

a.



K-Means ▼ ⋮

🔍 Recluster

Number of Clusters 7 ▼

- Cluster 1 (2487) ⋮
- Cluster 2 (2047) ⋮
- Cluster 3 (907) ⋮
- Cluster 4 (241) ⋮
- Cluster 5 (195) ⋮
- Cluster 6 (145) ⋮
- Cluster 7 (100) ⋮

Significant Feature Comparison ⊗

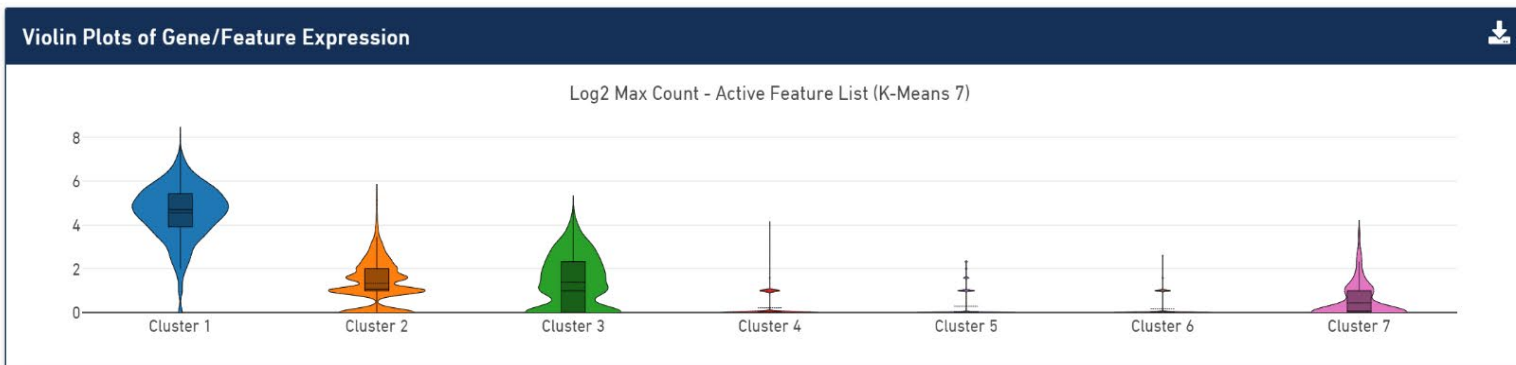
Globally Distinguishing ▼

Feature Type

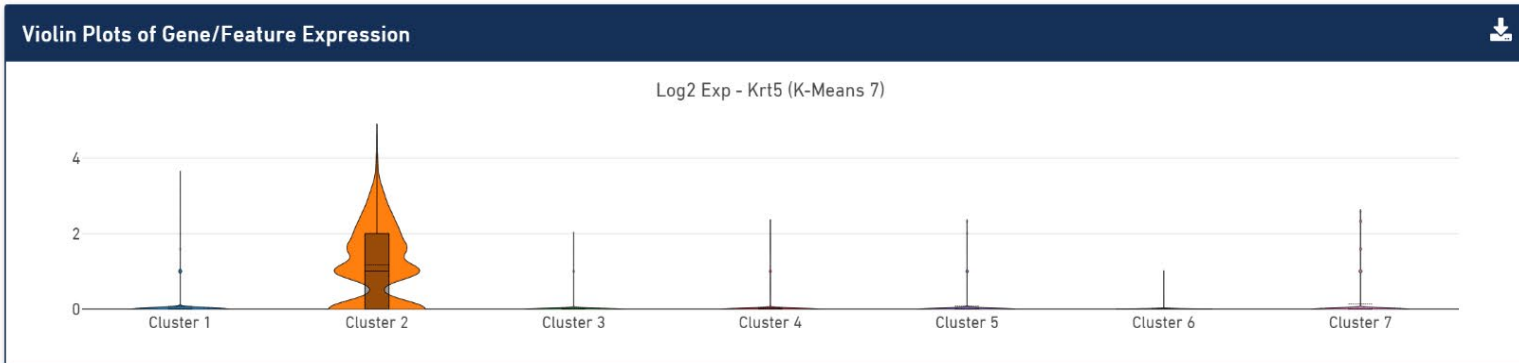
Gene ▼ 📊

Stage: **Gestational**
Animal ID: **G1**
Clustering method: **tSNE**
Clustering: **K-means**

Cluster 1 = **Krt18 high**
Cluster 2 = **Krt5 high**
Cluster 3 = **Krt18 low**
Clusters 4-7 = **other**



b.



Active Feature List

Search for a feature...

Krt5
Gene - ENSMUSG00000061527

Krt18
Gene - ENSMUSG00000023043

Scale & Attribute ⓘ
Log2 Feature Max

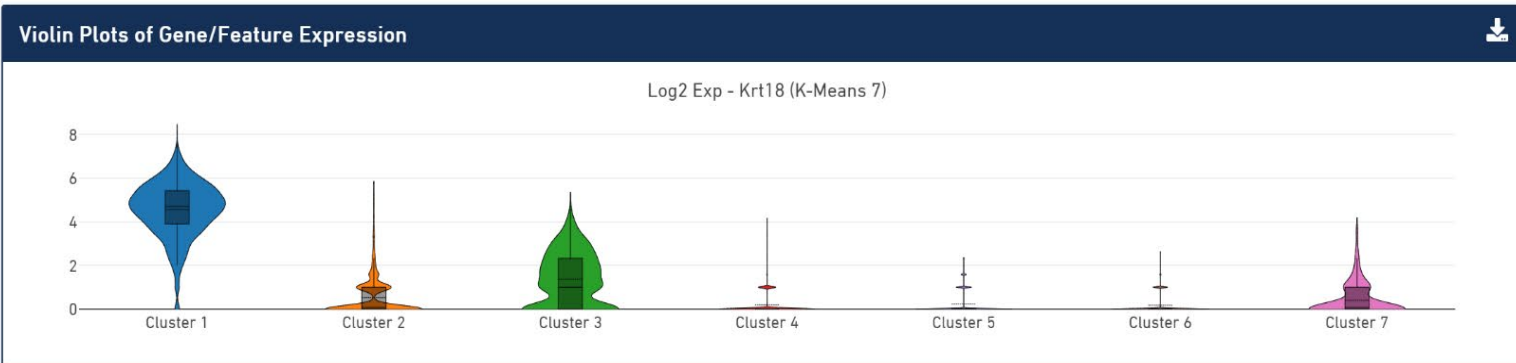
Select by Count - Krt5
> Enter a Number

Log2 Exp - Krt5
0.0 5.0

Stage: **Gestational**
Animal ID: **G1**
Clustering method: **tSNE**
Clustering: **Krt5**

Cluster 1 = **Krt18 high**
Cluster 2 = **Krt5 high**
Cluster 3 = **Krt18 low**
Clusters 4-7 = **other**

C.



Active Feature List

Search for a feature...

Krt5
Gene - ENSMUSG00000061527

Krt18
Gene - ENSMUSG00000023043

Scale & Attribute ⓘ

Log2 Feature Max

Select by Count - Krt18

> Enter a Number

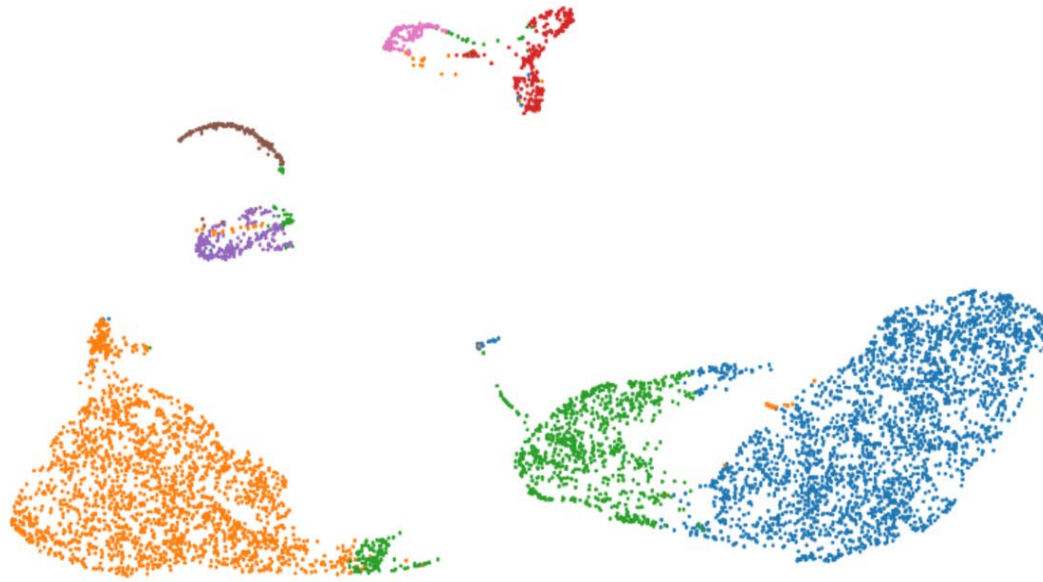
Log2 Exp - Krt18

0.0 8.0

Stage: **Gestational**
Animal ID: **G1**
Clustering method: **tSNE**
Clustering: **Krt18**

Cluster 1 = **Krt18 high**
Cluster 2 = **Krt5 high**
Cluster 3 = **Krt18 low**
Clusters 4-7 = **other**

d.



