



# gEAR - ARO MidWinter 2026

Presenting: Joshua Orvis  
Beatrice Milon  
Christopher Shults

WiFi: AROMWM26 (same password)

February 6, 2026



## The gEAR Team

**Joshua Orvis***Lead Engineer*

Institute for Genome Sciences

**Ricky Shaun Adkins***User interface and Analysis tools*

Institute for Genome Sciences

**Daniel Lesperance***Outreach, user testing, data curation and upload*

Institute for Genome Sciences

**Joe Receveur, PhD***Outreach, user testing, data curation and upload*

Institute for Genome Sciences

**Seth Ament, PhD***Informatics consultant*

Institute for Genome Sciences

**Brian Herb, PhD***Informatics consultant*

Institute for Genome Sciences

**Carlo Colantuoni, PhD***Informatics consultant*

Johns Hopkins University

**Ronna Hertzano, MD PhD***Principal Investigator*

NIH/NIDCD

**Anup Mahurkar***Co-Principal Investigator**Engineering and informatics oversight*

Institute for Genome Sciences

**Beatrice Milon, PhD***Curation, user testing*

NIH/NIDCD

**Christopher Shults, MS***Spatial transcriptomics*

NIH/NIDCD

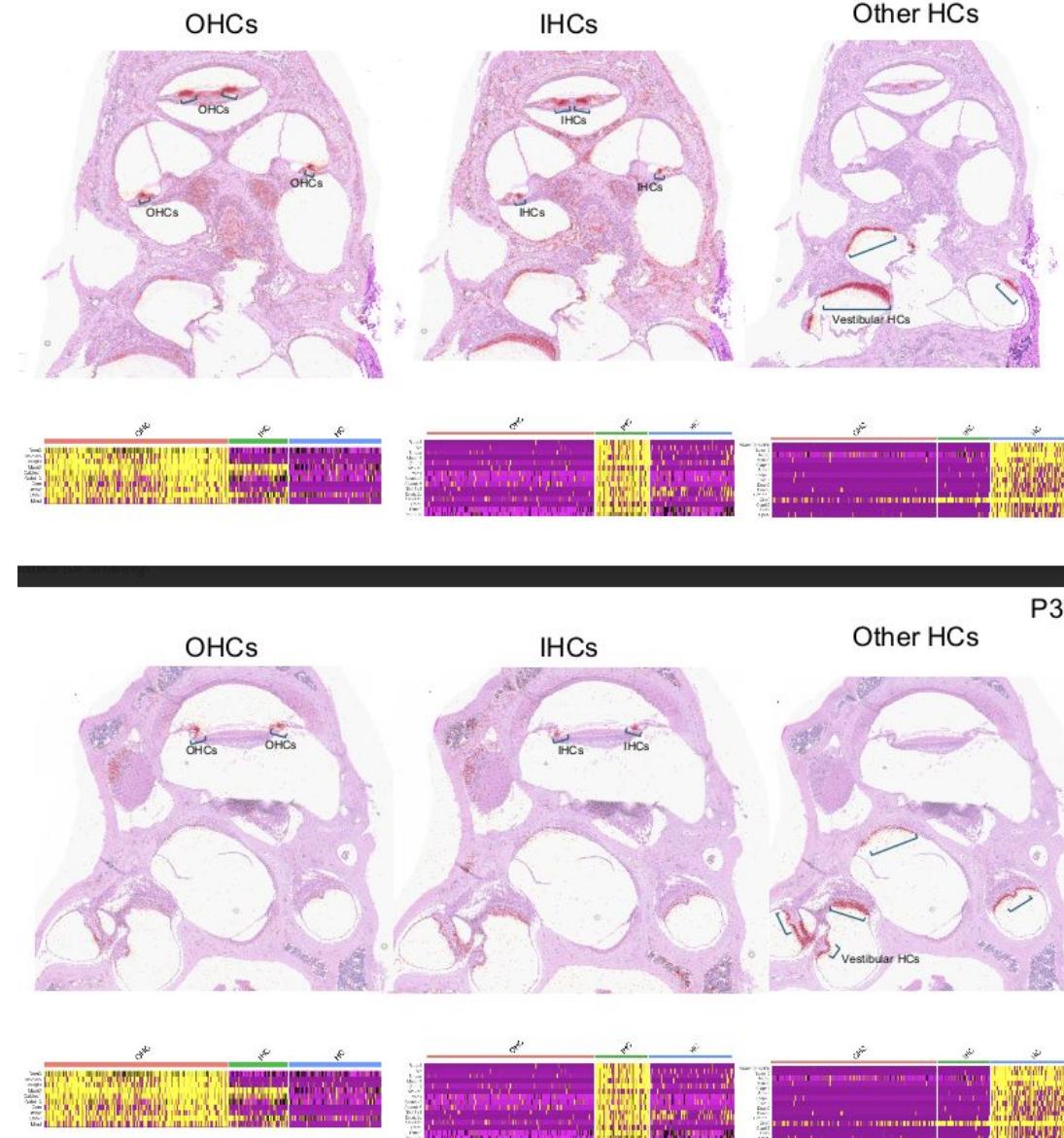
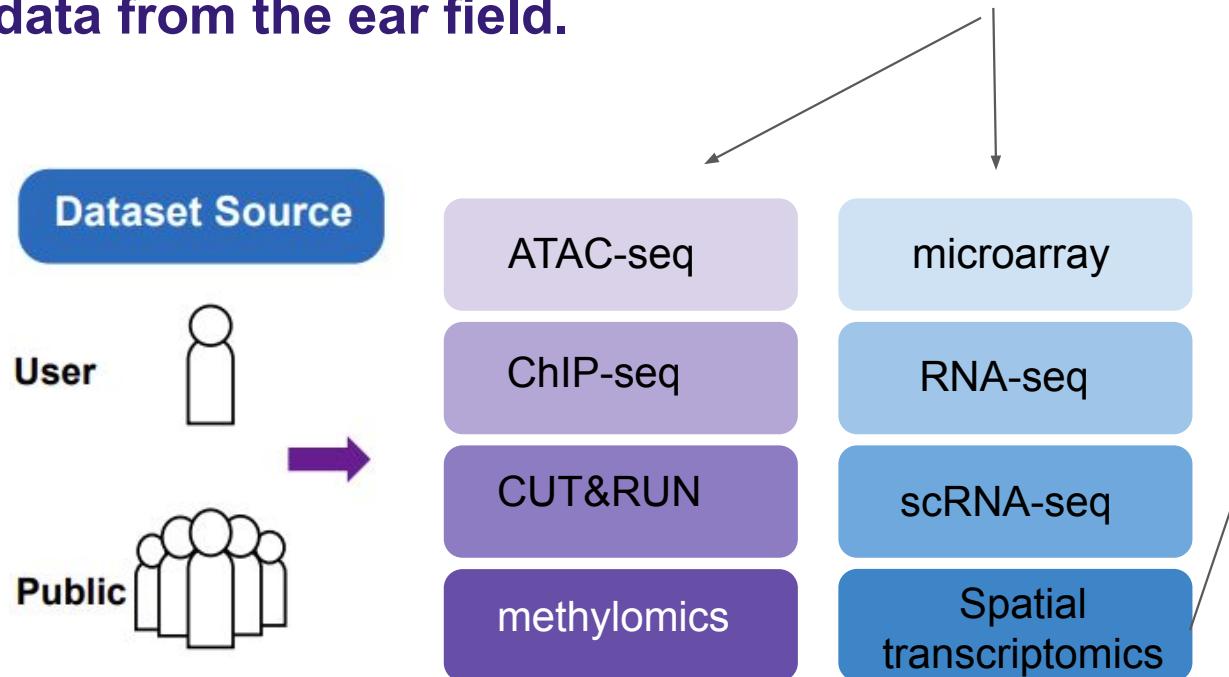
## Outline

Topics covered:

- Overview of Gene Expression Analysis Resource (gEAR)
- Looking up expression of single and multiple genes
- Compare expression between two conditions
- Explore scRNA-Seq datasets
- Explore dataset content of gEAR
- Dataset curation: single and multi-gene displays
- Viewing spatial RNA-Seq data
- Viewing epigenetic data

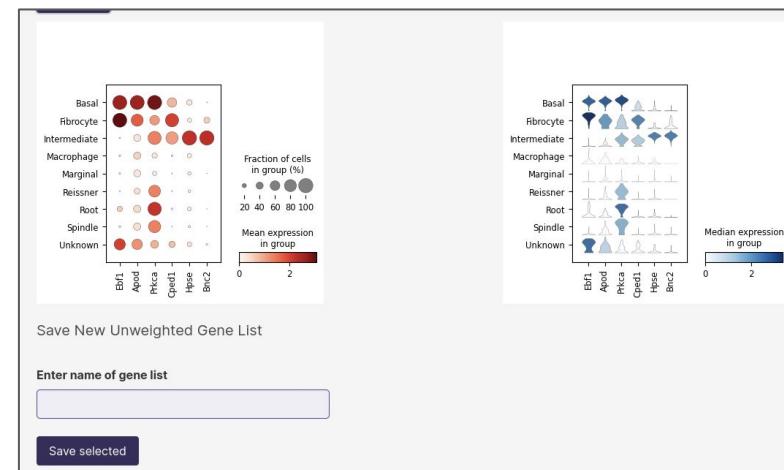
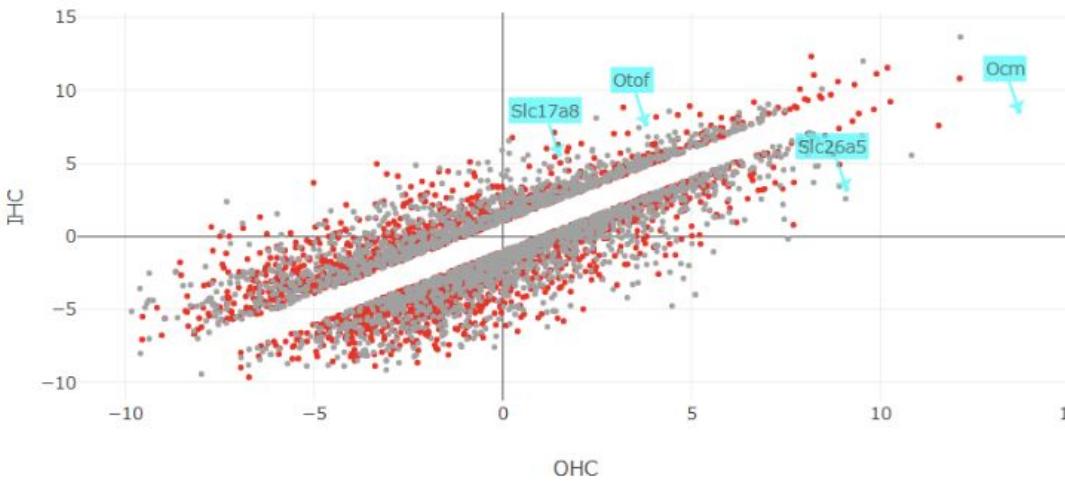
## gEAR - gene Expression Analysis Resource

'One-Stop-Shop' to access & analyze multi-omic data from the ear field.

