adult ova (Fan et al Nat Commun 2019) ⓘ	5	10,000	Expression

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Name ▼	Donor ▼	Cells/Spot	Data types ▼
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(Tirosh et. al. 2016)	8	400,000	scRNAseq\scATACse
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Next



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Metastatic melanoma HTAN Human (Tirosh et. al. 2016) 10x Visium, scRNAseq/scATACseq X

Layout

Select a layout type

Select a layout type:

- ☐ UMAP/t-SNE
- ☐ Spatial

Legend





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Metastatic melanoma HTAN Human (Tirosh et. al. 2016) 10x Visium, scRNAseq/scATACseq X

Layout

Select a layout type:

- ☒ UMAP/t-SNE
- ☐ Spatial

Select a UMAP/t-SNE layout

Select a UMAP/t-SNE layout:

Select a UMAP/t-SNE layout



Legend





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Metastatic melanoma HTAN Human (Tirosh et. al. 2016) 10x Visium, scRNAseq/scATACseq X

Layout

Select a UMAP/t-SNE layout

Select a layout type:

- ☒ UMAP/t-SNE
- ☐ Spatial

Select a UMAP/t-SNE layout:

Select a UMAP/t-SNE layout ▼

- scRNAseq (Tumor only, all patients)
- scRNAseq (All cells, all patients)
- scATACseq (Tumor only, all patients)
- scATACseq (All cells, all patients)
- scRNAseq + scATACseq (Seurat, Tumor)
- scRNAseq + scATACseq (Seurat, All cell)

Legend



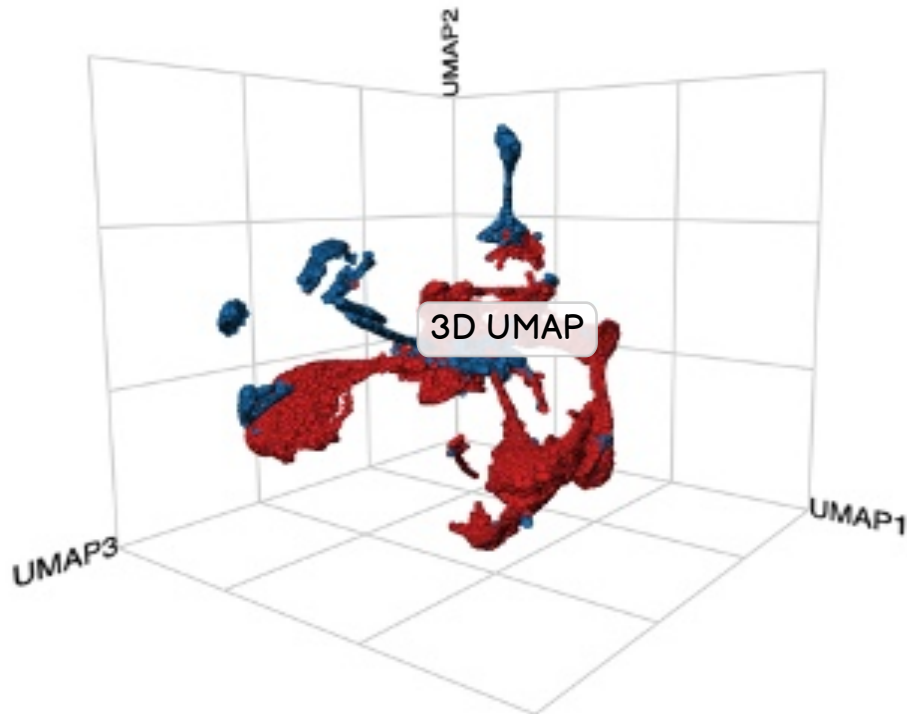
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Metastatic melanoma HTAN Human (Tirosh et. al. 2016) 10x Visium, scRNAseq/scATACseq X

Layout

Color by

Cells in View



Select a layout type:

☒ UMAP/t-SNE☐ Spatial

Select a UMAP/t-SNE layout:

scRNAseq + scATACseq (Seurat, All cells) ▼

Dot Size:



Legend

 scRNAseq

 scATACseq

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Metastatic melanoma HTAN Human (Tirosh et. al. 2016) 10x Visium, scRNAseq/scATACseq X

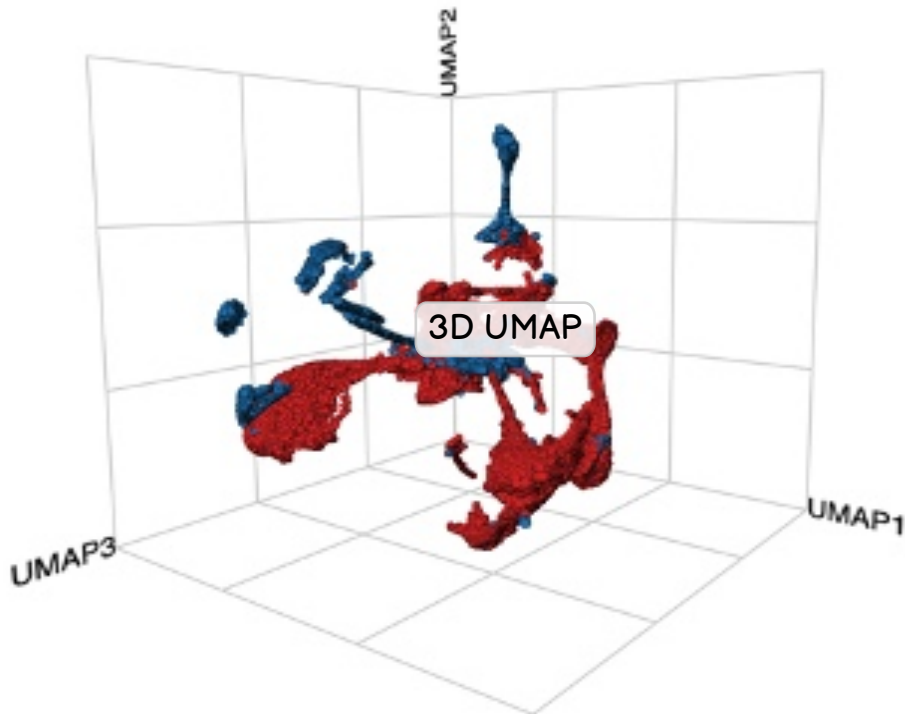
Layout

Color by

Cells in View

Select how to color cells

By dataset



Legend

scRNAseq

scATACseq

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Metastatic melanoma HTAN Human (Tirosh et. al. 2016) 10x Visium, scRNAseq/scATACseq X