K-Means Recluster

Number of Clusters:

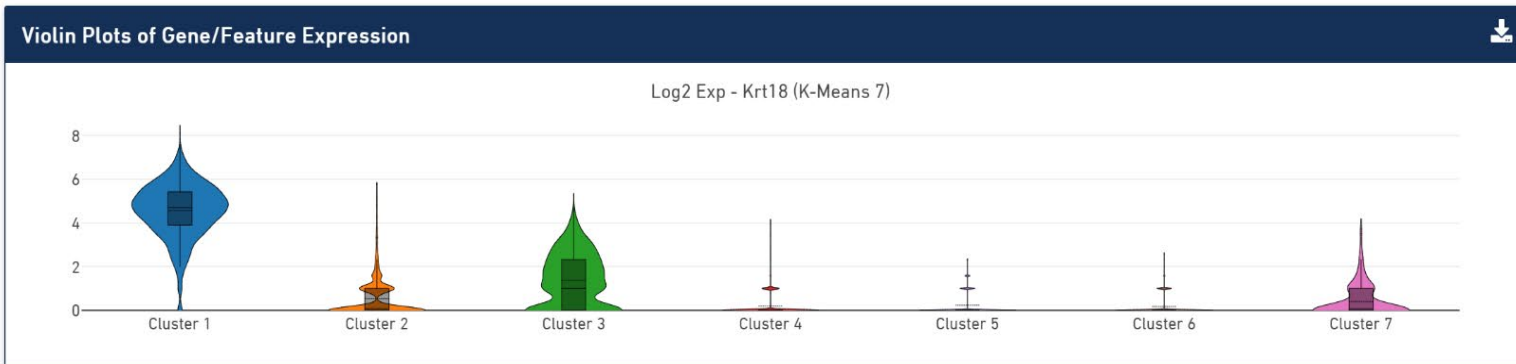
- Cluster 1 (2487)
- Cluster 2 (2047)
- Cluster 3 (907)
- Cluster 4 (241)
- Cluster 5 (195)
- Cluster 6 (145)
- Cluster 7 (100)

Significant Feature Comparison
Globally Distinguishing

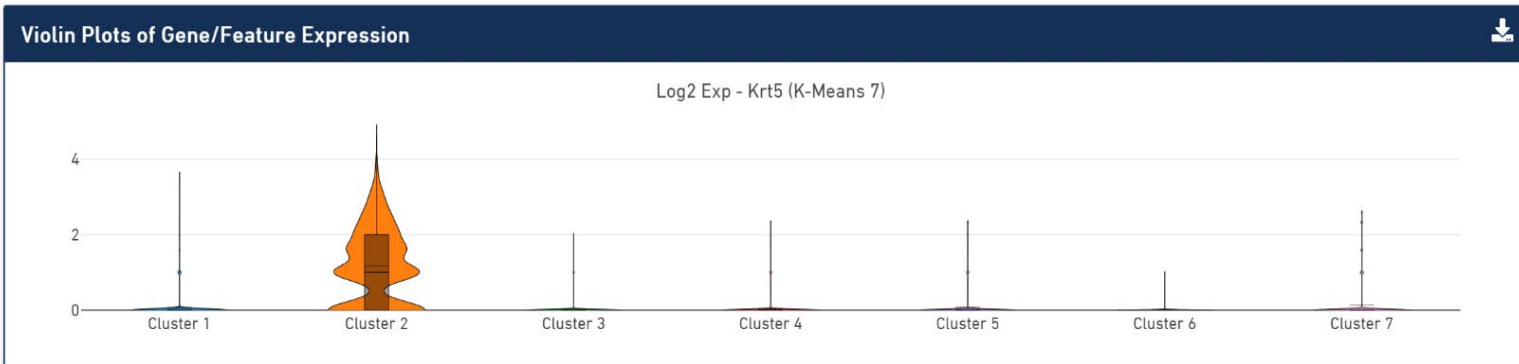
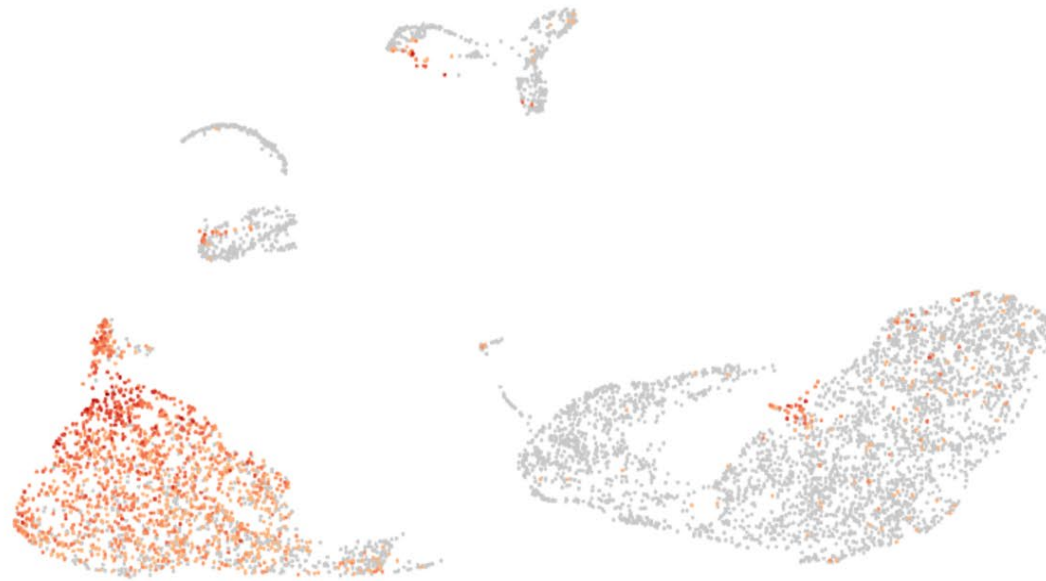
Feature Type
Gene

Stage: **Gestational**
Animal ID: **G1**
Clustering method: **UMAP**
Clustering : **K-means**

Cluster 1 = **Krt18 high**
Cluster 2 = **Krt5 high**
Cluster 3 = **Krt18 low**
Clusters 4-7 = **other**



e.



Active Feature List

Search for a feature...

Krt5
Gene - ENSMUSG00000061527

Krt18
Gene - ENSMUSG00000023043

Scale & Attribute ⓘ
Log2 Feature Max

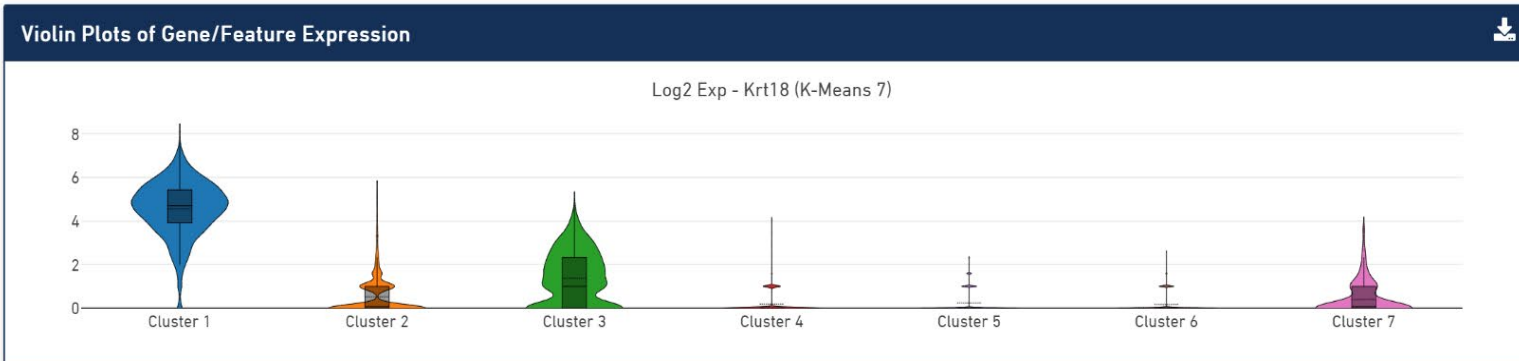
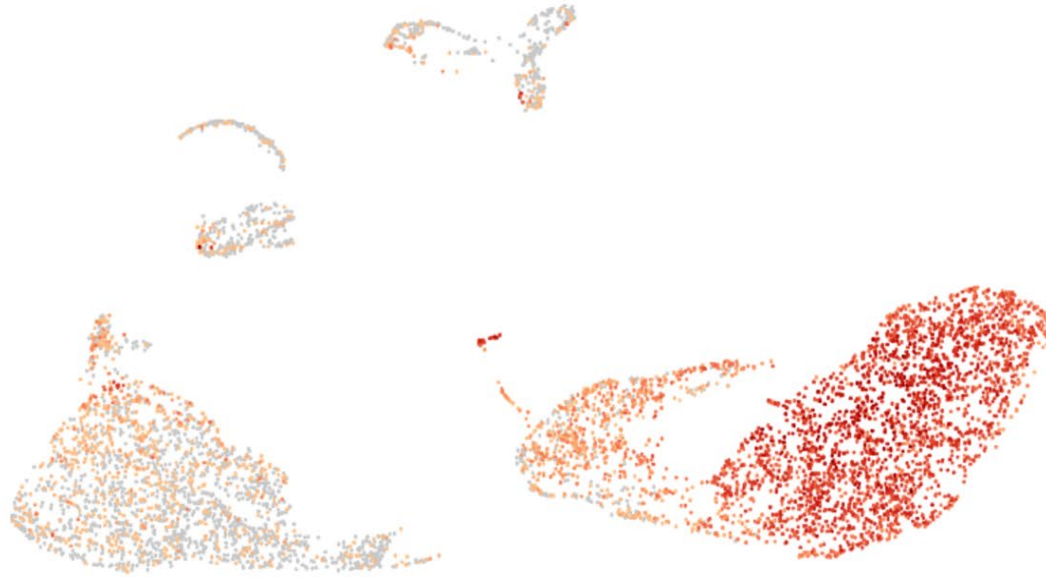
Select by Count - Krt5
> Enter a Number

Log2 Exp - Krt5
0.0 5.0

Stage: **Gestational**
Animal ID: **G1**
Clustering method: **UMAP**
Clustering: **Krt5**

Cluster 1 = **Krt18 high**
Cluster 2 = **Krt5 high**
Cluster 3 = **Krt18 low**
Clusters 4-7 = **other**

f.



Active Feature List

Search for a feature...

Krt5
Gene - ENSMUSG00000061527

Krt18
Gene - ENSMUSG00000023043

Scale & Attribute

Log2 Feature Max

Select by Count - Krt18

> Enter a Number

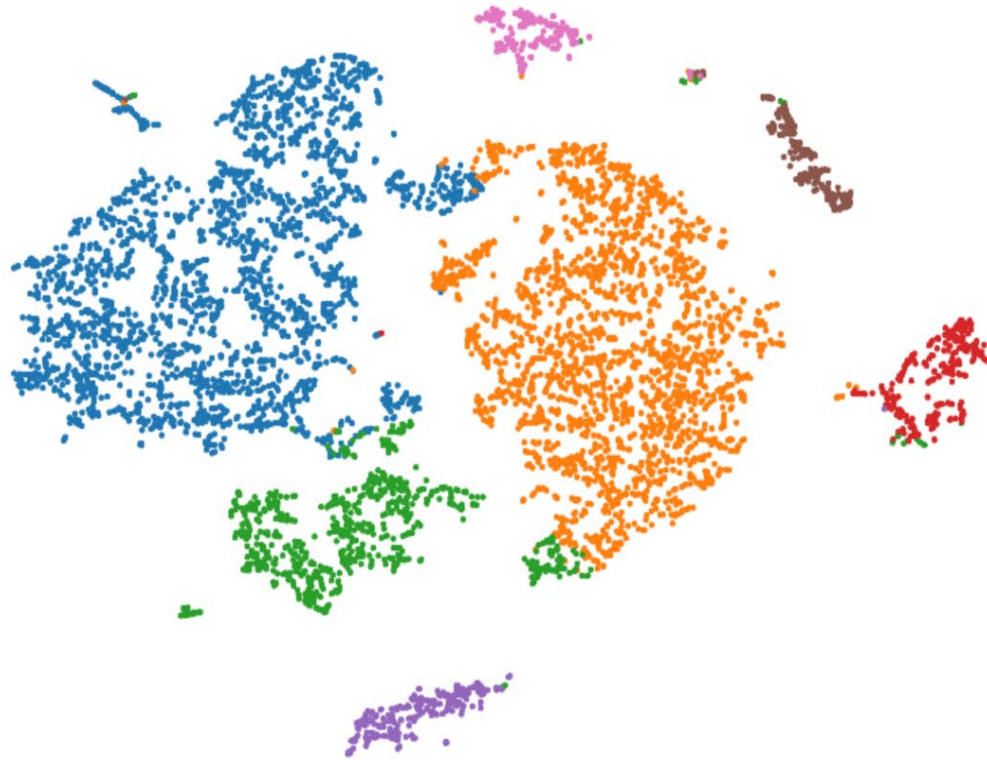
Log2 Exp - Krt18

0.0 8.0

Stage: **Gestational**
Animal ID: **G1**
Clustering method: **UMAP**
Clustering: **Krt18**

Cluster 1 = **Krt18 high**
Cluster 2 = **Krt5 high**
Cluster 3 = **Krt18 low**
Clusters 4-7 = **other**

g.