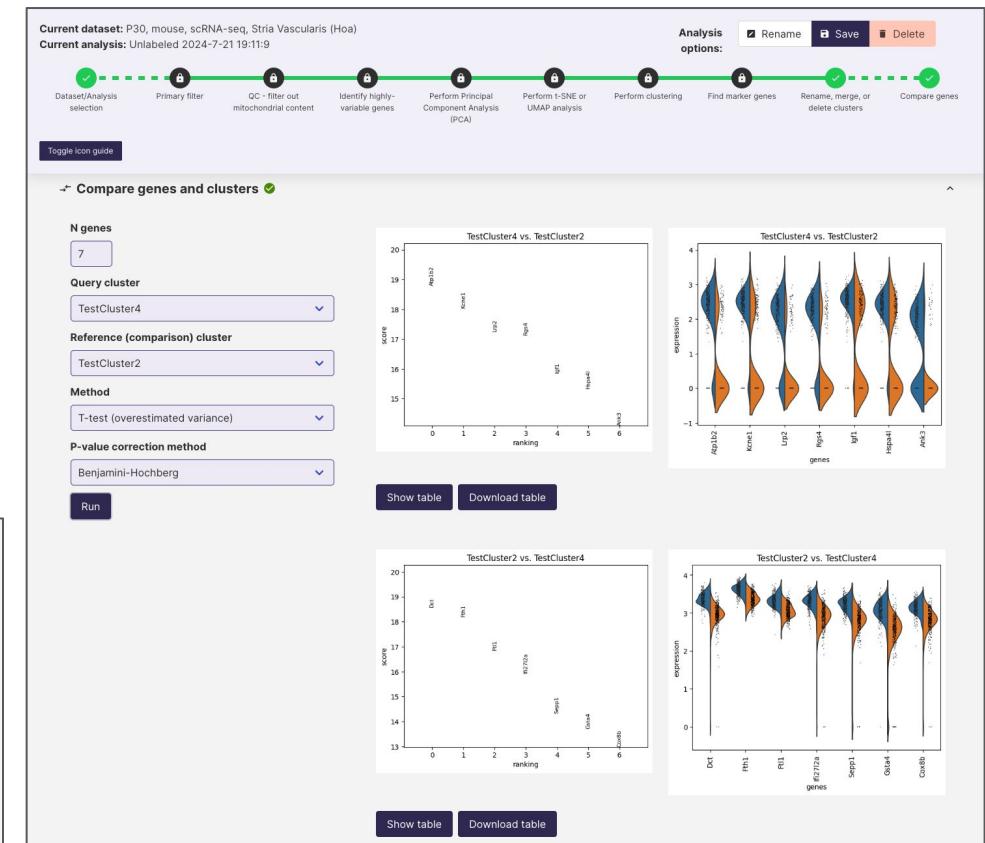


# Analysis tools

## Dataset comparisons



## Single-cell workbench



# Analysis tools

## Dataset projection

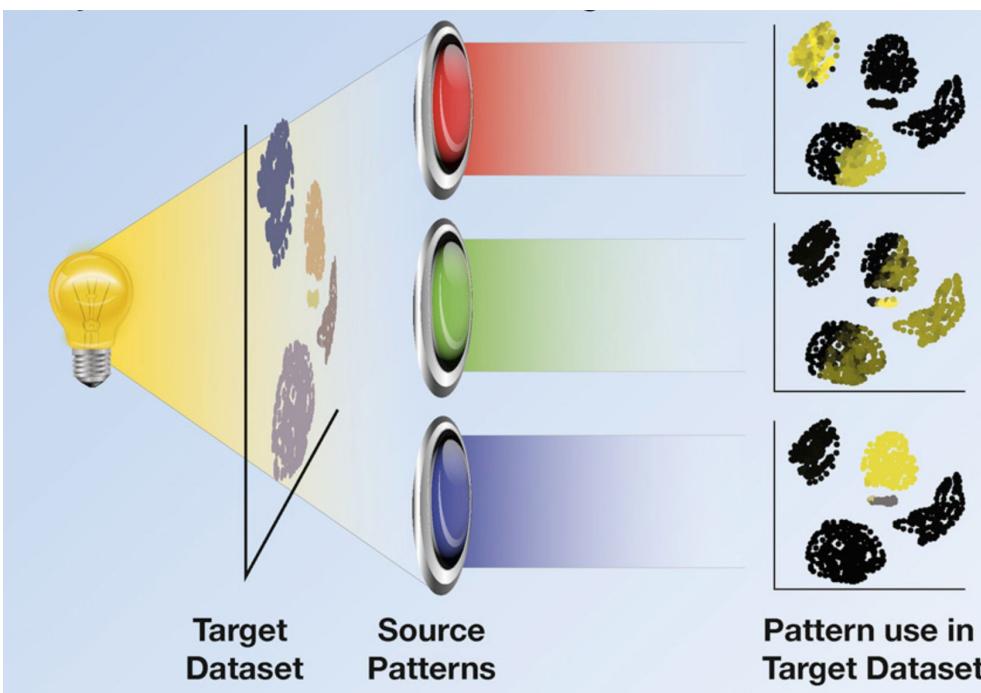
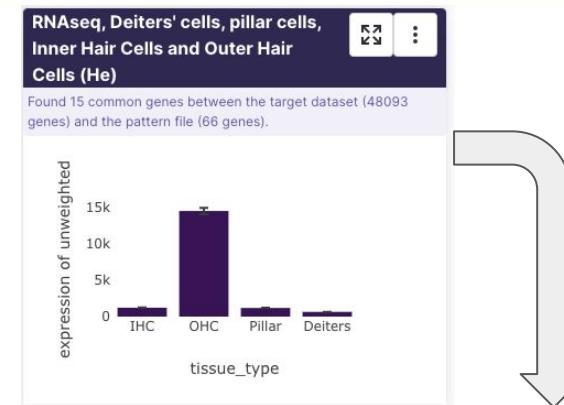
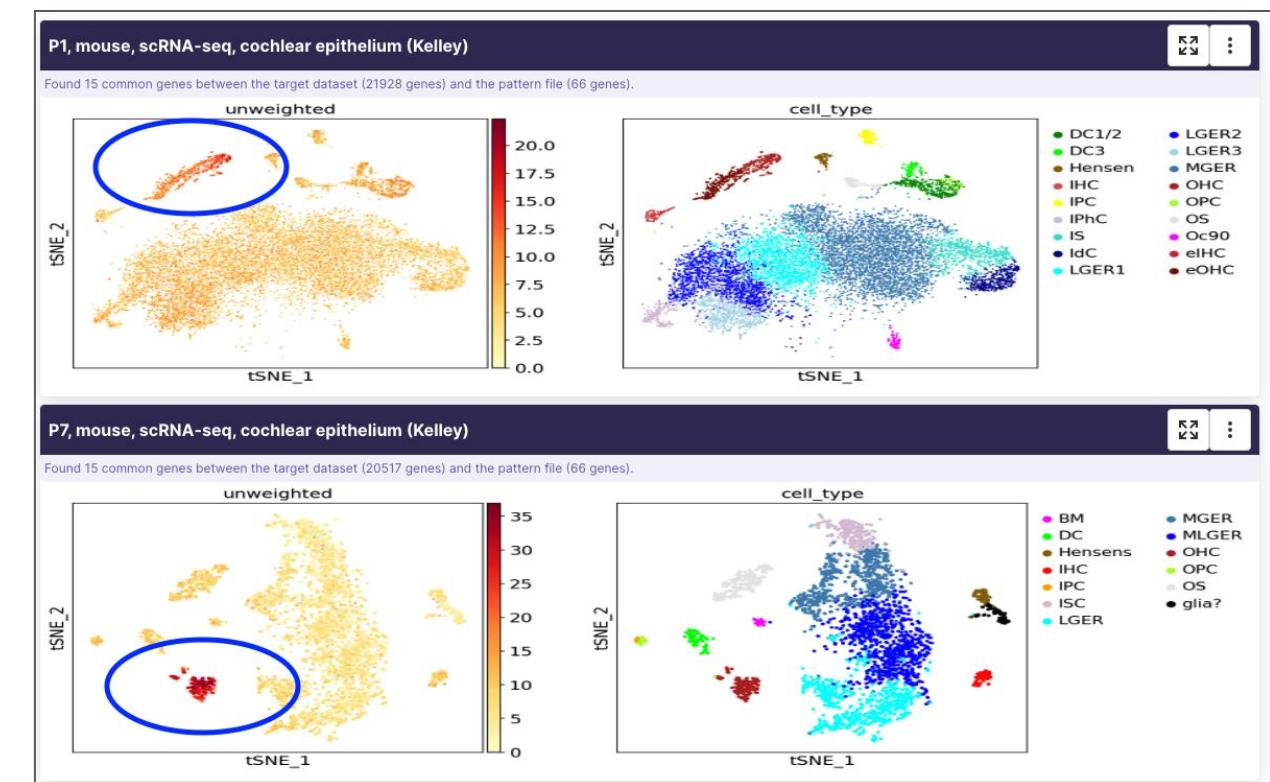


Image from: <https://doi.org/10.1016/j.cels.2019.04.004>

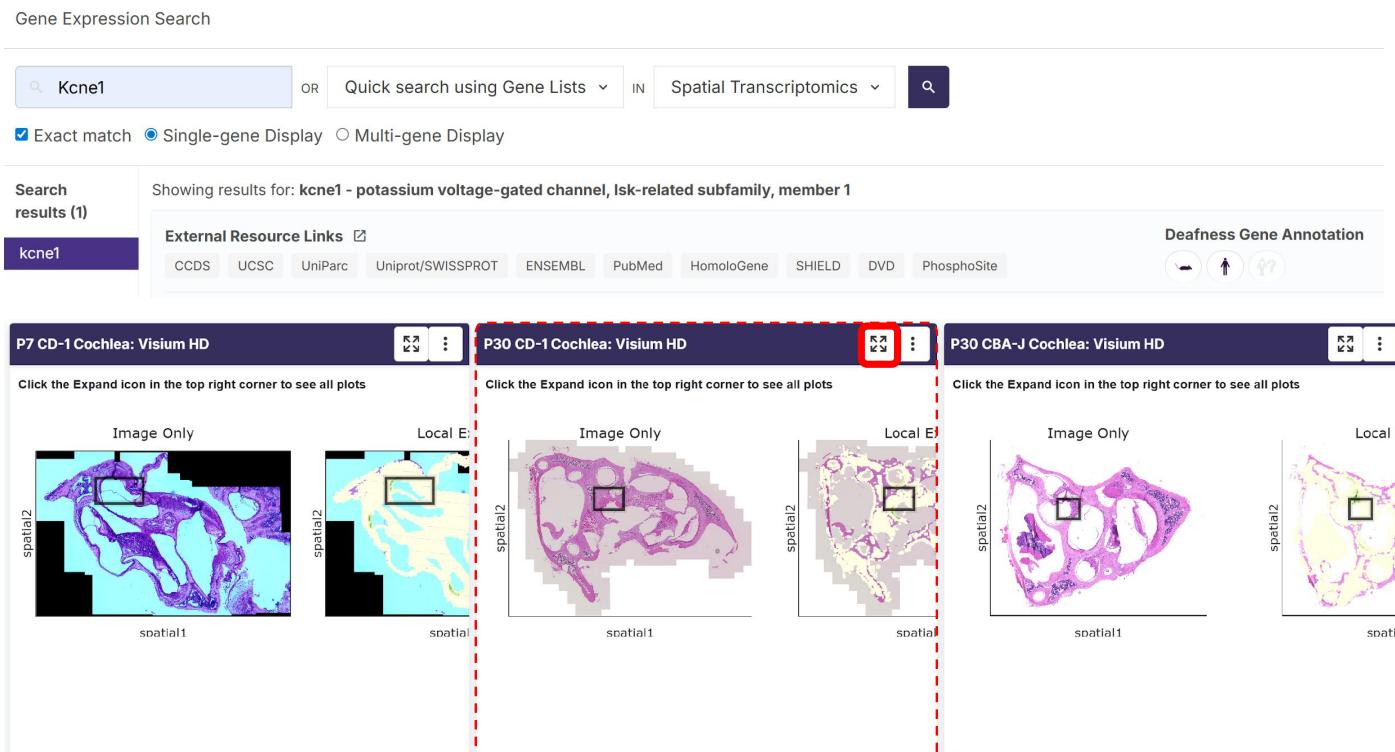


Looking at the P1 and P7 Kelley datasets, it seems that OHC expression grows stronger as the mouse matures.