Layout

Color by

Cells in View

Select how to color cells

By dataset

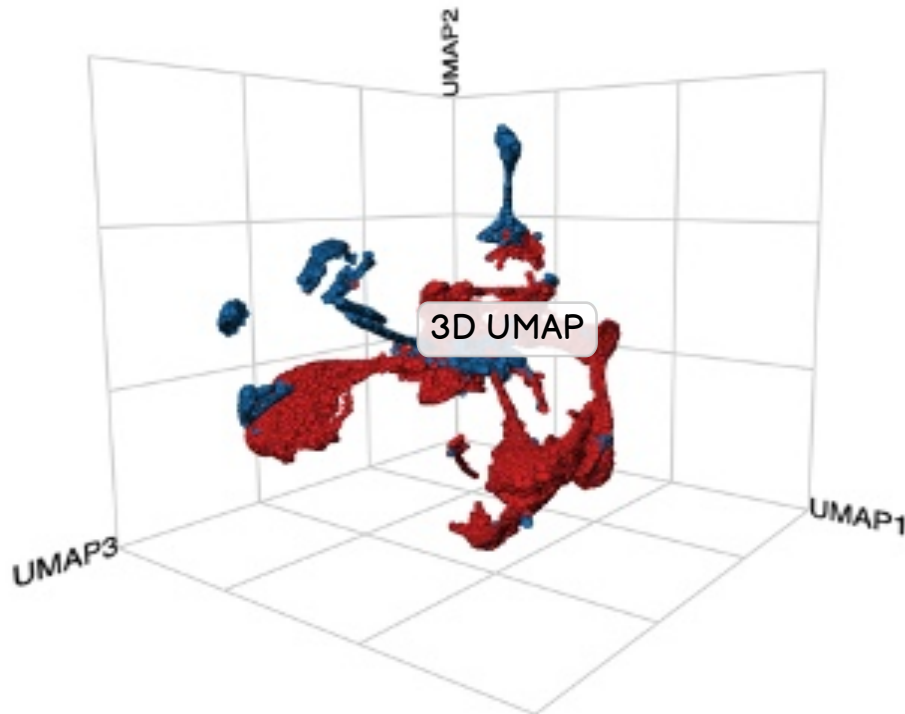


By donor

By cell type/cluster

By cell type/cluster probability

By gene



Legend

 scRNAseq scATACseq

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Metastatic melanoma HTAN Human (Tirosh et. al. 2016) 10x Visium, scRNAseq/scATACseq X

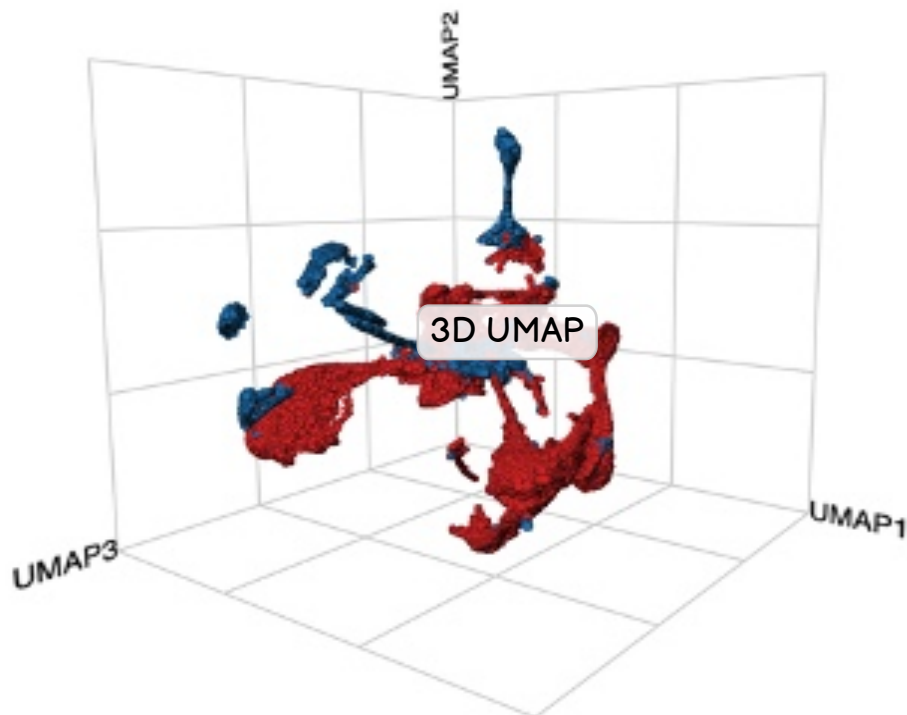
Layout

Color by

Cells in View

Select how to color cells

By donor



Legend

Donor 1

Donor 3

Donor 2

Donor 4



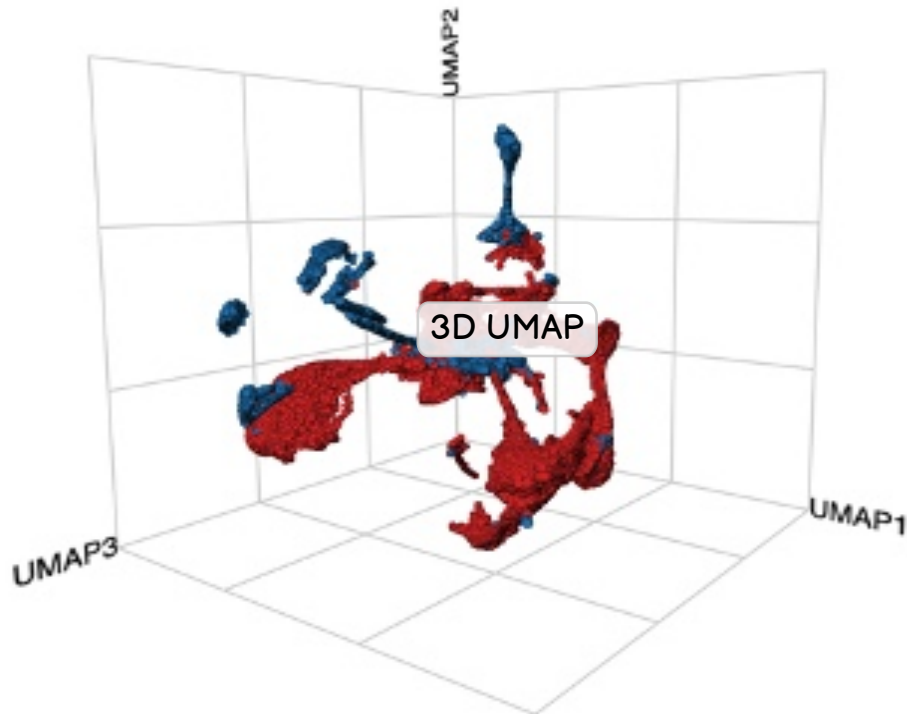
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Metastatic melanoma HTAN Human (Tirosh et. al. 2016) 10x Visium, scRNAseq/scATACseq X