K-Means ⌵ ⋮

🔍 Recluster

Number of Clusters 7 ⌵

- Cluster 1 (2506) ⋮
- Cluster 2 (2259) ⋮
- Cluster 3 (758) ⋮
- Cluster 4 (280) ⋮
- Cluster 5 (241) ⋮
- Cluster 6 (210) ⋮
- Cluster 7 (189) ⋮

Significant Feature Comparison ⊗

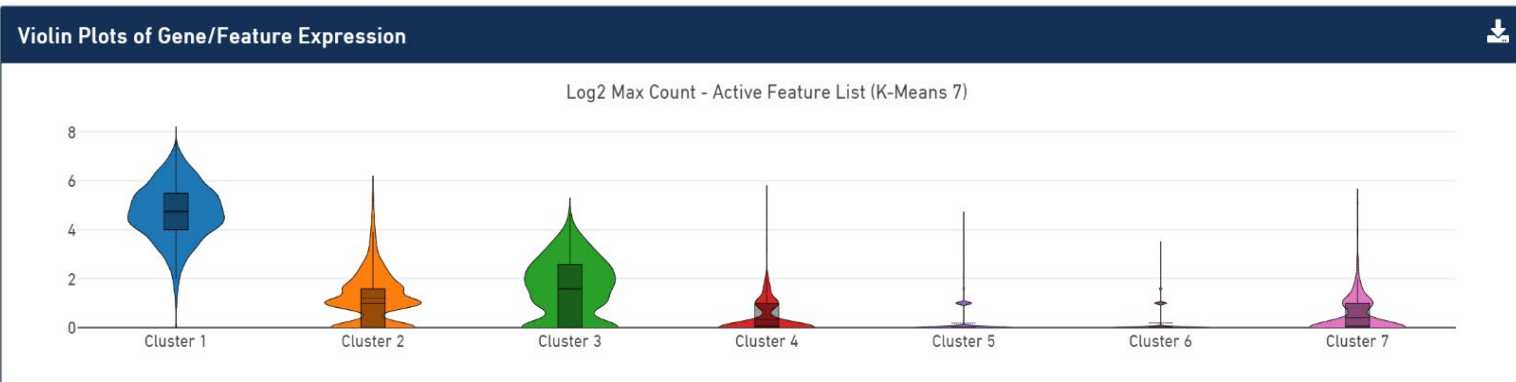
Globally Distinguishing ⌵

Feature Type

Gene ⌵ 📊

Stage: **Gestational**
Animal ID: **G2**
Clustering method: **tSNE**
Clustering: **K-means**

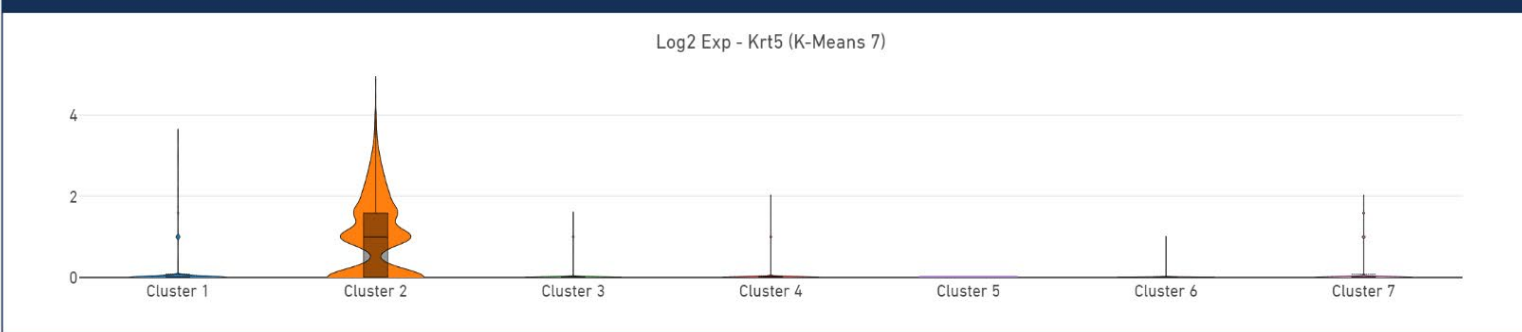
Cluster 1 = **Krt18 high**
Cluster 2 = **Krt5 high**
Cluster 3 = **Krt18 low**
Clusters 4-7 = **other**



h.



Violin Plots of Gene/Feature Expression



Active Feature List

Search for a feature...

Krt5
Gene · ENSMUSG00000061527

Krt18
Gene · ENSMUSG00000023043

Scale & Attribute

Log2 Feature Max

Select by Count - Krt5

> Enter a Number

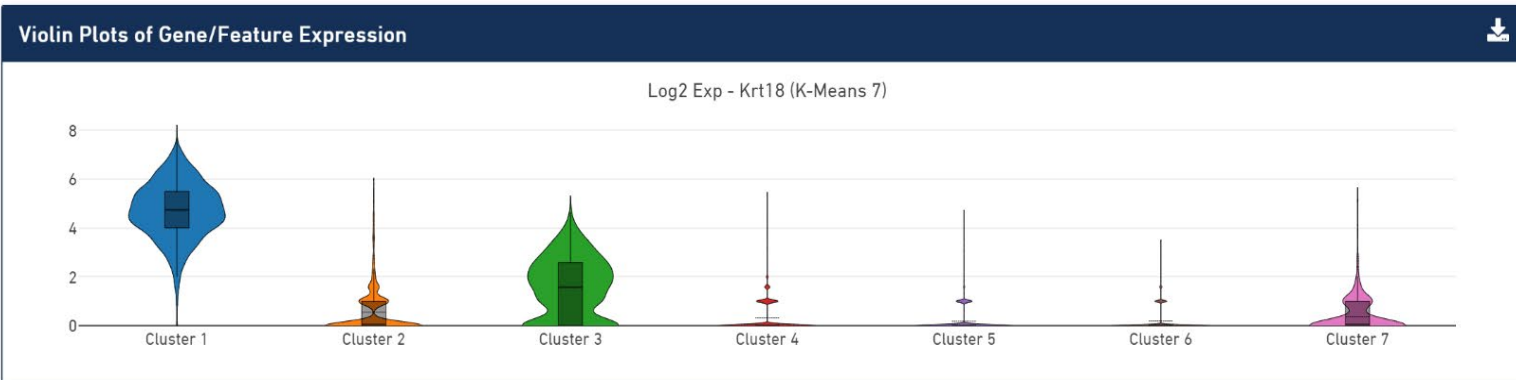
Log2 Exp - Krt5

0.0 5.0

Stage: **Gestational**
Animal ID: **G2**
Clustering method: **tSNE**
Clustering: **Krt5**

Cluster 1 = **Krt18 high**
Cluster 2 = **Krt5 high**
Cluster 3 = **Krt18 low**
Clusters 4-7 = **other**

i.



Active Feature List

Search for a feature...

Krt5
Gene · ENSMUSG00000061527

Krt18
Gene · ENSMUSG00000023043

Scale & Attribute

Log2 Feature Max

Select by Count - Krt18

> Enter a Number

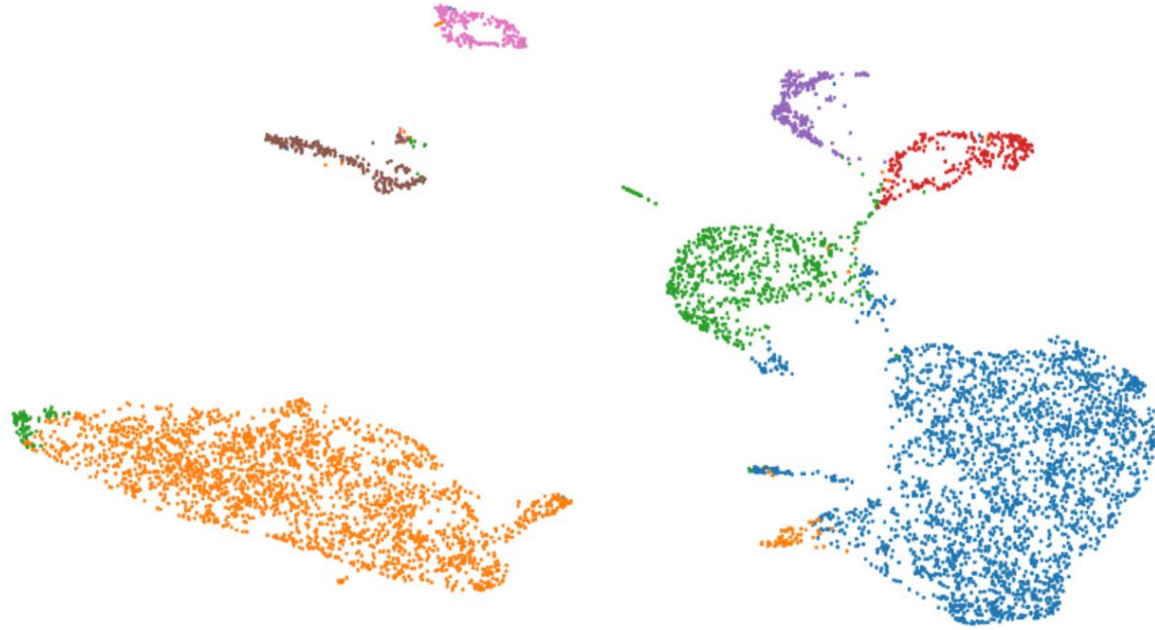
Log2 Exp - Krt18

0.0 8.0

Stage: **Gestational**
Animal ID: **G2**
Clustering method: **tSNE**
Clustering: **Krt18**

Cluster 1 = **Krt18 high**
Cluster 2 = **Krt5 high**
Cluster 3 = **Krt18 low**
Clusters 4-7 = **other**

j.