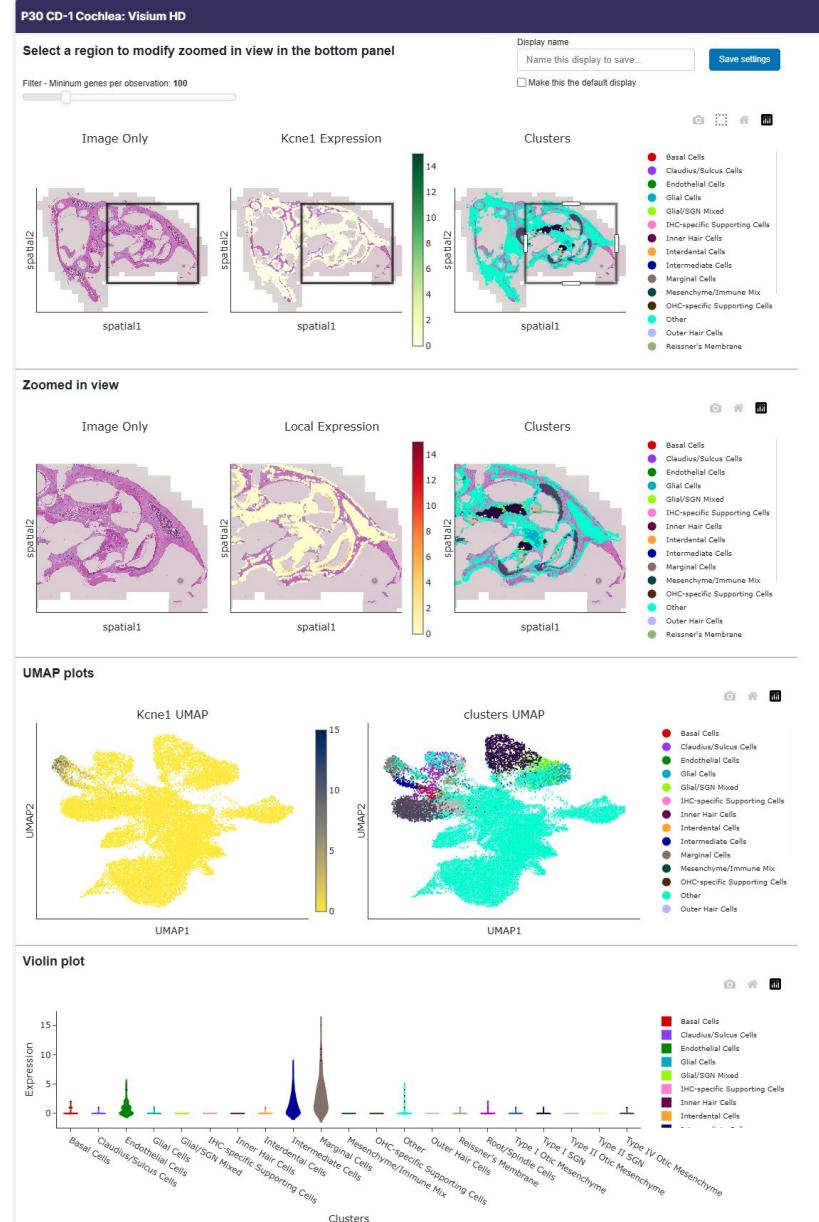
These marker genes also seem to show higher levels in OHC in the David He dataset as well.



# New: Spatial data displays



Full Image



ROI Zoom

UMAP Projection

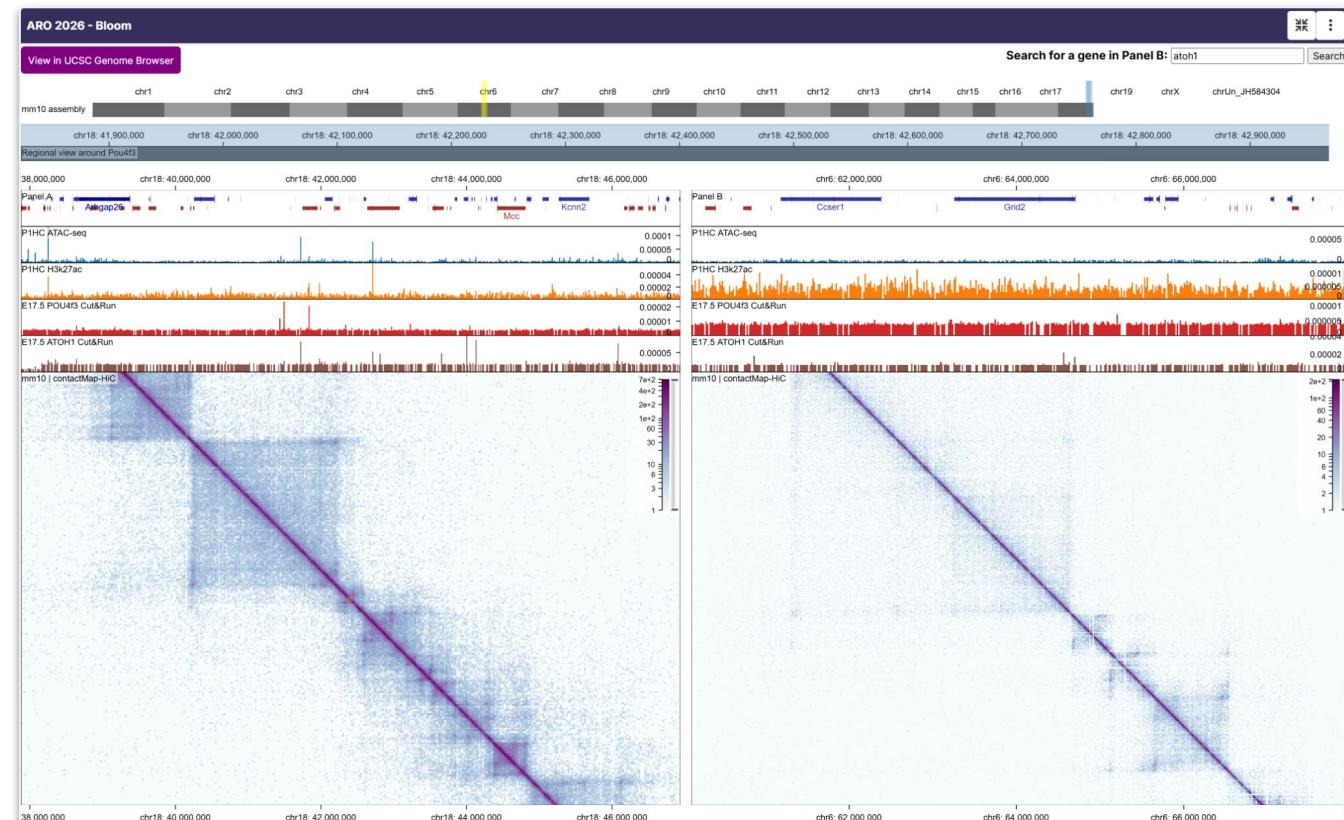
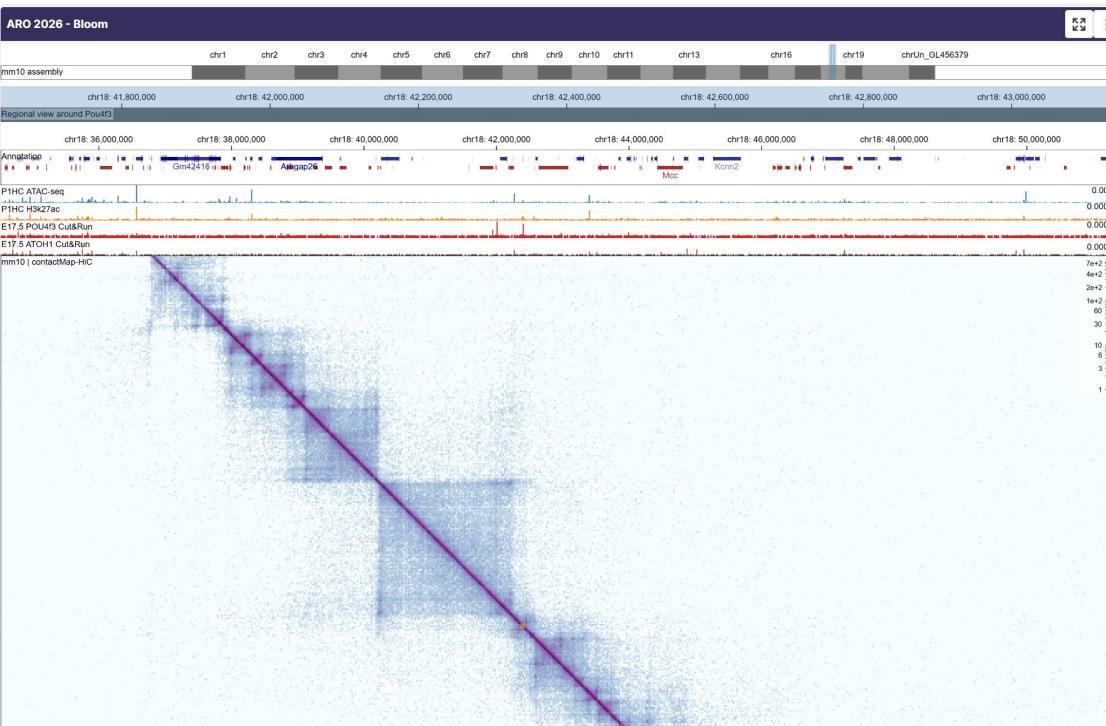
Violin Plot