Layout

Color by

Cells in View



Select how to color cells

By cell type/cluster ▼

Select a cell type/cluster

scRNAseq Louvain clusters ▼

Legend

Tumor

Neutrophils

T-cells

B-cells



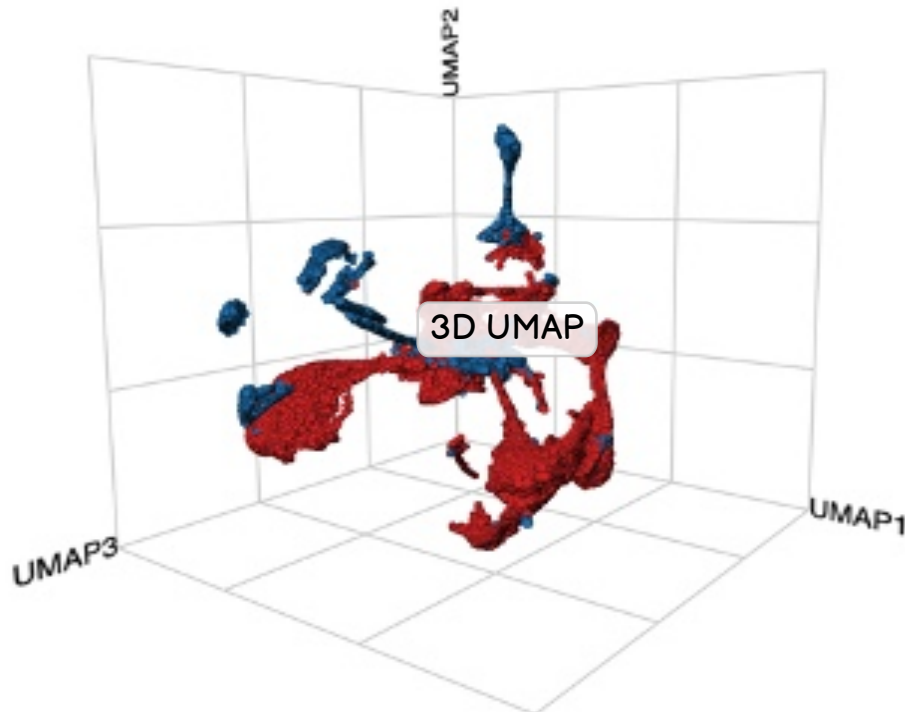
<https://singlecell.xena.net>

Metastatic melanoma HTAN Human (Tirosh et. al. 2016) 10x Visium, scRNAseq/scATACseq X

Layout

Color by

Cells in View



Select how to color cells

By cell type/cluster ▼

Select a cell type/cluster

Select a cell type/cluster ▼

Cell types/clusters ⓘ

scRNAseq cell cluster Louvain ⓘ

scRNAseq cell type Craft et al Science 2021

scATACseq cell cluster Louvain ⓘ

Transferred cell types/clusters ⓘ

scRNAseq -> scATACseq by MARIO ⓘ

Legend



Tumor



T-cells



Neutrophils



B-cells



<https://singlecell.xena.net>

Metastatic melanoma HTAN Human (Tirosh et. al. 2016) 10x Visium, scRNAseq/scATACseq X

Layout

Color by

Cells in View

Select how to color cells

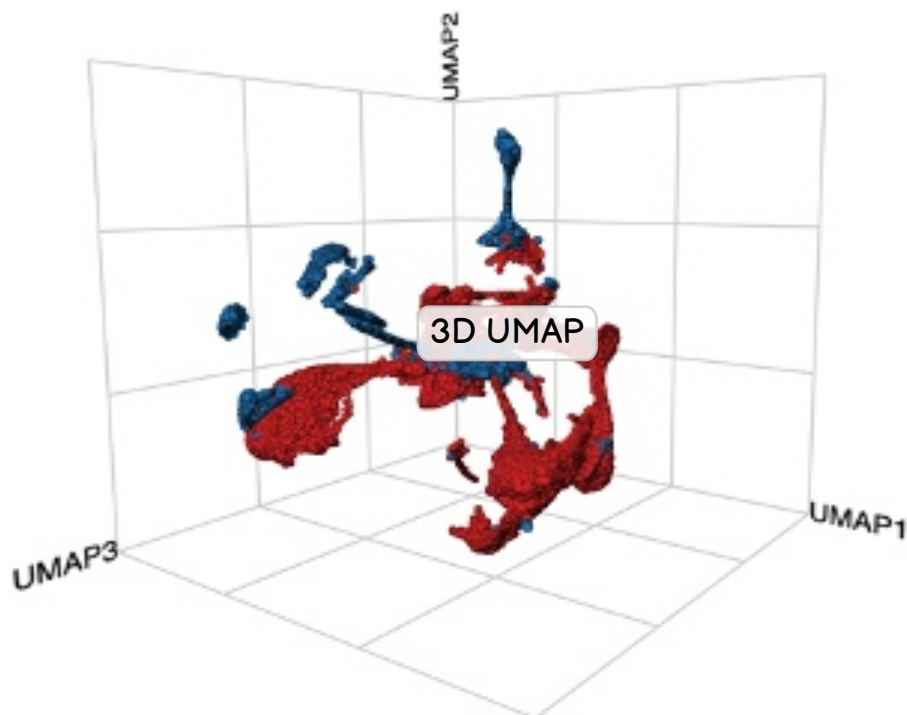
By cell type/cluster probability ▼

Select a transferred cell type/cluster:

scRNAseq -> scATACseq by MARIO ▼

Select cell type:

Select a cell type ▼



Legend

 Tumor

 Neutrophils

 T-cells

 B-cells



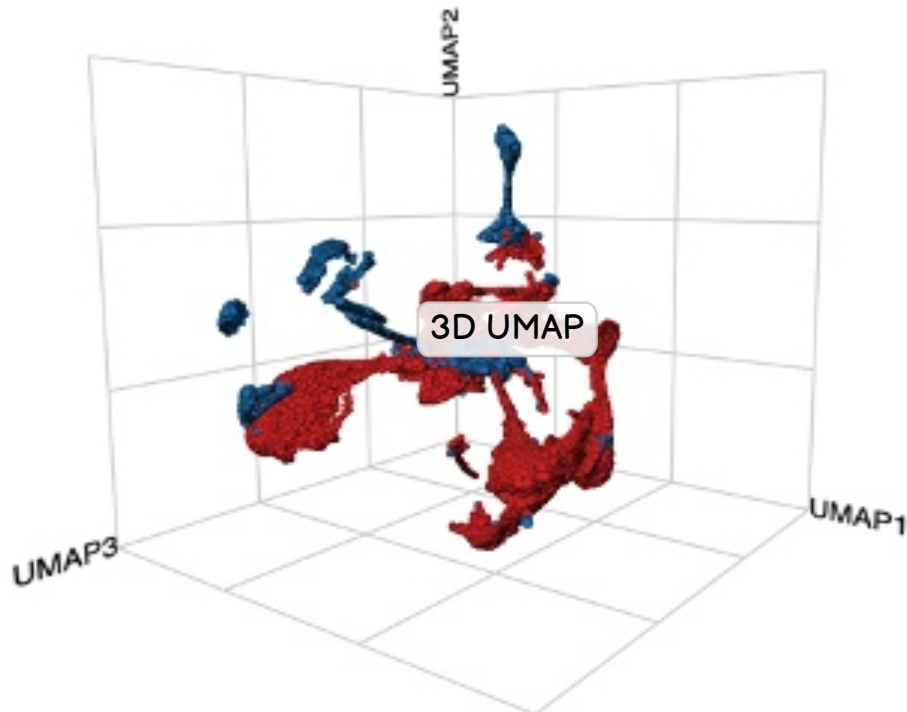
<https://singlecell.xena.net>

Metastatic melanoma HTAN Human (Tirosh et. al. 2016) 10x Visium, scRNAseq/scATACseq X

Layout

Color by

Cells in View



Select how to color cells

By cell type/cluster probability ▼

Select a transferred cell type/cluster:

scRNAseq -> scATACseq by MARIO ▼

Select cell type:

T cell ▼



Legend

T cell

17



35

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Metastatic melanoma HTAN Human (Tirosh et. al. 2016) 10x Visium, scRNAseq/scATACseq X

Layout

Color by

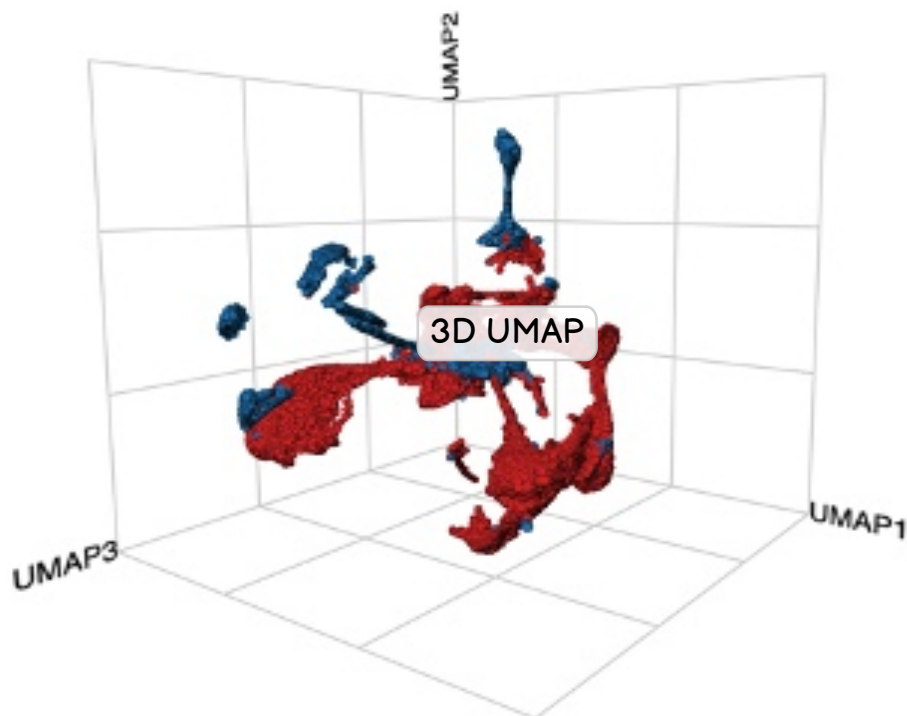
Cells in View

Select how to color cells

By gene expression/ATACseq peak

Select a gene:

Q Gene name



Legend

T cell 17 35

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Metastatic melanoma HTAN Human (Tirosh et. al. 2016) 10x Visium, scRNAseq/scATACseq X

Layout

Color by

Cells in View

Select how to color cells

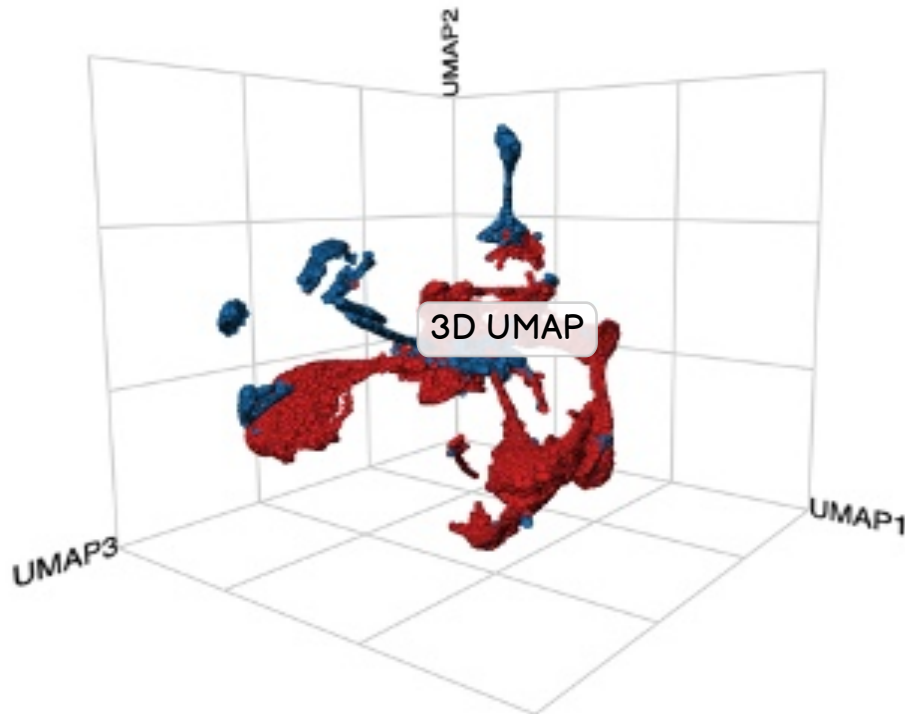
By gene expression/ATACseq peak

Select a gene:

Q PD1

PD1 - gene expression

PD1 - ATACseq peak



Legend

T cell

17



35

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Metastatic melanoma HTAN Human (Tirosh et. al. 2016) 10x Visium, scRNAseq/scATACseq X

Layout

Color by

Cells in View

Select how to color cells

By gene expression/ATACseq peak

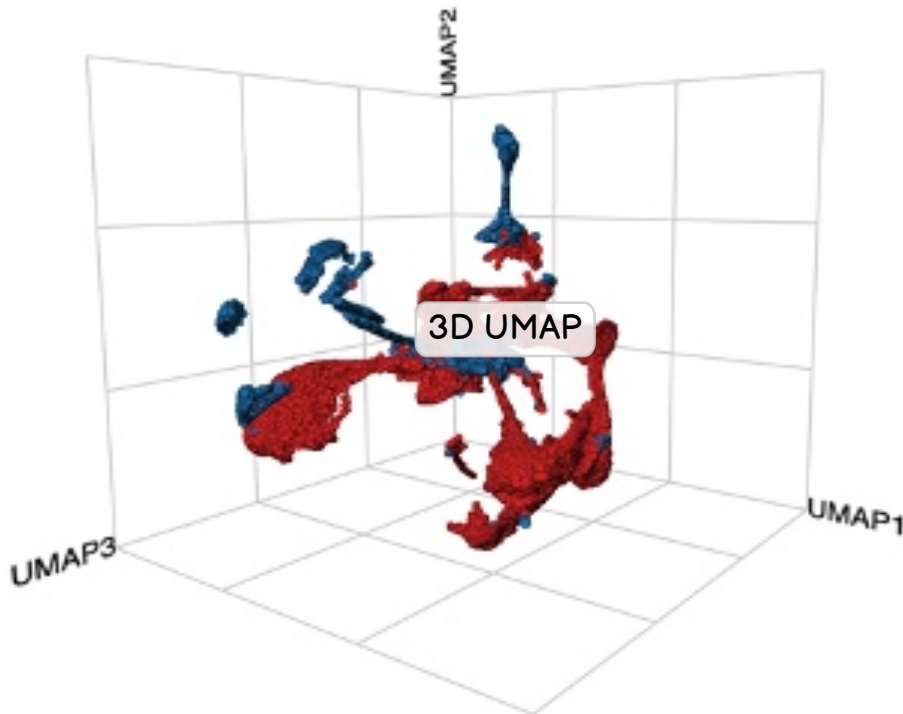
Select a gene:

Q PD1 - gene expression



Legend

PD1 - gen.. 17  35



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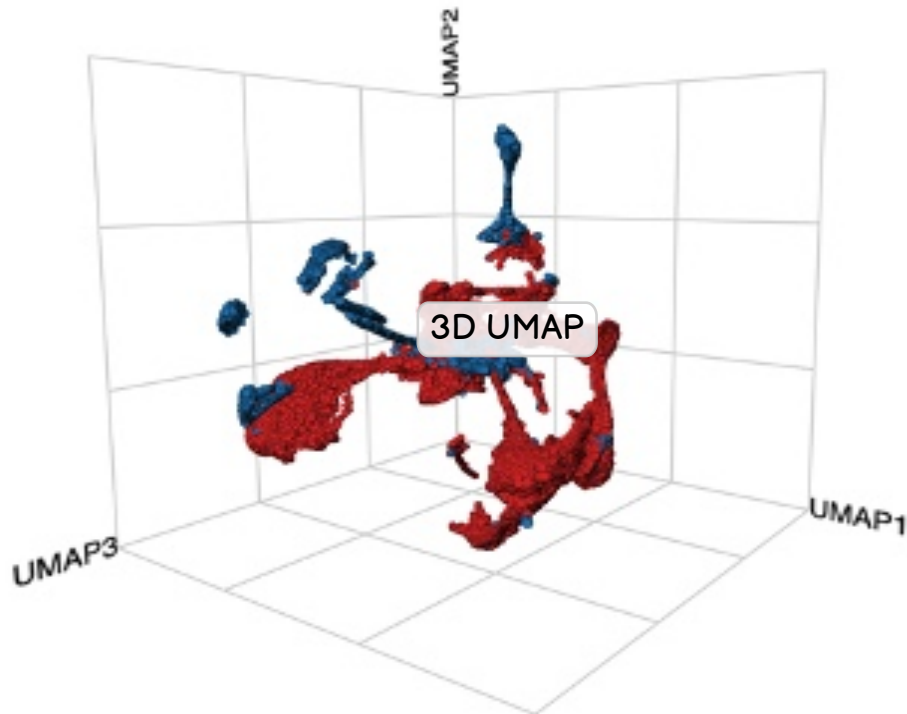
Metastatic melanoma HTAN Human (Tirosh et. al. 2016) 10x Visium, scRNAseq/scATACseq X

Layout

Color by

Cells in View

Select the cells you want to view

☒ All cells

Legend

PD1 - gen.. 17  35

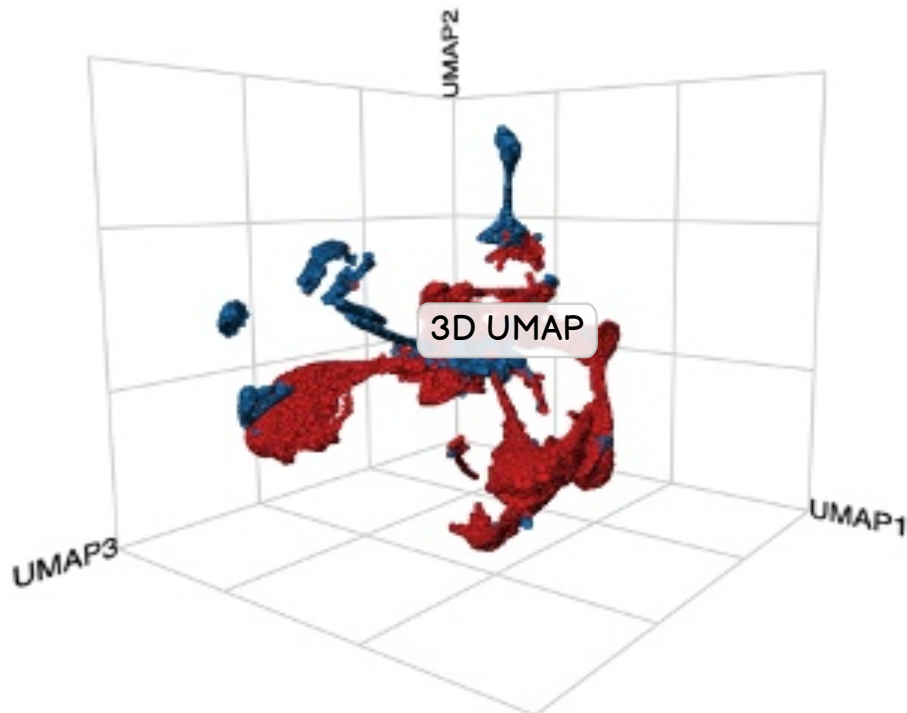
<https://singlecell.xena.net>

Metastatic melanoma HTAN Human (Tirosh et. al. 2016) 10x Visium, scRNAseq/scATACseq X