K-Means ▼ ⋮

🔄 Recluster

Number of Clusters ▼

- Cluster 1 (2506) ⋮
- Cluster 2 (2259) ⋮
- Cluster 3 (758) ⋮
- Cluster 4 (280) ⋮
- Cluster 5 (241) ⋮
- Cluster 6 (210) ⋮
- Cluster 7 (189) ⋮

Significant Feature Comparison ⊗

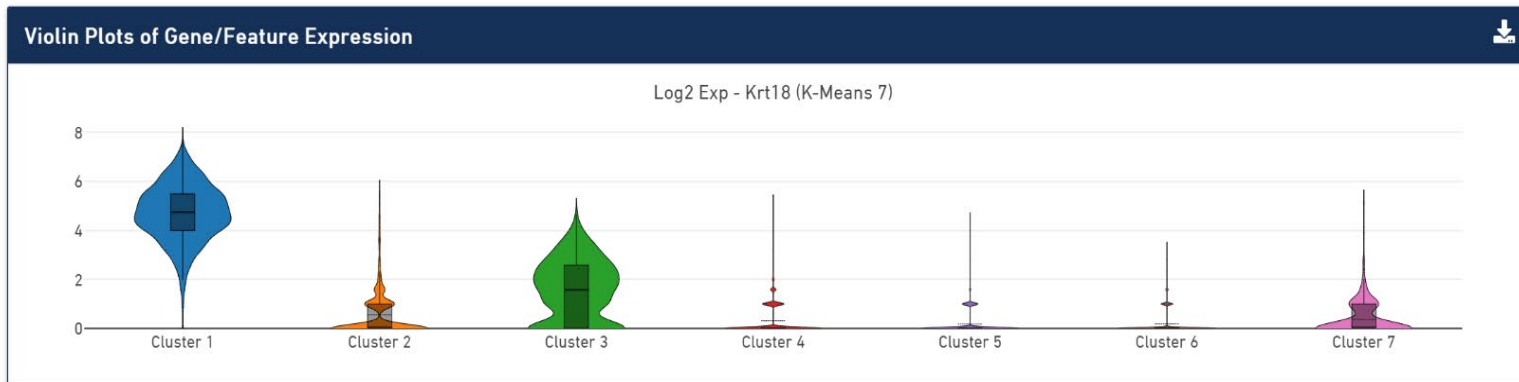
Globally Distinguishing ▼

Feature Type

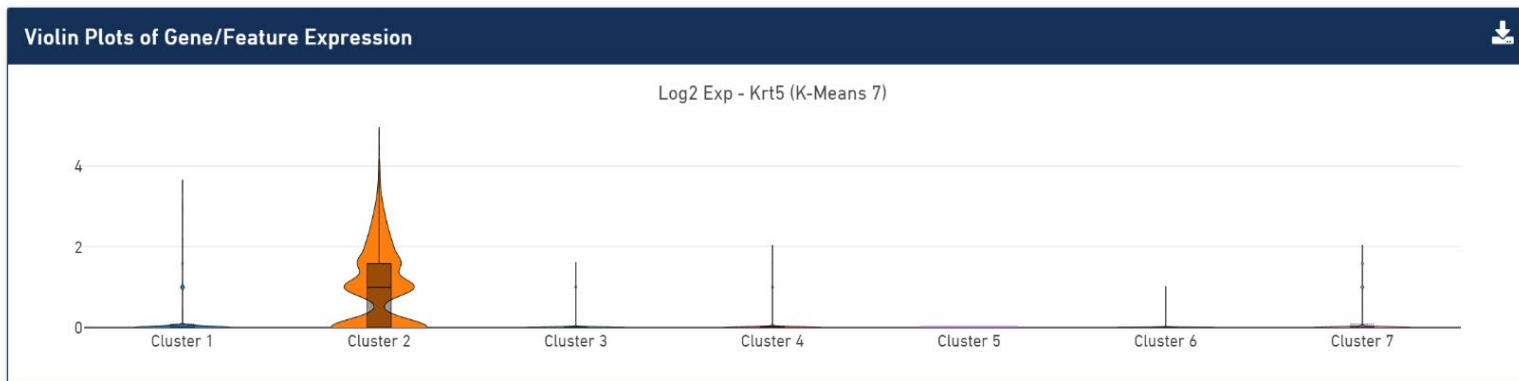
Gene ▼ 📊

Stage: **Gestational**
Animal ID: **G2**
Clustering method: **UMAP**
Clustering: **K-means**

Cluster 1 = **Krt18 high**
Cluster 2 = **Krt5 high**
Cluster 3 = **Krt18 low**
Clusters 4-7 = **other**



k.



Active Feature List

Search for a feature...

Krt5
Gene · ENSMUSG00000061527

Krt18
Gene · ENSMUSG00000023043

Scale & Attribute

Log2 Feature Max

Select by Count - Krt5

> Enter a Number

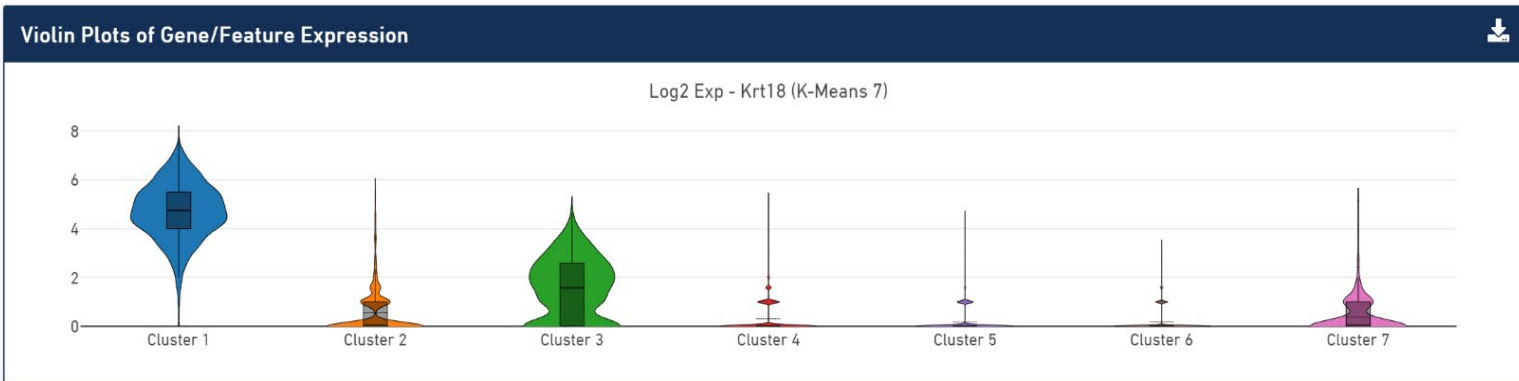
Log2 Exp - Krt5

0.0 5.0

Stage: **Gestational**
Animal ID: **G2**
Clustering method: **UMAP**
Clustering: **Krt5**

Cluster 1 = **Krt18 high**
Cluster 2 = **Krt5 high**
Cluster 3 = **Krt18 low**
Clusters 4-7 = **other**

I.



Active Feature List

Search for a feature...

Krt5
Gene · ENSMUSG00000061527

Krt18
Gene · ENSMUSG00000023043

Scale & Attribute

Log2 Feature Max

Select by Count - Krt18

> Enter a Number

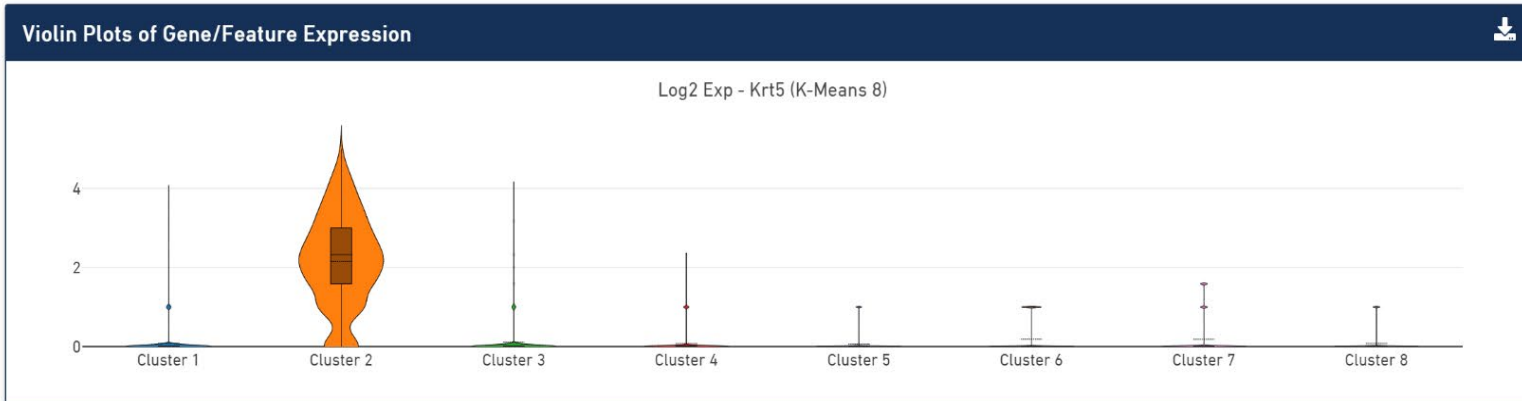
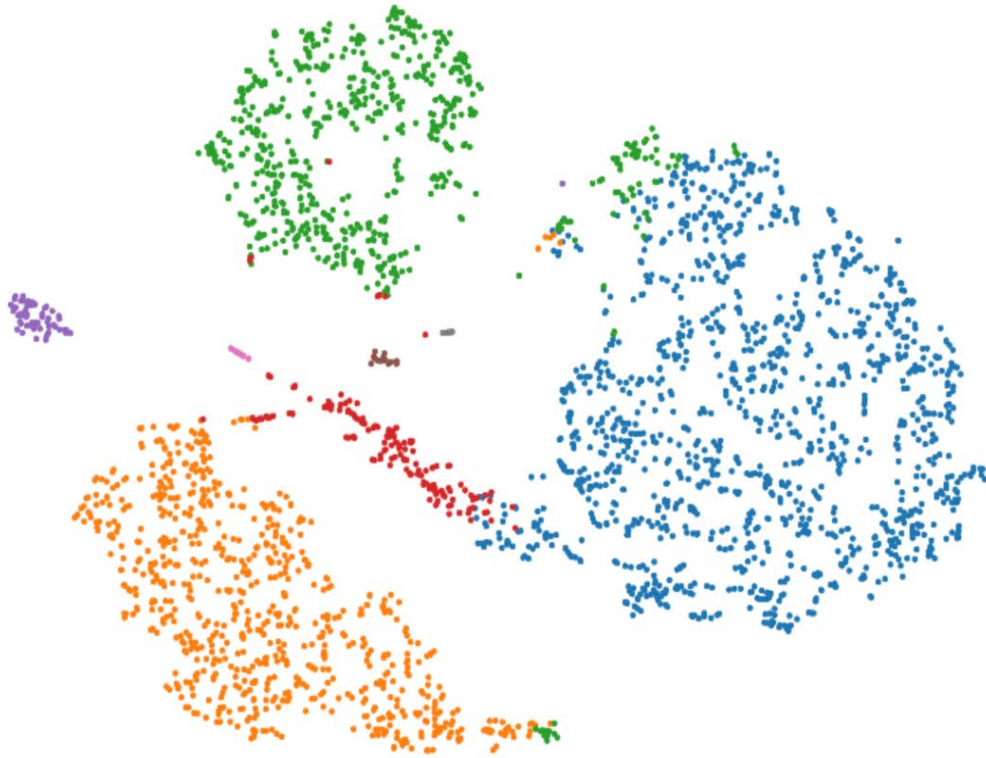
Log2 Exp - Krt18

0.0 8.0

Stage: **Gestational**
Animal ID: **G2**
Clustering method: **UMAP**
Clustering: **Krt18**

Cluster 1 = **Krt18 high**
Cluster 2 = **Krt5 high**
Cluster 3 = **Krt18 low**
Clusters 4-7 = **other**

m.