# New: Epigenomics data display

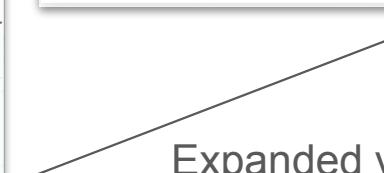


Gosling

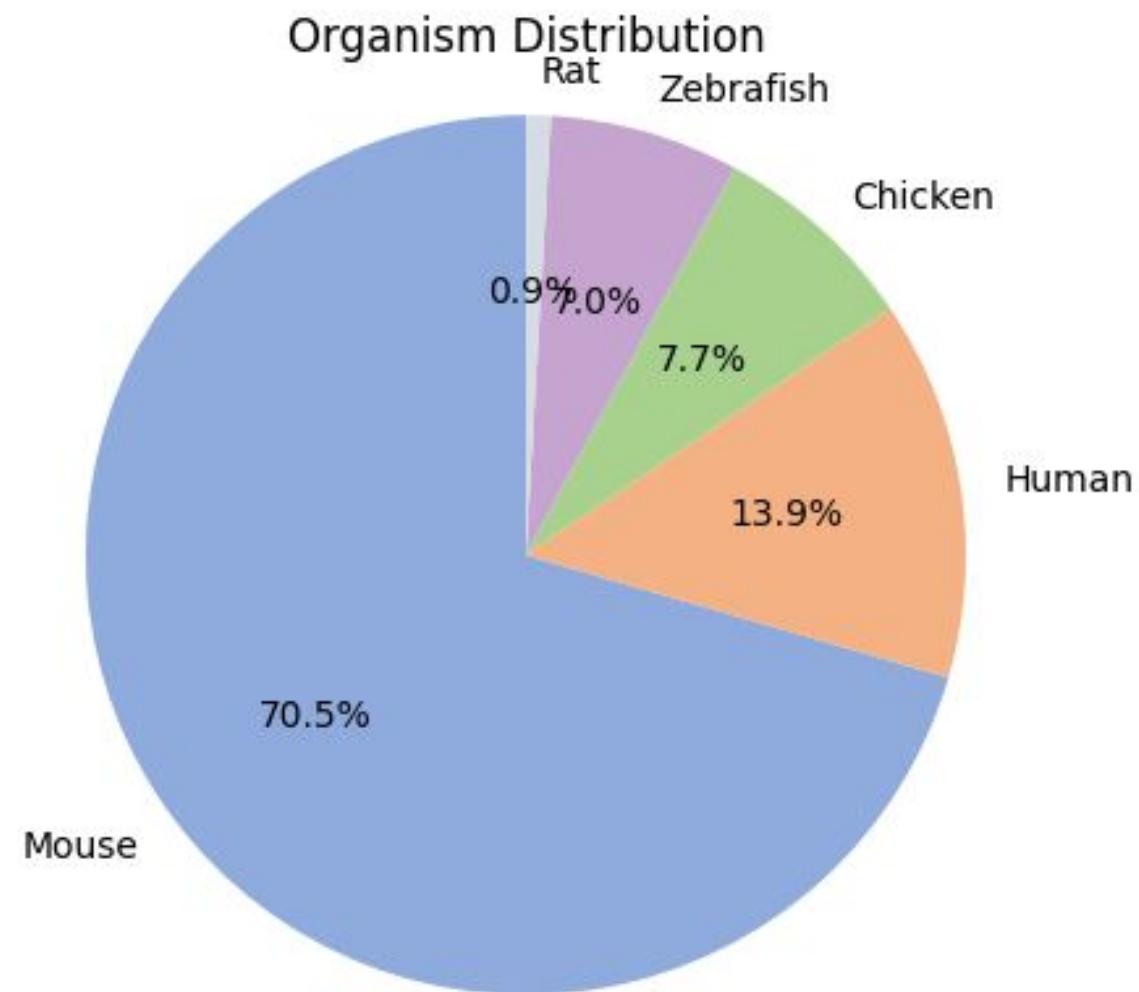
ATAC-seq  
ChIP-seq  
CUT&RUN  
Hi-C



Expanded view



## Many organisms supported



# gEAR - Usage statistics

## Cumulative stats:

 Users	2,613
 Datasets	1,319
 Datapoints	3.75 trillion

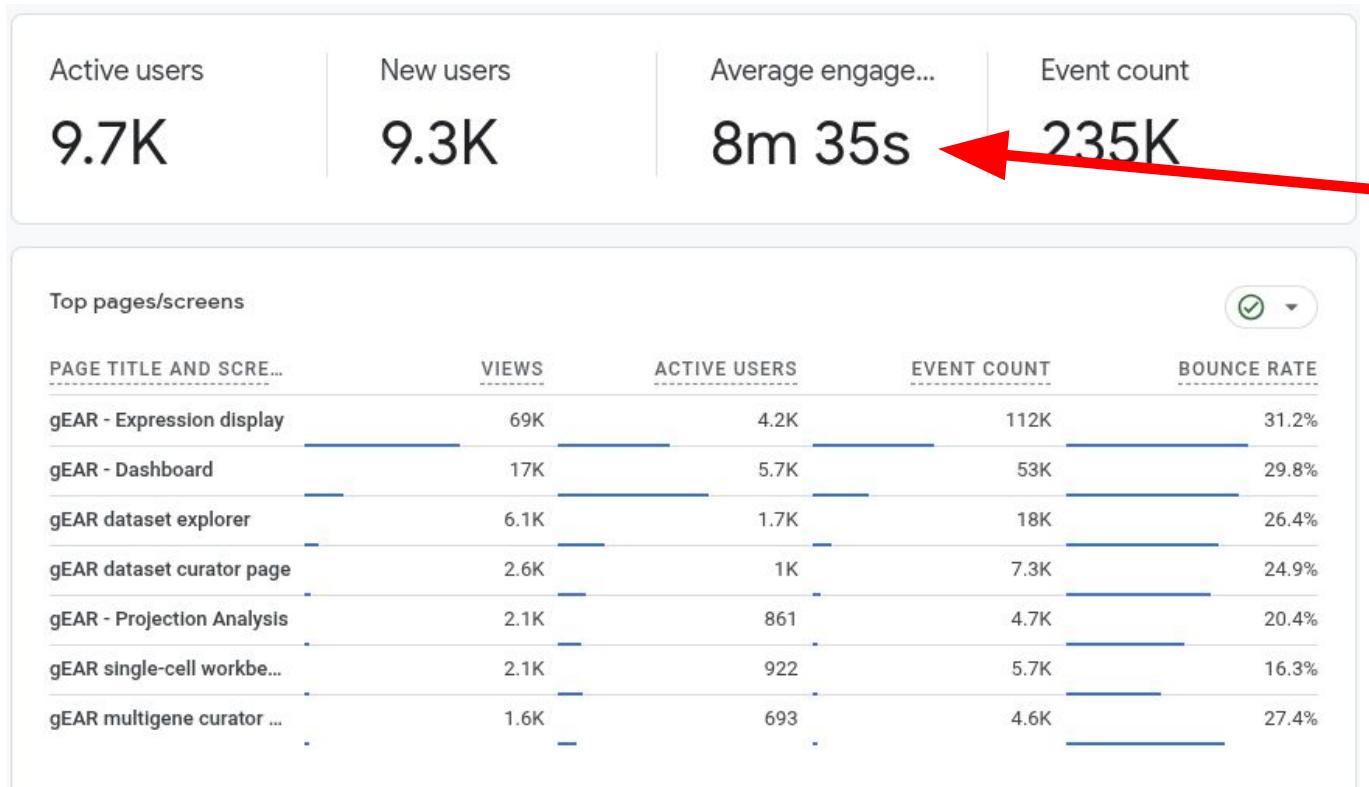
Used in 127 countries:



Map Data ©2026 Terms

COUNTRY	ACTIVE USERS
United States	14K
China	5.1K
Singapore	1.3K
Germany	904
Japan	833
United Kingdom	786
South Korea	713

## Active users



**Total page views: 235,000**

average web site usage time

All Images Videos Short videos Shopping Web Forums : More

AI Overview

The average time a user spends on a webpage is typically around 54 seconds. However, this can vary significantly depending on the website's purpose, the type of content, and the user's goals. Some studies, like one by [Backlinko](#), found that the average page load time is 10.3 seconds on desktop and 27.3 seconds on mobile.

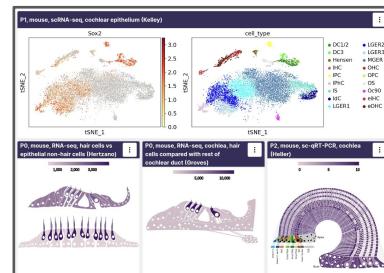
# Life cycle of data in gEAR

	A	B
1	ensembl.ID	gene_symbol
2	ENSMUSG00000000028	Cdc45
3	ENSMUSG00000000031	H19
4	ENSMUSG00000000037	Scml2
5	ENSMUSG00000000049	Apoh
6	ENSMUSG00000000056	Narf
7	ENSMUSG00000000058	Cav2
8	ENSMUSG00000000078	Klf6
9	ENSMUSG00000000085	Scmh1

Prepare data



Make datasets  
public

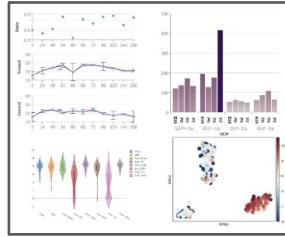


gEAR becomes  
primary viewer

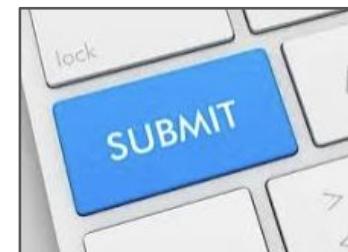
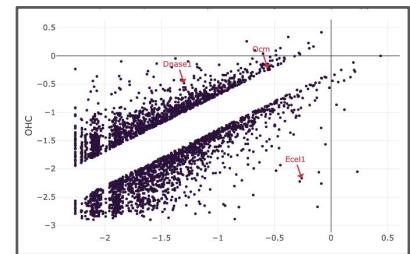


Upload  
(privately)  
to gEAR

Create  
visualizations



Perform  
analysis on  
the platform



Submit  
manuscript  
w/permalink

Independent  
bioinformatics  
analysis

# Life cycle of data in gEAR

	A	B
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3	ENSMUSG00000000031	H19
4	ENSMUSG00000000037	Scml2
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6	ENSMUSG00000000056	Narf
7	ENSMUSG00000000058	Cav2
8	ENSMUSG00000000078	Klf6
9	ENSMUSG00000000085	Scmh1

Prepare data

## Step: Prepare data

Expression data can be uploaded in common formats. These include:

- MEX format (from CellRanger)
- Excel spreadsheets
- R Seurat objects

	A	B
1	ensembl_ID	gene_symbol
2	ENSMUSG00000000028	Cdc45
3	ENSMUSG00000000031	H19
4	ENSMUSG00000000037	Scml2
5	ENSMUSG00000000049	Apoh
6	ENSMUSG00000000056	Narf
7	ENSMUSG00000000058	Cav2
8	ENSMUSG00000000078	Klf6
9	ENSMUSG00000000085	Scmh1

	A	B	C
1	ensembl_ID	2945-TAH-1_P7	2945-TAH-11_P7
2	ENSMUSG00000000028	2.346902957	3.800793352
3	ENSMUSG00000000031	1.83946448	2.86726516
4	ENSMUSG00000000037	11.22707631	9.535323673
5	ENSMUSG00000000049	0.126859619	0.066680585
6	ENSMUSG00000000056	103.5174494	99.15403008
7	ENSMUSG00000000058	44.0202879	30.80643033
8	ENSMUSG00000000078	152.5486922	175.7700224
9	ENSMUSG00000000085	53.9153382	56.81185853

# Life cycle of data in gEAR

	A	B
1	ensembl.ID	gene_symbol
2	ENSMUSG00000000028	Cdc45
3	ENSMUSG00000000031	H19
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6	ENSMUSG00000000056	Narf
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Prepare data



Upload  
(privately)  
to gEAR

# Step: Upload to gEAR

Uploads to gEAR are private by default.

## Step 1: Upload metadata

Upload an expression dataset

Joshua Orvis ▾

Enter metadata      Upload dataset      Dataset processing      Finalize submission      Curate dataset

Use the form or provided template to enter metadata for your dataset.

Choose your dataset format and upload directly or provide a supported URL.

Your dataset is processed and checked on the server.

Your dataset gets fully integrated into the system here.

Get the most out of your dataset by doing curation steps here.

**Step - Enter metadata (via form OR upload)**

The 'metadata' is the data describing your dataset, including things like title, authorship, sequencing protocols used, etc. This is the first step in uploading a dataset to the portal. All data uploaded are initially private to only your account (you can change this later in the Dataset Explorer)

Enter the metadata manually below OR fill out and upload from a spreadsheet template.

**Title** ⓘ

Title of your dataset

Or upload a metadata file

Choose No file chosen

**Longer description** ⓘ

A concise description of the experiments performed. Describing how the data were produced.

Upload

**Dataset type** ⓘ

Select one

**Annotation metadata**

**Annotation source** ⓘ

Select one

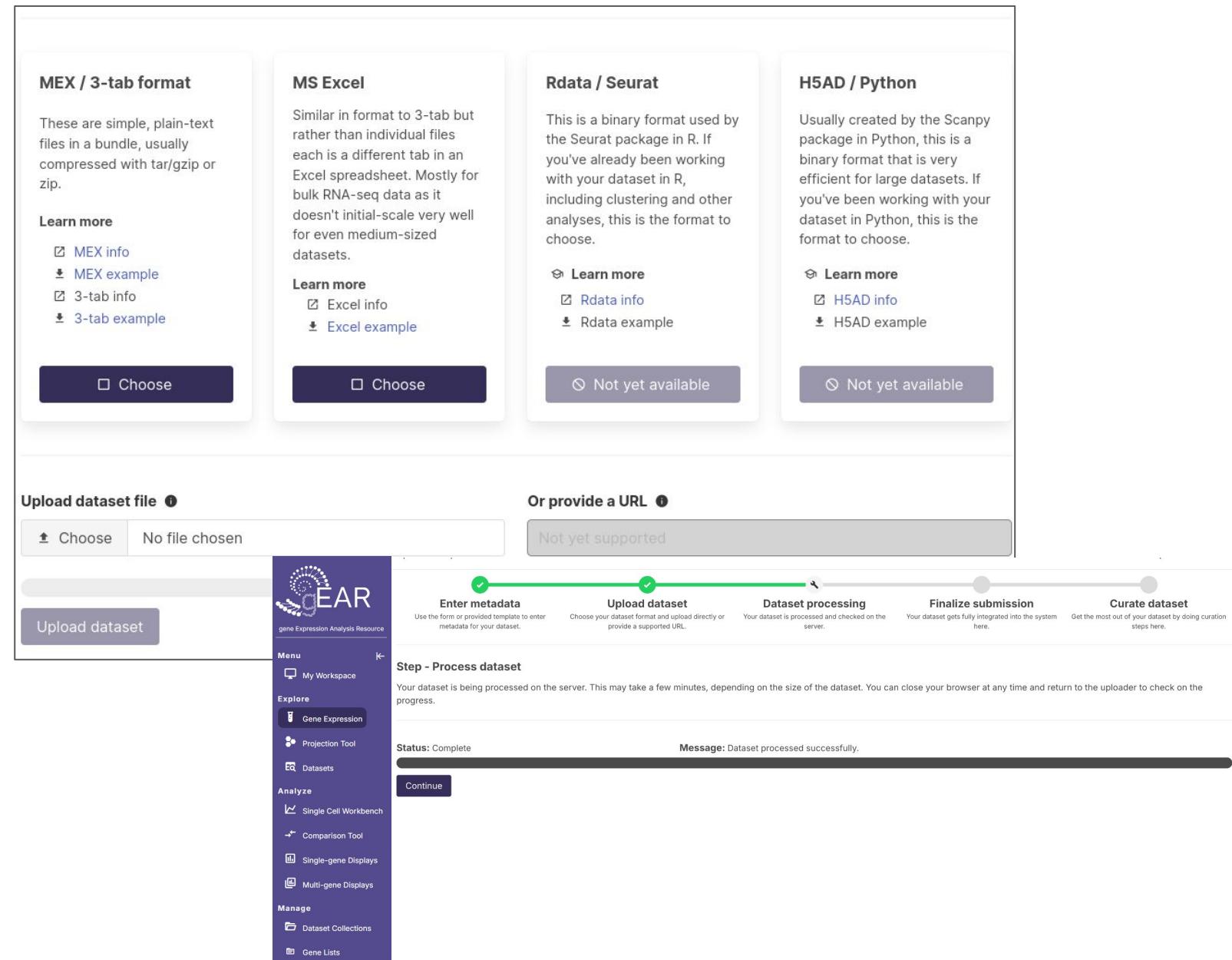
**Annotation release name/number** ⓘ

# Step: Upload to gEAR

Uploads to gEAR are private by default.