Layout

Color by

Cells in View



Select a layout type:

☒ UMAP/t-SNE☐ Spatial

Select a UMAP/t-SNE layout:

scRNAseq + scATACseq (Seurat, All cells) ▼

Dot Size:



Legend

PD1 - gen.. 17  35



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Metastatic melanoma HTAN Human (Tirosh et. al. 2016) 10x Visium, scRNAseq/scATACseq X

Layout

Select a layout type:

- ☐ UMAP/t-SNE
- ☒ Spatial

Select a Spatial layout

Select a spatial layout

Select a spatial layout



Legend





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Metastatic melanoma HTAN Human (Tirosh et. al. 2016) 10x Visium, scRNAseq/scATACseq X

Layout

Select a layout type:

- ☐ UMAP/t-SNE
- ☒ Spatial

Select a Spatial layout

Select a spatial layout

Select a spatial layout ▼

Patient 1 Tumor
Patient 1 Normal
Patient 2 Tumor
Patient 2 Normal

Legend

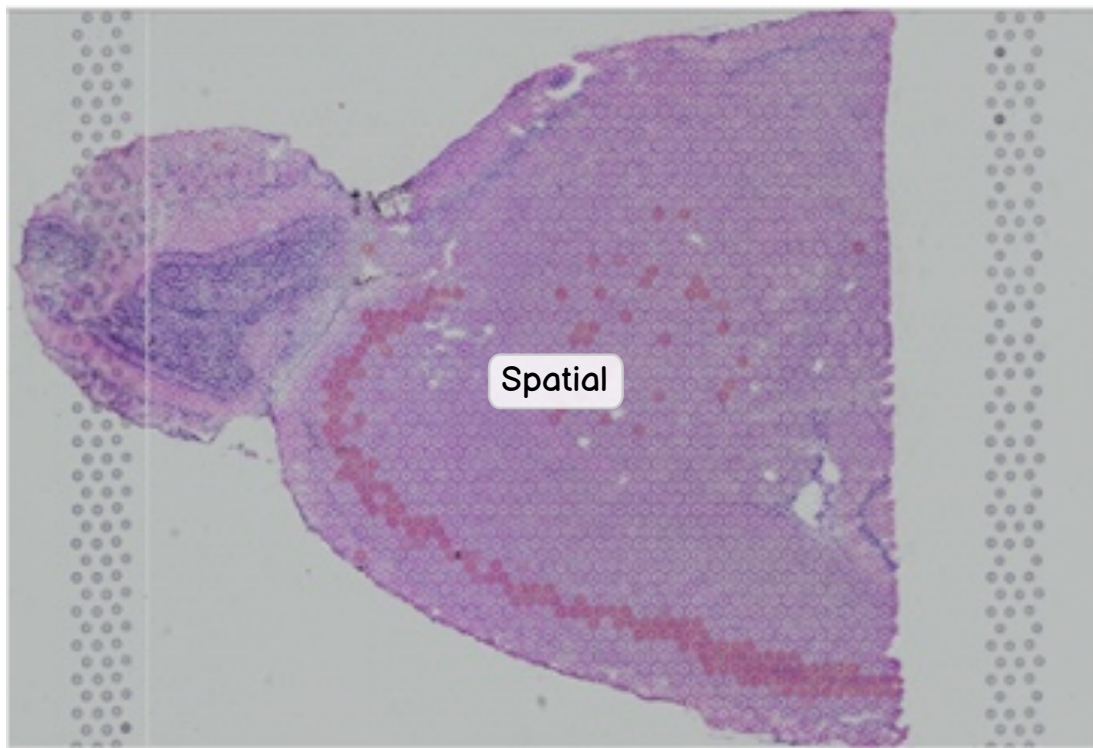
<https://singlecell.xena.net>

Metastatic melanoma HTAN Human (Tirosh et. al. 2016) 10x Visium, scRNAseq/scATACseq X

Layout

Color by

Cells in View



Select a layout type:

☐ UMAP/t-SNE☒ Spatial

Select a spatial layout

Patient 2 Normal

Dot Size:

Legend

 Tumor T-cells Neutrophils B-cells

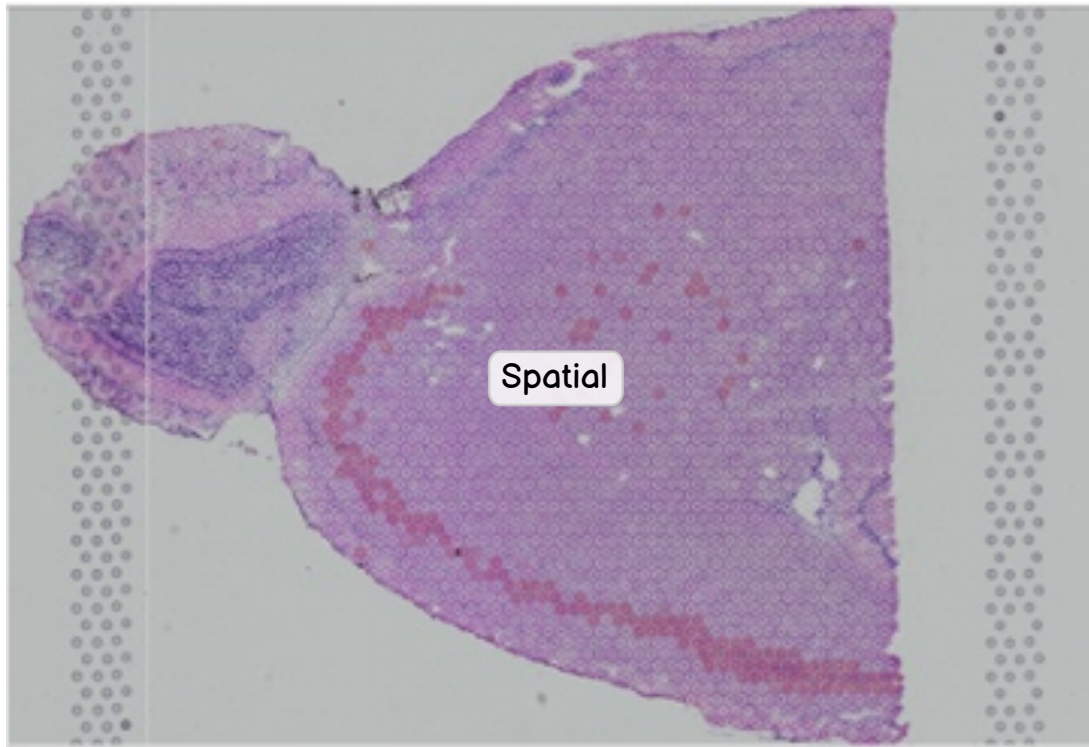
<https://singlecell.xena.net>

Metastatic melanoma HTAN Human (Tirosh et. al. 2016) 10x Visium, scRNAseq/scATACseq X

Layout

Color by

Cells in View



Select how to color cells

By cell type/cluster ▼

Select a cell type/cluster

Visium cell types ▼

Legend



Tumor



T-cells



Neutrophils



B-cells



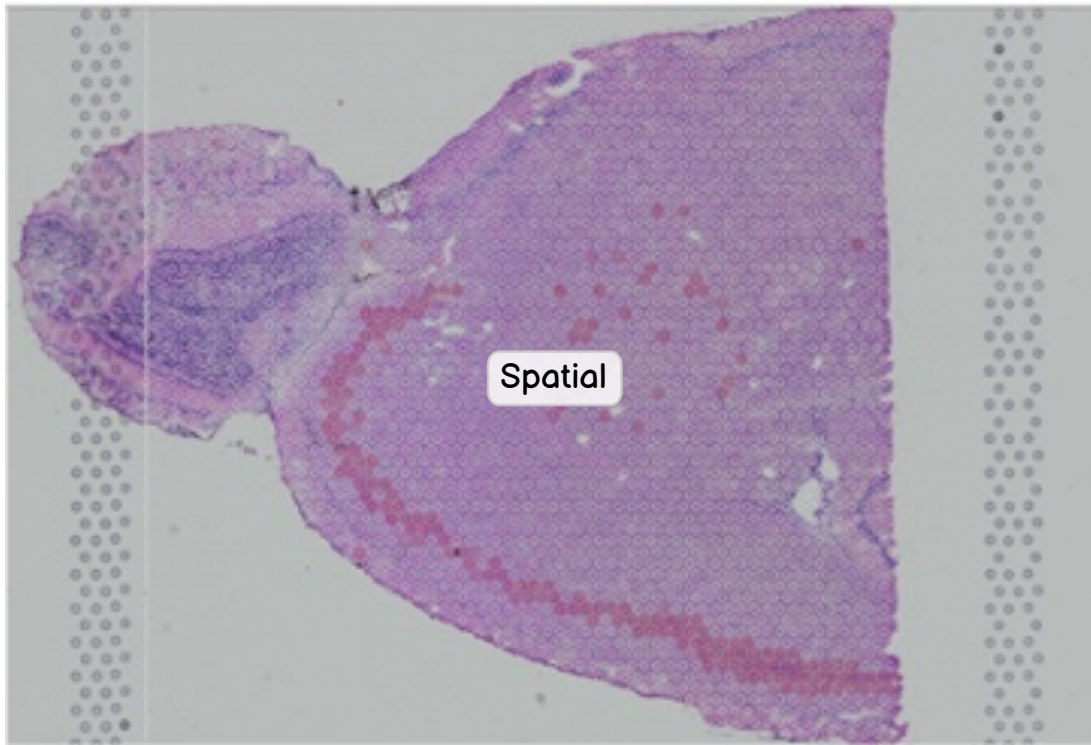
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Metastatic melanoma HTAN Human (Tirosh et. al. 2016) 10x Visium, scRNAseq/scATACseq X

Layout

Color by

Cells in View



Select how to color cells

By cell type/cluster

Select a cell type/cluster

Select a cell type/cluster

Cell types/clusters

Visium cell types

Transferred cell types/clusters

scRNAseq Lieden cell types-> Visium

Legend



Tumor



T-cells



Neutrophils



B-cells



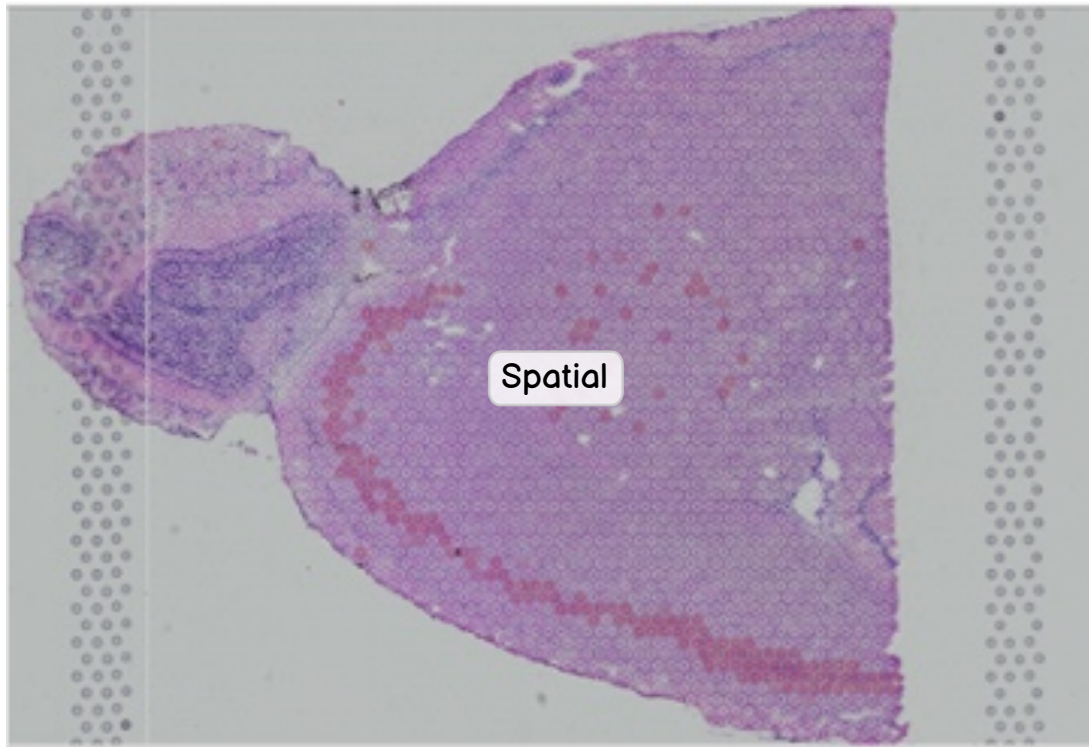
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Layout