K-Means Recluster

Number of Clusters: 8

- Cluster 1 (1296)
- Cluster 2 (750)
- Cluster 3 (630)
- Cluster 4 (154)
- Cluster 5 (62)
- Cluster 6 (16)
- Cluster 7 (14)
- Cluster 8 (13)

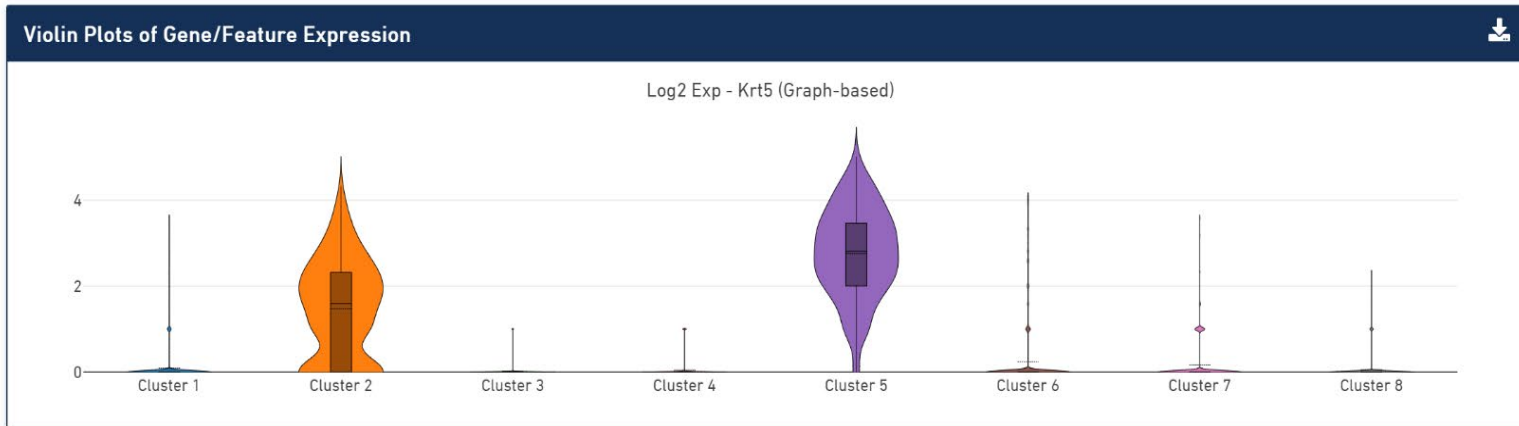
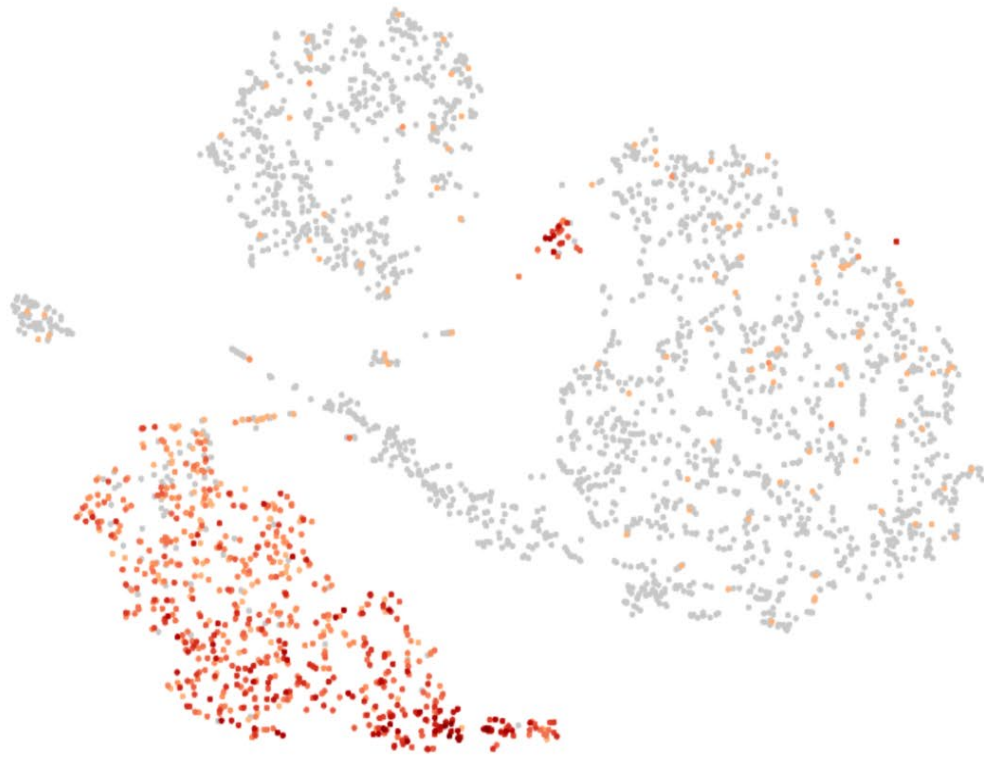
Significant Feature Comparison: Globally Distinguishing

Feature Type: Gene

Stage: **Nulliparous**
Animal ID: **NP1**
Clustering method: **tSNE**
Clustering: **K-means**

Cluster 1,3 = Krt18 high
Cluster 2 = Krt5 high
Cluster 4,5 = Krt18 low
Cluster 6-8 = other

n.



Active Feature List

Search for a feature...

Krt5
Gene · ENSMUSG00000061527

Krt18
Gene · ENSMUSG00000023043

Scale & Attribute

Log2 Feature Max

Select by Count - Krt5

> Enter a Number

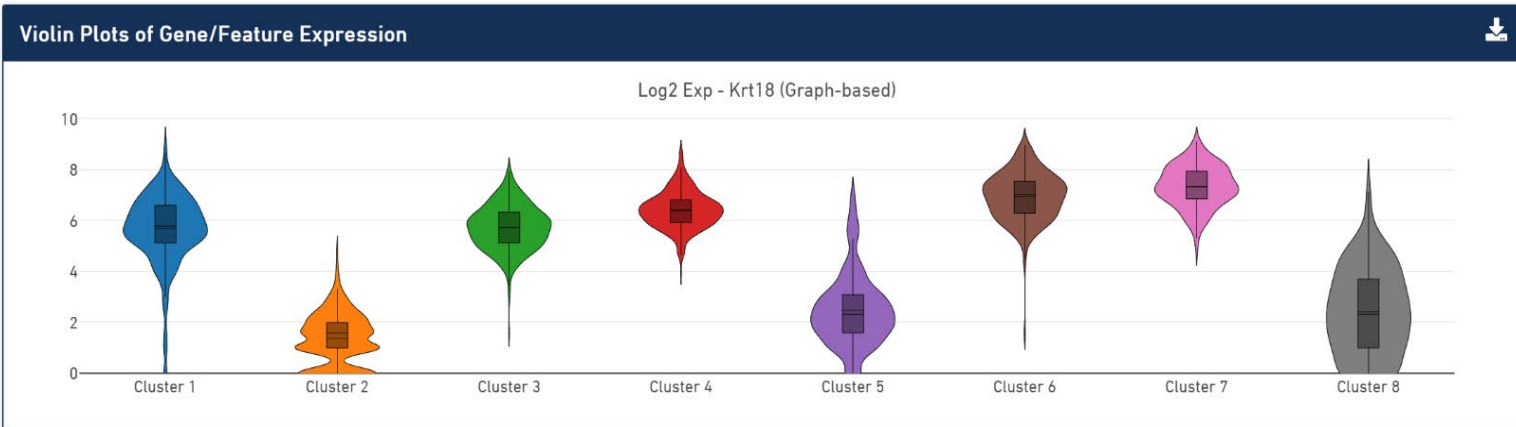
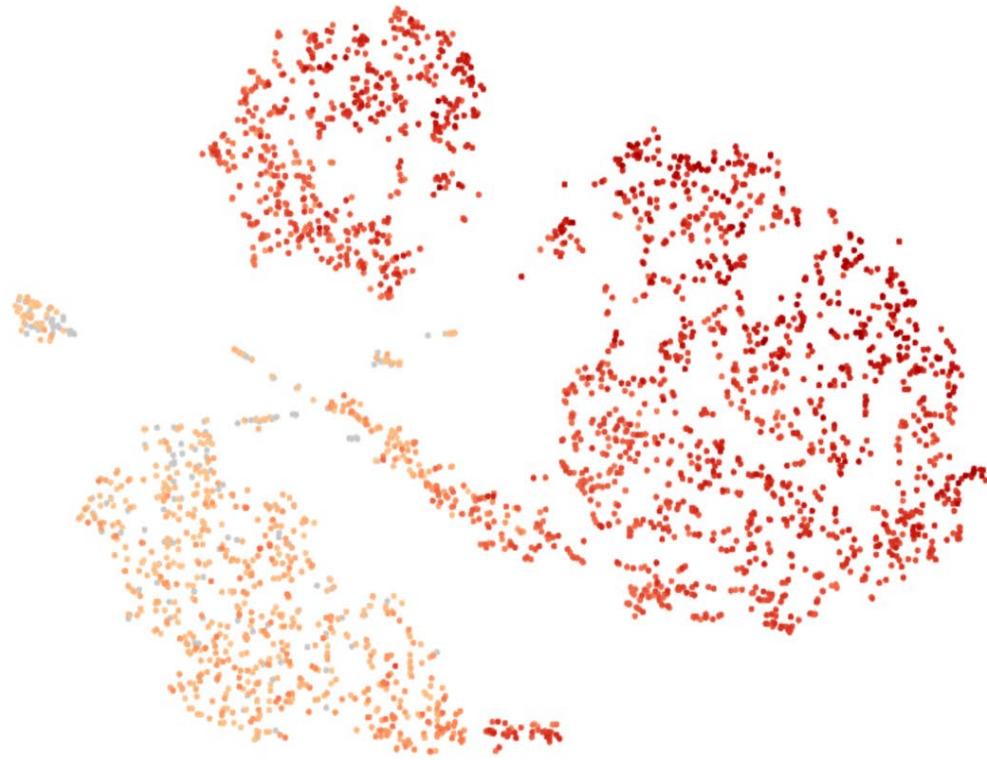
Log2 Exp - Krt5

0.0 5.0

Stage: **Nulliparous**
Animal ID: **NP1**
Clustering method: **tSNE**
Clustering: **Krt5**

Cluster 1,3 = **Krt18 high**
Cluster 2 = **Krt5 high**
Cluster 4,5 = **Krt18 low**
Cluster 6-8 = **other**

O.