Step 2: Upload expression data

Step 3: Wait for processing



The screenshot shows the gEAR dataset upload interface. At the top, there are four sections for supported file formats:

- MEX / 3-tab format**: Described as simple, plain-text files in a bundle, usually compressed with tar/gzip or zip. Includes "Learn more" links for MEX info and 3-tab info, and download links for MEX example and 3-tab example. A "Choose" button is present.
- MS Excel**: Similar in format to 3-tab but each is a different tab in an Excel spreadsheet. Mostly for bulk RNA-seq data as it doesn't initial-scale very well for even medium-sized datasets. Includes "Learn more" links for Excel info and download links for Excel example. A "Choose" button is present.
- Rdata / Seurat**: A binary format used by the Seurat package in R. If you've already been working with your dataset in R, including clustering and other analyses, this is the format to choose. Includes "Learn more" links for Rdata info and download links for Rdata example. A "Not yet available" button is present.
- H5AD / Python**: Usually created by the Scanpy package in Python, this is a binary format that is very efficient for large datasets. If you've been working with your dataset in Python, this is the format to choose. Includes "Learn more" links for H5AD info and download links for H5AD example. A "Not yet available" button is present.

Below these sections, there are two main upload methods:

- Upload dataset file**: A file input field showing "No file chosen" and a "Choose" button. Below it is a "Upload dataset" button.
- Or provide a URL**: A text input field showing "Not yet supported".

The right side of the interface shows a process flow:

- Enter metadata**: Use the form or provided template to enter metadata for your dataset.
- Upload dataset**: Choose your dataset format and upload directly or provide a supported URL.
- Dataset processing**: Your dataset is processed and checked on the server.
- Finalize submission**: Your dataset gets fully integrated into the system here.
- Curate dataset**: Get the most out of your dataset by doing curation steps here.

At the bottom, a status message indicates "Status: Complete" and "Message: Dataset processed successfully." with a "Continue" button.

## Life cycle of data in gEAR

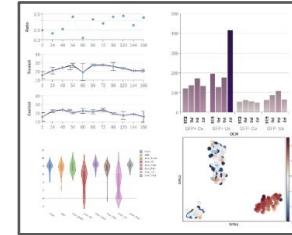
	A	B
1	ensembl.ID	gene_symbol
2	ENSMUSG00000000028	Cdc45
3	ENSMUSG00000000031	H19
4	ENSMUSG00000000037	Scml2
5	ENSMUSG00000000049	Apoh
6	ENSMUSG00000000056	Narf
7	ENSMUSG00000000058	Cav2
8	ENSMUSG00000000078	Klf6
9	ENSMUSG00000000085	Scmh1

Prepare data



Upload  
(privately)  
to gEAR

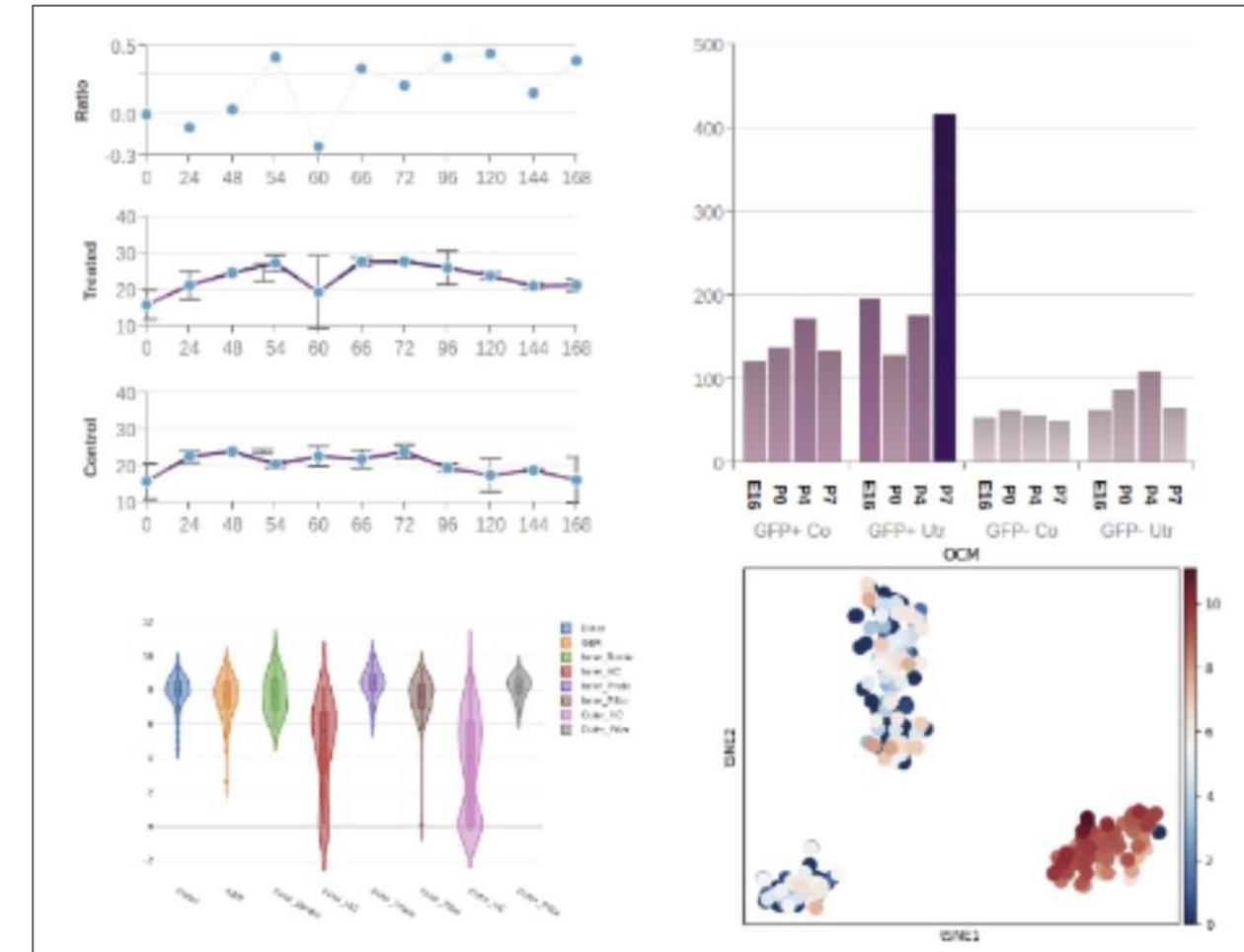
Create  
visualizations



## Step: Create visualizations

After a successful upload  
you'll be directed to  
'curate' your dataset,  
which creates  
visualizations for it.

These can be based on  
your raw data, or analyses  
you've performed already.



## Life cycle of data in gEAR

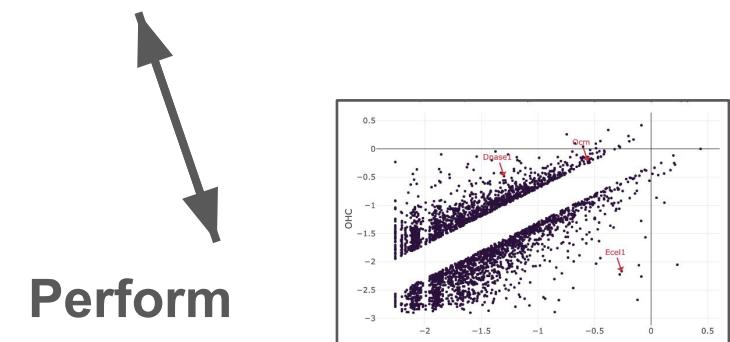
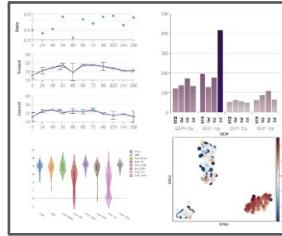
	A	B
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4	ENSMUSG00000000037	Scml2
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7	ENSMUSG00000000058	Cav2
8	ENSMUSG00000000078	Klf6
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Prepare data