Color by

Cells in View



Select how to color cells

By cell type/cluster



Select a cell type/cluster

Visium cell types



Legend



Tumor



T-cells



Neutrophils



B-cells



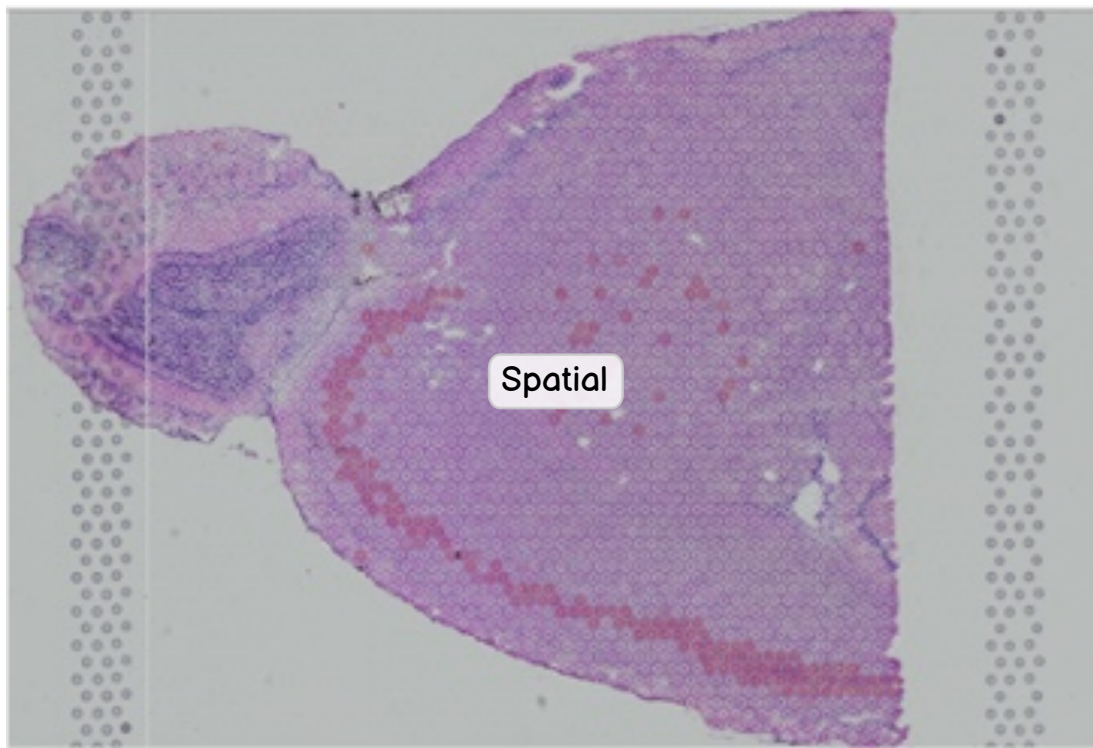
<https://singlecell.xena.net>

Metastatic melanoma HTAN Human (Tirosh et. al. 2016) 10x Visium, scRNAseq/scATACseq X

Layout

Color by

Cells in View



Select how to color cells

By cell type/cluster

By cell type/cluster probability

By gene

Visium cell types

Legend



Tumor



T-cells



Neutrophils



B-cells



<https://singlecell.xena.net>

Metastatic melanoma HTAN Human (Tirosh et. al. 2016) 10x Visium, scRNAseq/scATACseq [x](#)

Layout

Color by

Cells in View

Select how to color cells

By cell type/cluster



By cell type/cluster probability

By gene

Visium cell types



Legend



Tumor



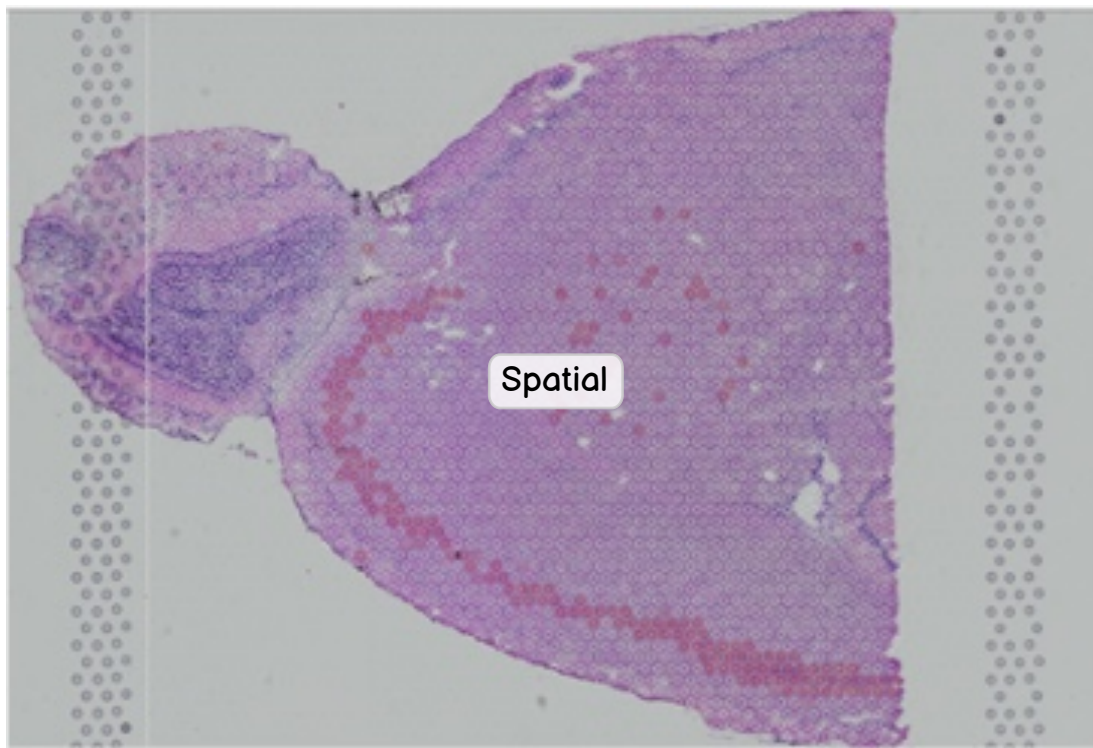
T-cells



Neutrophils



B-cells





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