Active Feature List

Search for a feature...

Krt5
Gene - ENSMUSG00000061527

Krt18
Gene - ENSMUSG00000023043

Scale & Attribute

Log2 Feature Max

Select by Count - Krt18

> Enter a Number

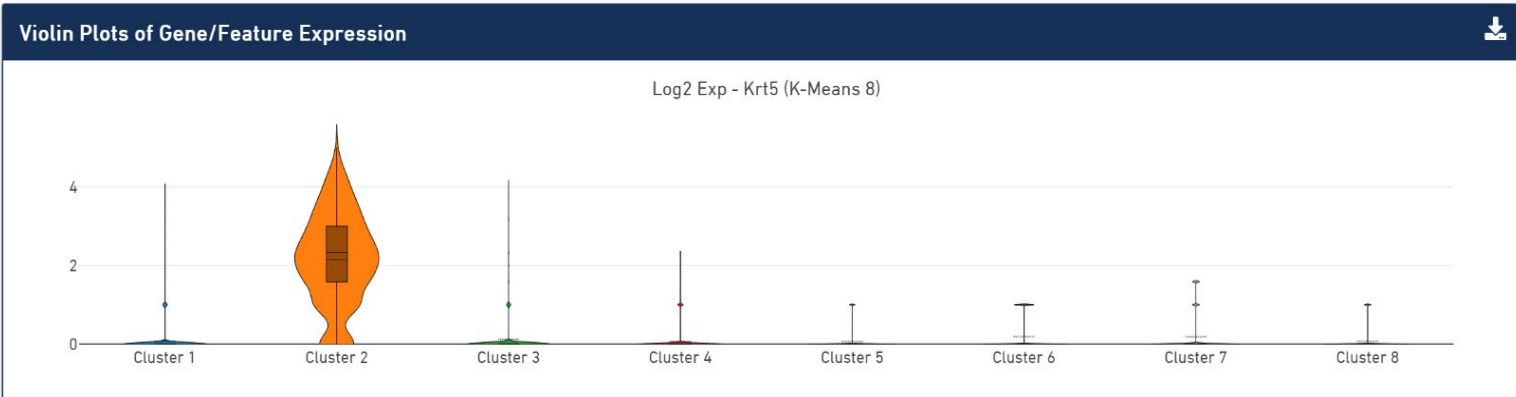
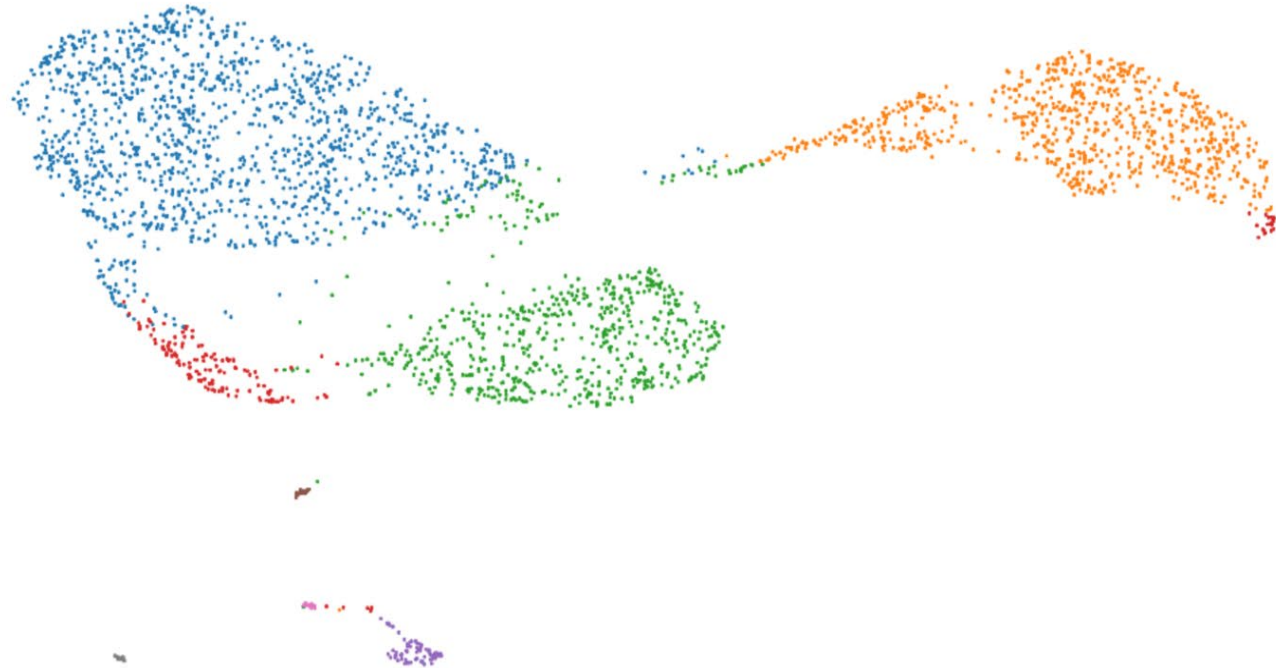
Log2 Exp - Krt18

0.0 10.0

Stage: **Nulliparous**
Animal ID: **NP1**
Clustering method: **tSNE**
Clustering: **Krt18**

Cluster 1,3 = **Krt18 high**
Cluster 2 = **Krt5 high**
Cluster 4,5 = **Krt18 low**
Cluster 6-8 = **other**

p.



K-Means

Recluster

Number of Clusters: 8

- Cluster 1 (1296)
- Cluster 2 (750)
- Cluster 3 (630)
- Cluster 4 (154)
- Cluster 5 (62)
- Cluster 6 (16)
- Cluster 7 (14)
- Cluster 8 (13)

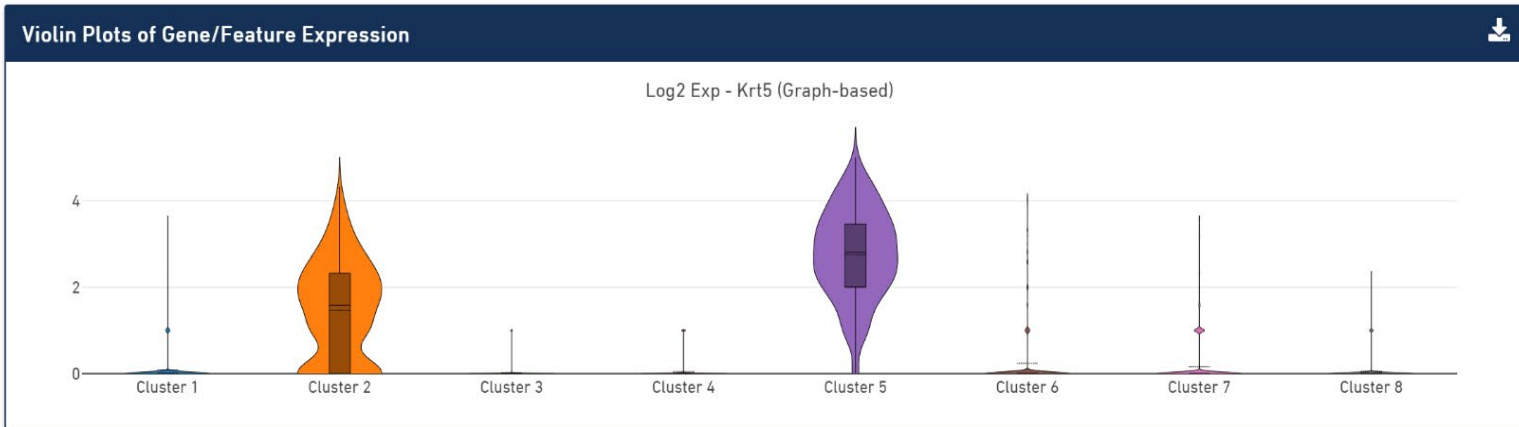
Significant Feature Comparison: Globally Distinguishing

Feature Type: Gene

Stage: **Nulliparous**
Animal ID: **NP1**
Clustering method: **UMAP**
Clustering: **K-means**

Cluster 1,3 = **Krt18 high**
Cluster 2 = **Krt5 high**
Cluster 4,5 = **Krt18 low**
Cluster 6-8 = **other**

q.



Active Feature List

Search for a feature...