Upload  
(privately)  
to gEAR

Create  
visualizations



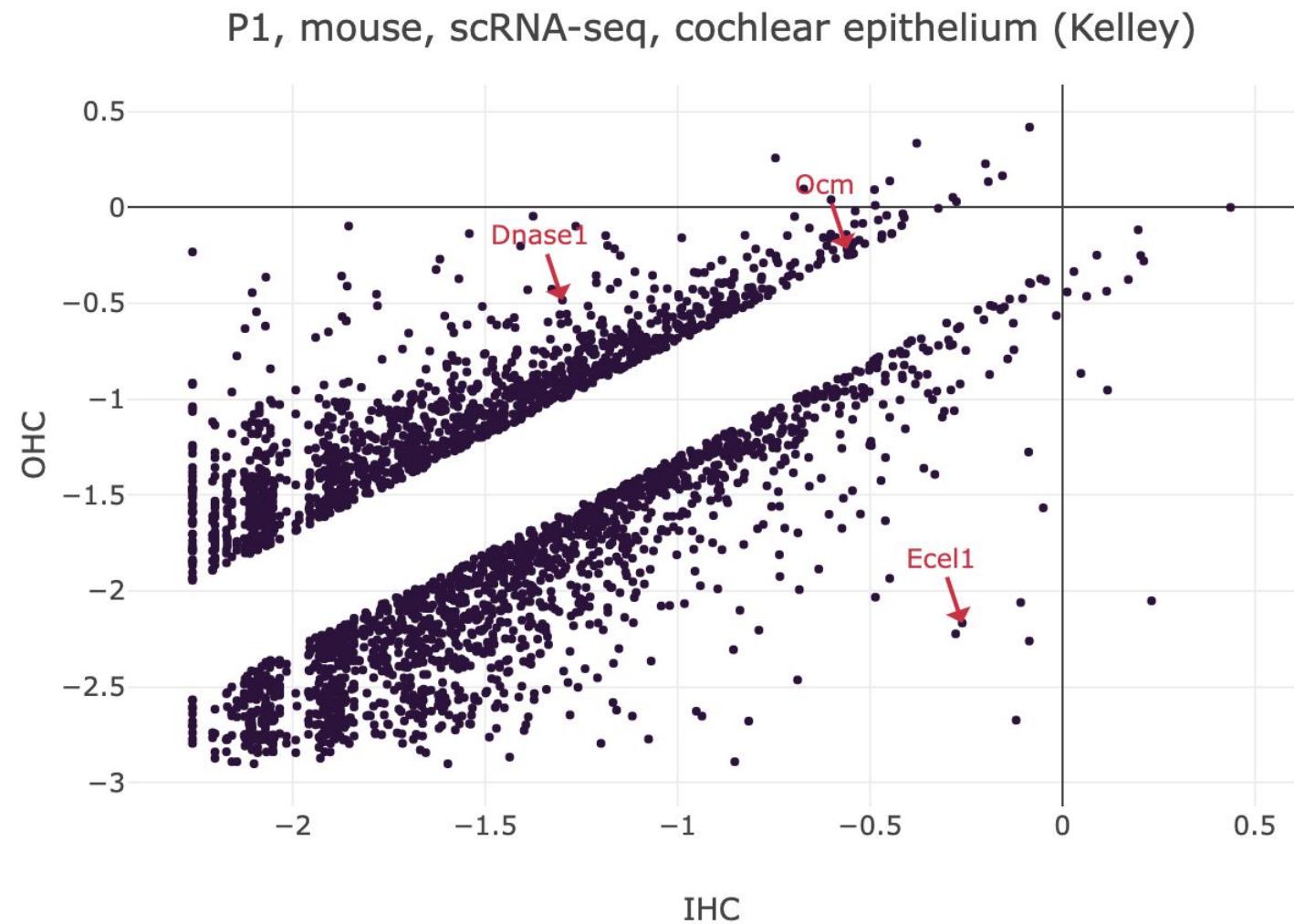
Perform  
analysis on  
the platform



Independent  
bioinformatics  
analysis

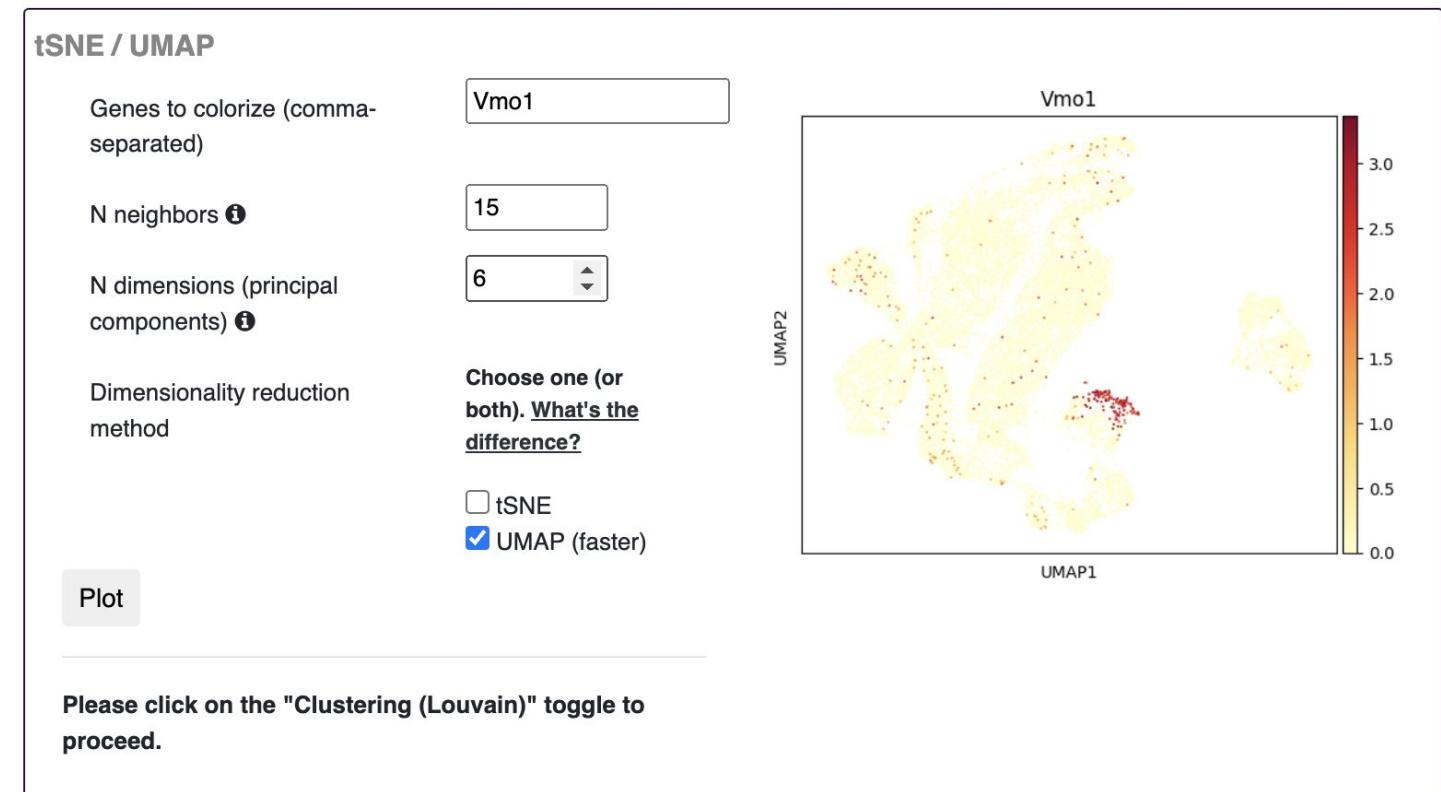
## Step: Perform analyses

Analyses you perform within gEAR can then be used to create new visual curations.



## Step: Perform analyses

After using the scRNA-seq workbench to create a UMAP analysis, for example, you can then use the curator to create a visualization of that type to highlight any gene searched. This is especially useful after generating cluster data



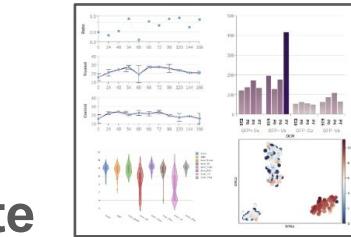
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9	ENSMUSG00000000085	Scmh1

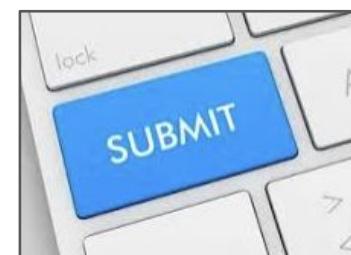
Prepare data



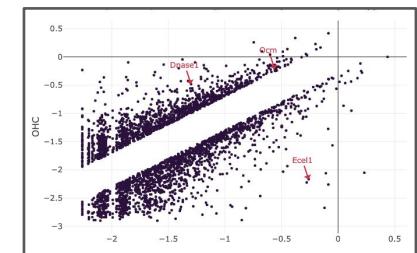
Upload  
(privately)  
to gEAR



Create  
visualizations



Submit  
manuscript  
w/permalink



Perform  
analysis on  
the platform



Independent  
bioinformatics  
analysis

## Step: Submit your manuscript

gEAR has a system of short URLs called ‘permalinks’ which can be included in your manuscript to take readers directly to your dataset, or even a collection of datasets.

Dataset Explorer

Collection management - View: Sort by: Date uploaded

Showing 1 - 9 of 9 results

Joshua Orvis

Filter controls

Search by keyword

Keyword search

Show from this collection only

Yes

Ownership

All

Your datasets

Group-affiliated datasets

Datasets shared with you

Public datasets

Organism

All

Chicken

Human

Marmoset

Mouse

Rat

Zebrafish

Dataset type

2-4 months, mouse, RNA-seq, cochlea, 2h post noise exposure day/night, with or without glucocorticoids (Canlon)

Organism: Mouse Owner: curator Type: bulk-rnaseq Added: Mon Aug 12 2019 Annotation source: Ensemble ID Source version: 93 PubMed ID: 31353184 GEO ID: GSE107086

P2, mouse, sc-qRT-PCR, cochlea (Heller)

Organism: Mouse Owner: Ronna Hertzano Type: svg-expression Added: Tue Feb 09 2016 Annotation source: Not given Source version: Not given PubMed ID: 26027927 GEO ID: Not available

P0, mouse, RNA-seq, cochlea, hair cells compared with rest of cochlear duct (Groves)

Organism: Mouse Owner: Ronna Hertzano Type: svg-expression Added: Tue Feb 09 2016 Annotation source: Not given Source version: Not given PubMed ID: 25855195 GEO ID: Not available

## Step: Submit your manuscript

In the dataset explorer, you can get the permalink by finding your dataset and clicking the “Share” button:

The screenshot shows the sgEAR Dataset Explorer interface. On the left, a sidebar menu includes links for My Workspace, Gene Expression, Projection Tool, Datasets (which is selected), Analyze, Manage, and Dataset Uploader. The main area displays a 'Dataset Explorer' with a collection titled 'Hearing (default)'. It features a search bar, filter controls (including 'Show from this collection only' set to 'Yes'), and a 'Sort by' dropdown set to 'Date uploaded'. Three datasets are listed:

- 2-4 months, mouse, RNA-seq, cochlea, 2h post noise exposure day/night, with or without glucocorticoids (Canlon)**  
Organism: Mouse  
Annotation source: Ensemble ID  
Source version: 93  
Type: bulk-rnaseq  
PubMed ID: 31353184  
GEO ID: GSE107086
- P2, mouse, sc-qRT-PCR, cochlea (Heller)**  
Organism: Mouse  
Annotation source: Not given  
Source version: Not given  
Type: svg-expression  
PubMed ID: 26027927  
GEO ID: Not available
- P0, mouse, RNA-seq, cochlea, hair cells compared with rest of cochlear duct (Groves)**  
Organism: Mouse  
Annotation source: Not given  
Source version: Not given  
Type: svg-expression  
PubMed ID: 25855195  
GEO ID: Not available

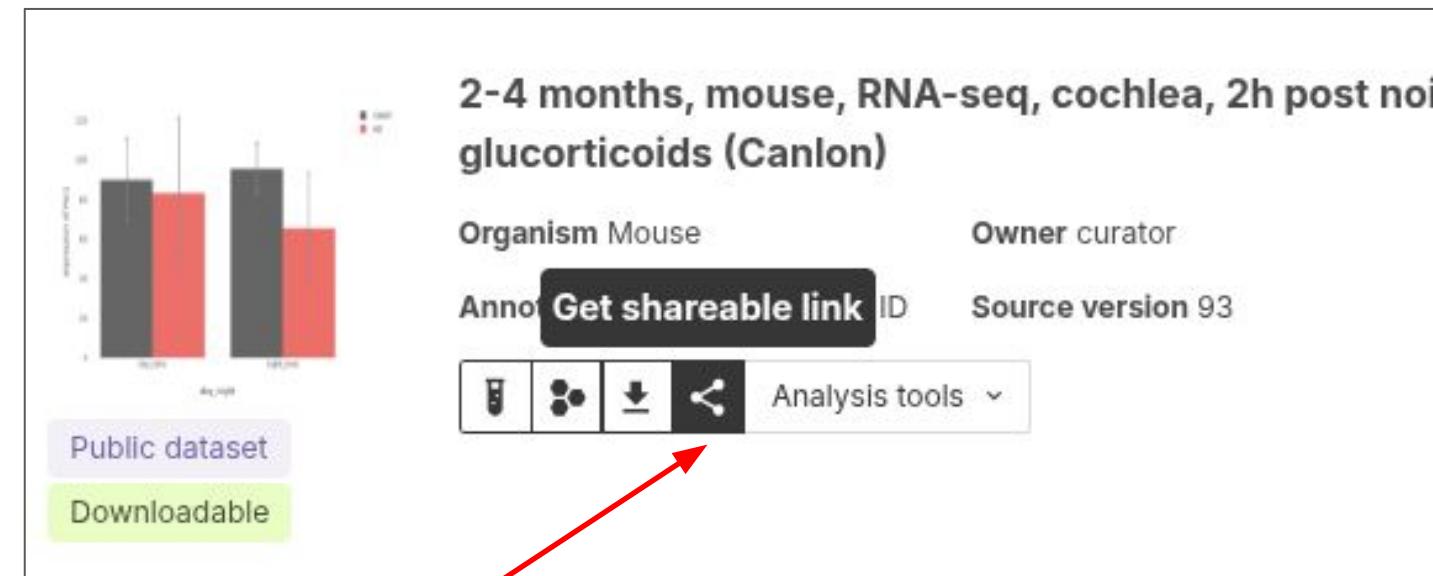
Each dataset card includes a 'Share' icon (represented by a person icon with a plus sign) which is highlighted with a red arrow.

## Step: Submit your manuscript

Clicking the share link copies the URL to your clipboard, but it looks something like this:

[umgear.org/p?s=78c3aa45](http://umgear.org/p?s=78c3aa45)

This takes any user directly to that dataset, ready for gene searches or analysis.



Important note: Permalinks work whether your data are public or private, so share them only with those you intend to view your dataset.

## Step: Submit your manuscript

If you create a **collection of datasets** and want to use that in your publication you can just select the sharing link on your profile instead. That creates a link which looks like this:

[umgear.org/p?l=32b9e270](http://umgear.org/p?l=32b9e270)

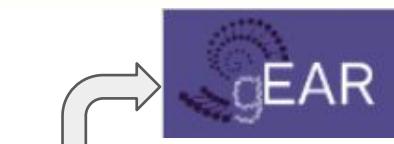
But the last part can be customized by you!



## Life cycle of data in gEAR

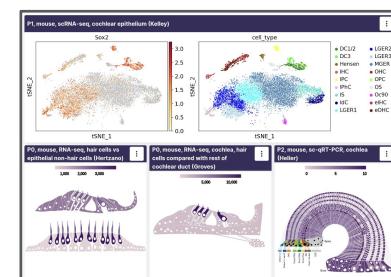
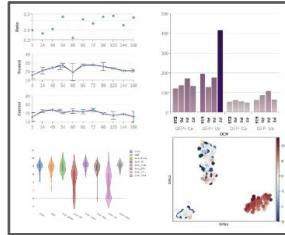
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6	ENSMUSG00000000056	Narf
7	ENSMUSG00000000058	Cav2
8	ENSMUSG00000000078	Klf6
9	ENSMUSG00000000085	Scmh1

Prepare data



Upload  
(privately)  
to gEAR

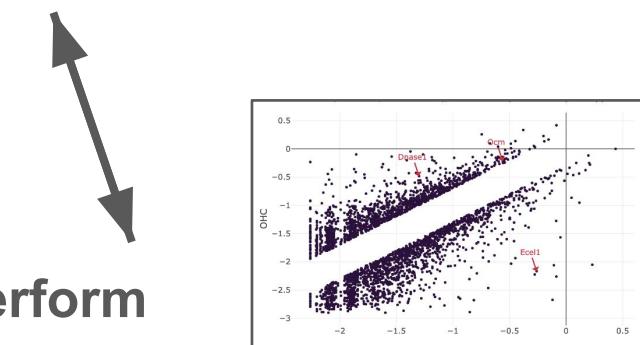
Create  
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gEAR becomes  
primary viewer



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manuscript  
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Perform  
analysis on  
the platform

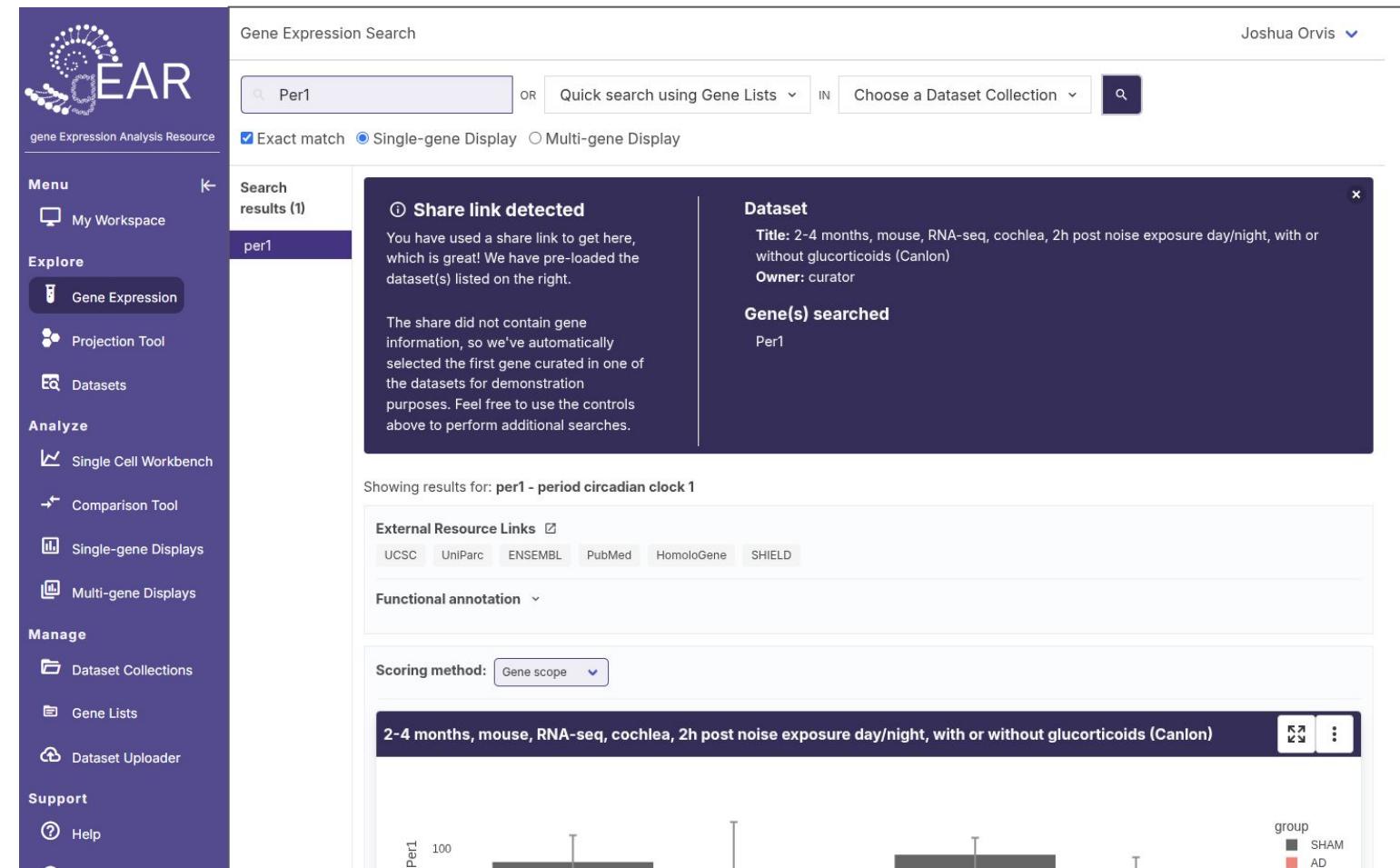


Independent  
bioinformatics  
analysis

## Step: Primary viewer

Example view of a single dataset after clicking a permalink.

Readers are taken directly to your dataset and can search a gene of interest



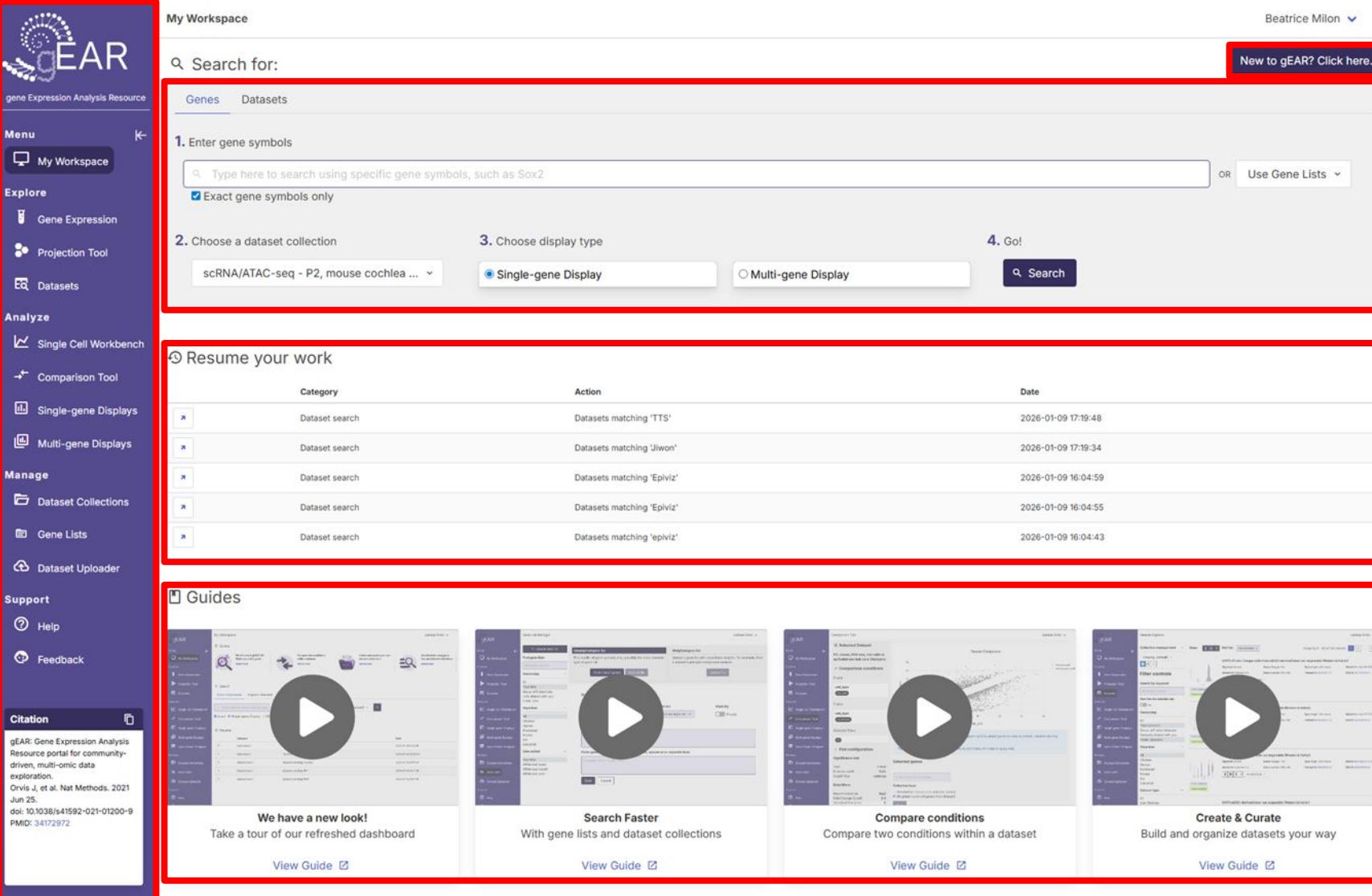
## Step: Primary viewer

Following a profile permalink pre-loads this profile in the interface and automatically searches a default gene.

The screenshot shows the GEAR (Gene Expression Analysis Resource) primary viewer interface. On the left is a dark sidebar with the GEAR logo at the top, followed by sections for Menu (My Workspace), Explore (Gene Expression, Projection Tool, Datasets), Analyze (Single Cell Workbench, Comparison Tool, Single-gene Displays, Multi-gene Displays), Manage (Dataset Collections, Gene Lists, Dataset Uploader), and Support (Help). The main content area has a header "Gene Expression Search" with a search bar containing "Pou4f3". Below the search bar are checkboxes for "Exact match", "Single-gene Display" (which is selected), and "Multi-gene Display". A red arrow points from the sidebar's "Gene Expression" link towards the search results. The search results section shows "Search results (1)" for "pou4f3". It includes a message about a share link being detected, stating that the share did not contain gene information so it automatically selected Pou4f3. To the right of this message is a "Dataset Collection" panel for "Adult" datasets, owned by Joshua Orvis, containing the gene "Pou4f3". Below this is a "Gene(s) searched" section for "Pou4f3". The main content area also displays "Showing results for: pou4f3 - POU domain, class 4, transcription factor 3" and "External Resource Links" for UCSC, UniParc, ENSEMBL, PubMed, HomoloGene, SHIELD, and DVD. It shows functional annotation and scoring methods (Gene scope). At the bottom, there are two bar charts: one for "RNAseq, Deiters' cells, pillar cells, Inner Hair Cells and Outer Hair Cells (He)" and another for "P7-adult, mouse, RNA-seq, medial geniculate and primary auditory cortex (A1) (Hackett)". A legend indicates gender: M (dark purple) and F (light purple). The x-axis for the charts is labeled "Pou4f3", "MG", and "A1". The y-axis for the first chart ranges from 0 to 100, with a value of 100 indicated for the M bar. The y-axis for the second chart ranges from 0 to 10, with a value of 10 indicated for the M bar.

# My Workspace details (umgear.org)

New navigation menu, present on all pages of the site.



The screenshot shows the 'My Workspace' page of the umgear.org website. A red box highlights the left sidebar, which contains a navigation menu with sections like 'Explore', 'Analyze', 'Manage', and 'Support'. Another red box highlights the search interface at the top, which includes a search bar, dropdown menus for 'Genes' and 'Datasets', and numbered steps for entering gene symbols, choosing a dataset collection, selecting a display type (Single-gene Display or Multi-gene Display), and performing the search. A third red box highlights the 'Resume your work' section, which displays a history of dataset search actions with their dates. A fourth red box highlights the 'Guides' section, which features four video thumbnails with titles: 'We have a new look!', 'Search Faster', 'Compare conditions', and 'Create & Curate'.