Krt5
Gene - ENSMUSG000000061527

Krt18
Gene - ENSMUSG000000023043

Scale & Attribute

Log2 Feature Max

Select by Count - Krt5

> Enter a Number

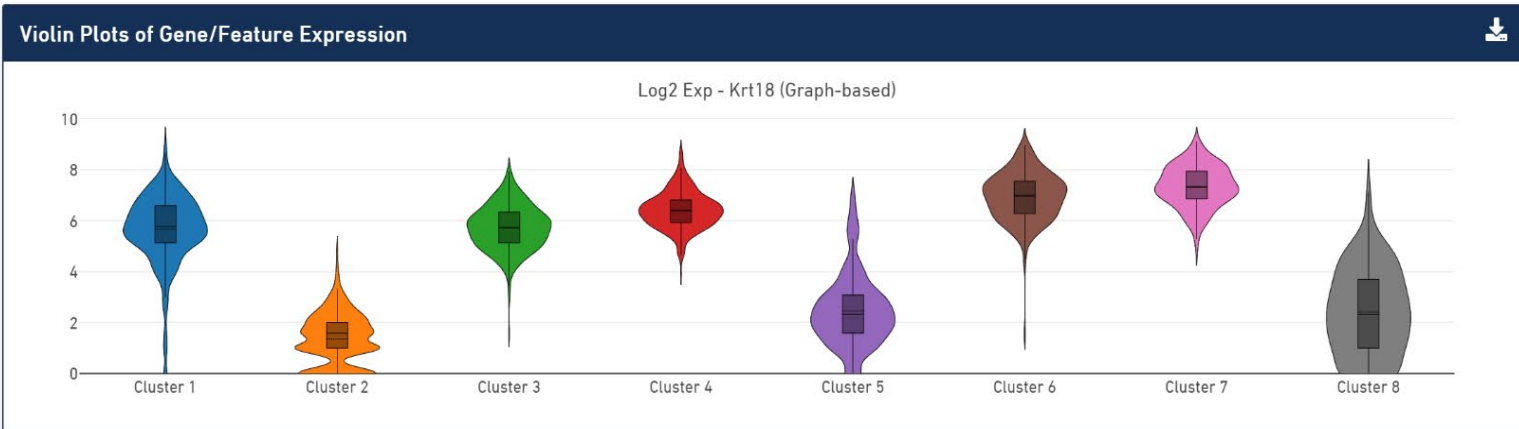
Log2 Exp - Krt5

0.0 5.0

Stage: **Nulliparous**
Animal ID: **NP1**
Clustering method: **UMAP**
Clustering: **Krt5**

Cluster 1,3 = **Krt18 high**
Cluster 2 = **Krt5 high**
Cluster 4,5 = **Krt18 low**
Cluster 6-8 = **other**

r.



Active Feature List

Search for a feature...

Krt5
Gene - ENSMUSG00000061527

Krt18
Gene - ENSMUSG00000023043

Scale & Attribute

Log2 Feature Max

Select by Count - Krt18

> Enter a Number

Log2 Exp - Krt18

0.0 10.0

Stage: **Nulliparous**
Animal ID: **NP1**
Clustering method: **UMAP**
Clustering: **Krt18**

Cluster 1,3 = **Krt18 high**
Cluster 2 = **Krt5 high**
Cluster 4,5 = **Krt18 low**
Cluster 6-8 = **other**

S.



K-Means ▼ ⋮

🔄 Recluster

Number of Clusters 7 ▼

- Cluster 1 (1448) ⋮
- Cluster 2 (444) ⋮
- Cluster 3 (321) ⋮
- Cluster 4 (135) ⋮
- Cluster 5 (103) ⋮
- Cluster 6 (28) ⋮
- Cluster 7 (19) ⋮

Significant Feature Comparison ⊗

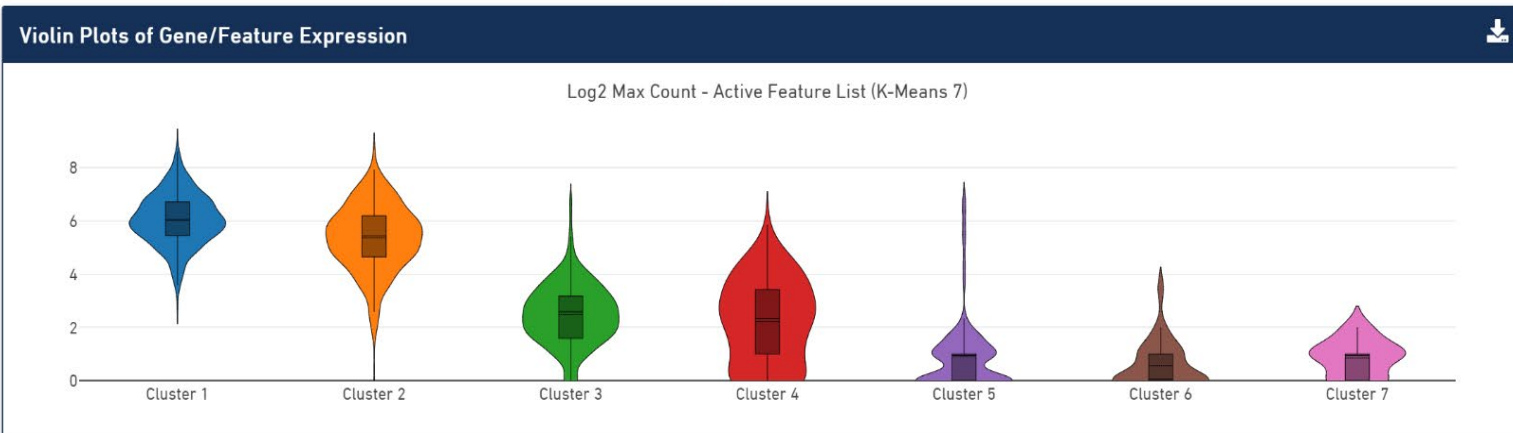
Globally Distinguishing ▼

Feature Type

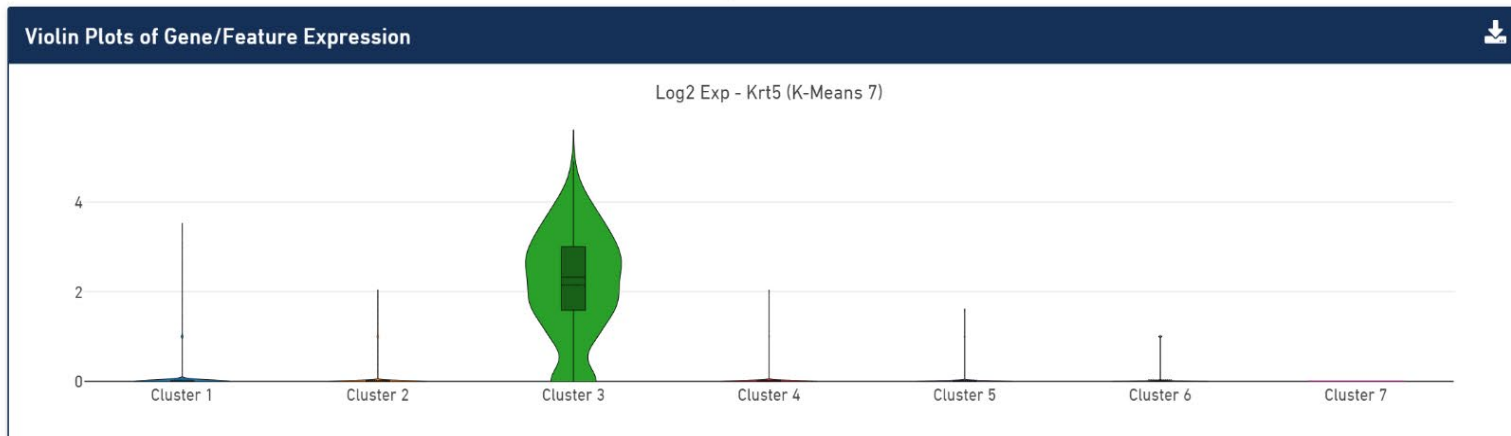
Gene ▼ 📊

Stage: **Nulliparous**
Animal ID: **NP2**
Clustering method: **tSNE**
Clustering: **K-means**

Cluster 1,2 = Krt18 high
Cluster 3= Krt5 high
Cluster 4,5 = Krt18 low
Cluster 6-8 = other



t.



Active Feature List

Search for a feature...

Krt5
Gene - ENSMUSG00000061527

Krt18
Gene - ENSMUSG00000023043

Scale & Attribute

Log2 Feature Max

Select by Count - Krt5

> Enter a Number

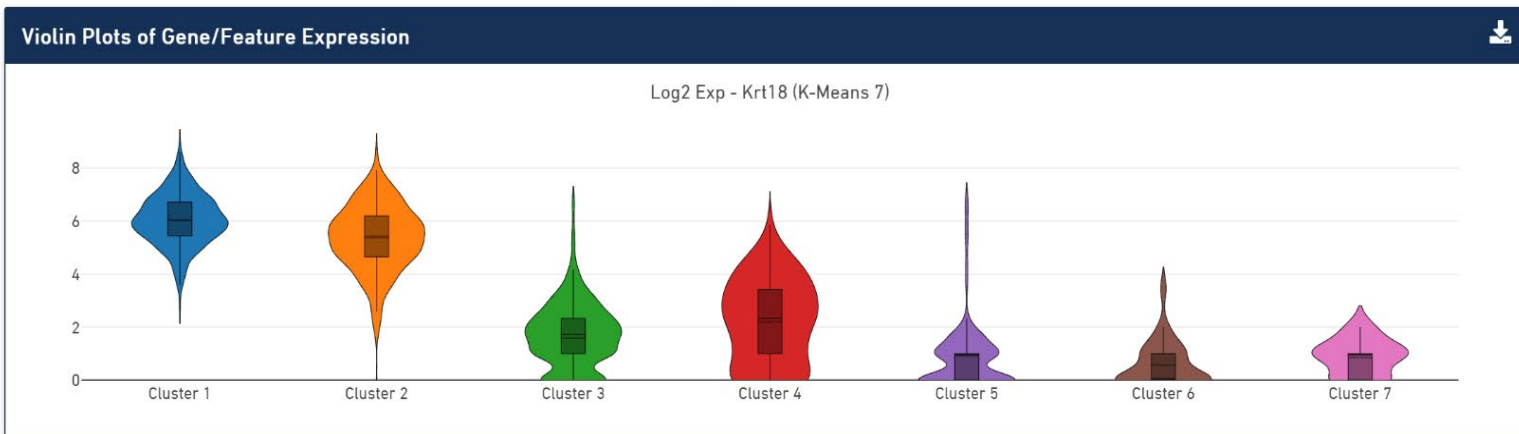
Log2 Exp - Krt5

0.0 5.0

Stage: **Nulliparous**
Animal ID: **NP2**
Clustering method: **tSNE**
Clustering: **Krt5**

Cluster 1,2 = **Krt18 high**
Cluster 3 = **Krt5 high**
Cluster 4,5 = **Krt18 low**
Cluster 6-8 = **other**

U.



Active Feature List

Search for a feature...

Krt5
Gene - ENSMUSG00000061527

Krt18
Gene - ENSMUSG00000023043

Scale & Attribute

Log2 Feature Max

Select by Count - Krt18

> Enter a Number

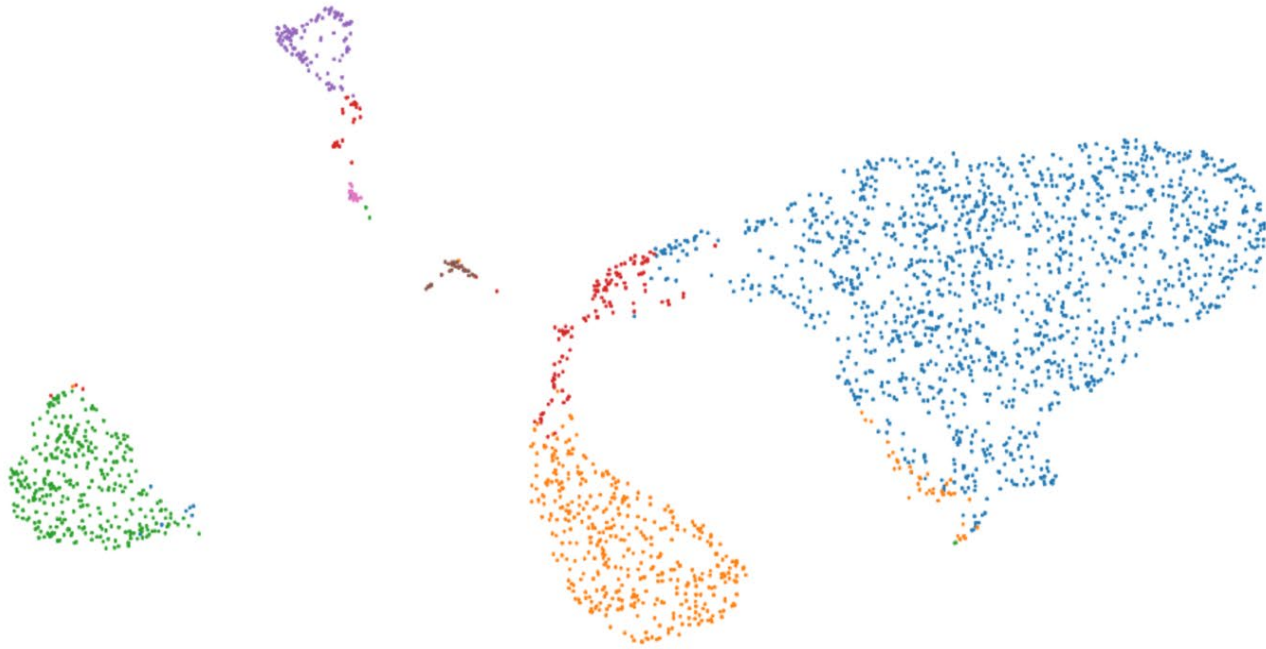
Log2 Exp - Krt18

0.0 9.0

Stage: **Nulliparous**
Animal ID: **NP2**
Clustering method: **tSNE**
Clustering: **Krt18**

Cluster 1,2 = **Krt18 high**
Cluster 3 = **Krt5 high**
Cluster 4,5 = **Krt18 low**
Cluster 6-8 = **other**

V.



K-Means ⌵ ⋮

🔍 Recluster

Number of Clusters 7 ⌵

- Cluster 1 (1448) ⋮
- Cluster 2 (444) ⋮
- Cluster 3 (321) ⋮
- Cluster 4 (135) ⋮
- Cluster 5 (103) ⋮
- Cluster 6 (28) ⋮
- Cluster 7 (19) ⋮

Significant Feature Comparison ⊗

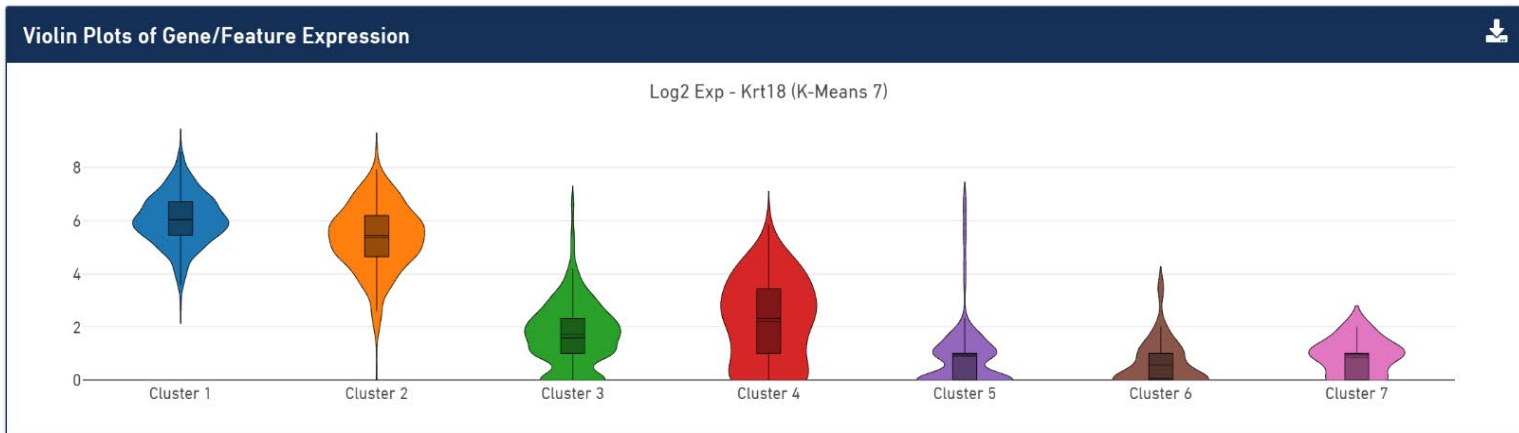
Globally Distinguishing ⌵

Feature Type

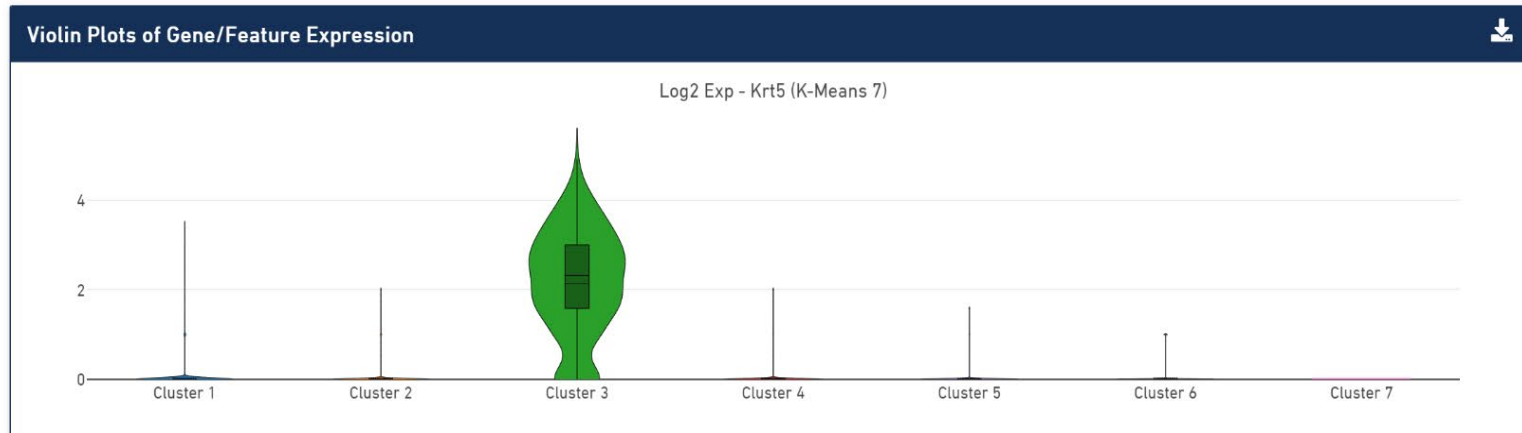
Gene ⌵ 📊

Stage: **Nulliparous**
Animal ID: **NP2**
Clustering method: **UMAP**
Clustering: **K-means**

Cluster 1,2 = **Krt18 high**
Cluster 3 = **Krt5 high**
Cluster 4,5 = **Krt18 low**
Cluster 6-8 = **other**



W.



Active Feature List

Search for a feature...

Krt5
Gene - ENSMUSG00000061527

Krt18
Gene - ENSMUSG00000023043

Scale & Attribute
Log2 Feature Max

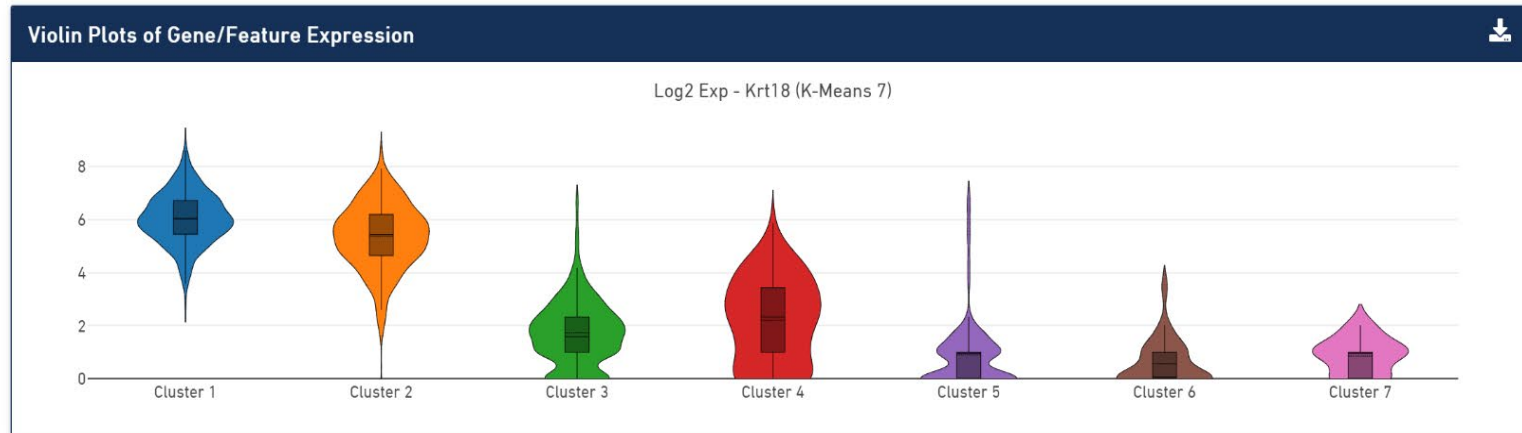
Select by Count - Krt5
> Enter a Number

Log2 Exp - Krt5
0.0 5.0

Stage: **Nulliparous**
Animal ID: **NP2**
Clustering method: **UMAP**
Clustering: **Krt5**

Cluster 1,2 = **Krt18 high**
Cluster 3 = **Krt5 high**
Cluster 4,5 = **Krt18 low**
Cluster 6-8 = **other**

X.



Active Feature List

Search for a feature...

Krt5
Gene · ENSMUSG000000061527

Krt18
Gene · ENSMUSG000000023043

Scale & Attribute

Log2 Feature Max

Select by Count - Krt18

> Enter a Number

Log2 Exp - Krt18

0.0 9.0

Stage: **Nulliparous**
Animal ID: **NP2**
Clustering method: **UMAP**
Clustering: **Krt18**

Cluster 1,2 = **Krt18 high**
Cluster 3 = **Krt5 high**
Cluster 4,5 = **Krt18 low**
Cluster 6-8 = **other**