Click here for a quick tutorial

Expanded search capabilities

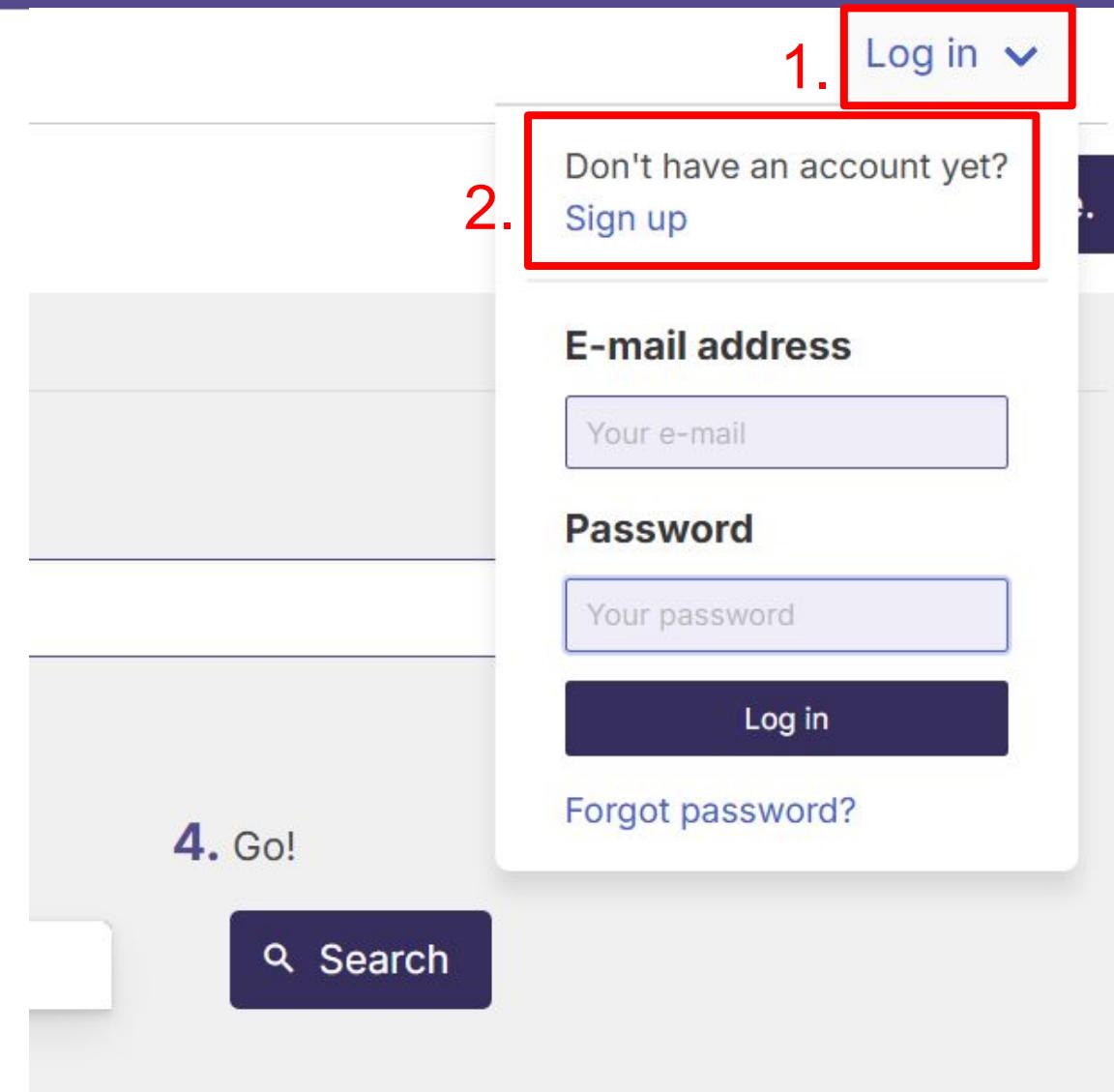
User history of actions, each can be clicked to revisit previous work

Walkthrough videos for key site pages



## Creating A New User

1. Click Log in at the top right corner of the page
2. Click on Sign Up. (Note you will need a working email address to create a user)



# Creating A New User

1. Enter the information in each box
2. \*Optional\* select the color-blind box or get regular updates box
3. Click “Create Account” button
4. Email verification step

Creating a free account allows you to save your work, share it with others, and access additional features.

1.

Name

Dan Alias

Institution

IGS

Email

danielias@fakeemail.com

Password

.....

Retype password

.....

Password requirements: (Annoying, we know, but helps ensure your data stay private!)

- ✓ At least 8 characters
- ✓ At least one uppercase letter
- ✓ At least one lowercase letter
- ✓ At least one number
- ✓ At least one special character

2.

Click to view all plots using a color scheme suitable for those with color-vision deficiencies.

Get regular email updates?

3.

Create Account

## Creating A New User

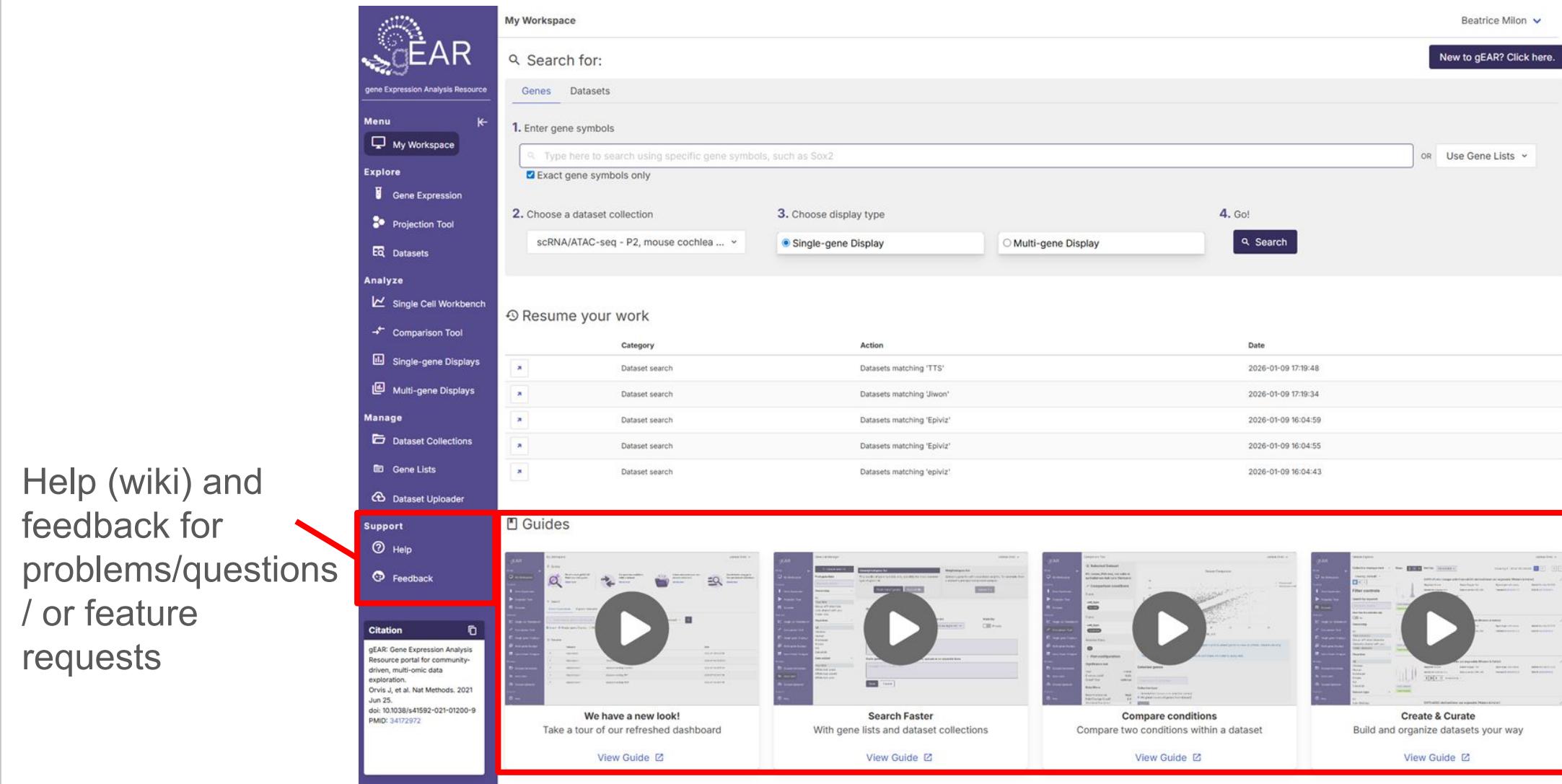
You'll be e-mailed a verification code. Enter that in the interface and your account will be created, and you'll be automatically logged in.

## User support

We provide support for and are available to:

- Any site issues
- Help formatting and uploading datasets
- Get feedback on new site features
- Create new display types for your data
- Create custom pages to show your data off for publication
  
- We are funded to support you!

# Finding help and reporting an issue



The screenshot shows the gEAR website's main search interface. On the left, a sidebar menu includes sections for My Workspace, Explore (Gene Expression, Projection Tool, Datasets), Analyze (Single Cell Workbench, Comparison Tool, Single-gene Displays, Multi-gene Displays), Manage (Dataset Collections, Gene Lists, Dataset Uploader), and Support (Help, Feedback). A red box highlights the 'Support' section. Below the sidebar is a 'Citation' box. The main content area has a search bar at the top with tabs for Genes and Datasets. Below the search bar is a step-by-step guide: 1. Enter gene symbols, 2. Choose a dataset collection, 3. Choose display type (radio buttons for Single-gene Display or Multi-gene Display), and 4. Go! A 'Search' button is also present. Underneath this is a 'Resume your work' section showing a table of recent dataset searches. At the bottom, there is a 'Guides' section with four video thumbnails and their titles: 'We have a new look!', 'Search Faster', 'Compare conditions', and 'Create & Curate'.

Help (wiki) and feedback for problems/questions / or feature requests

1. Enter gene symbols  
2. Choose a dataset collection  
3. Choose display type  
4. Go!

Search

Resume your work

Category Action Date

Dataset search Datasets matching 'TTS' 2026-01-09 17:19:48

Dataset search Datasets matching 'Jiwon' 2026-01-09 17:19:34

Dataset search Datasets matching 'Epiviz' 2026-01-09 16:04:59

Dataset search Datasets matching 'Epiviz' 2026-01-09 16:04:55

Dataset search Datasets matching 'epiviz' 2026-01-09 16:04:43

Guides

We have a new look! Take a tour of our refreshed dashboard View Guide

Search Faster With gene lists and dataset collections View Guide

Compare conditions Compare two conditions within a dataset View Guide

Create & Curate Build and organize datasets your way View Guide

Video and slideshow guides for key pages found throughout the site

# 1. Lookup expression of a gene



You just joined a lab that studies the role of the transcription factor POU4F3. You are interested to find out:

1. Where is *Pou4f3* expressed in the inner ear?
2. Is it expressed in type I and type II HC in the vestibular system?
3. Do mutations in *Pou4f3* cause hearing loss in human or in mouse?
4. You want to see the expression of *Pou4f3* in the following dataset from your lab: P8, mouse, scRNA-seq, hair cells, Anc80-Ikzf2 transduced and control (Hertzano)

## Menu



My Workspace

Beatrice Milon

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Single Cell Workbench

Comparison Tool

Single-gene Displays

Multi-gene Displays

## Manage

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Dataset Uploader

## Support

Help

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## Citation

## My Workspace

Search for:

New to gEAR? Click here.

Genes

Datasets

## 1. Enter gene symbols

Pou4f3

 Exact gene symbols only

OR Use Gene Lists

## 2. Choose a dataset collection

Hearing (default) ▾

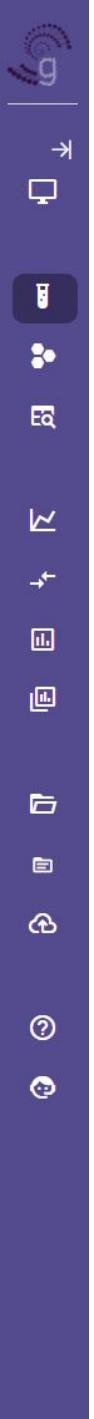
## 3. Choose display type

 Single-gene Display Multi-gene Display

## 4. Go!

Search

1. Where is *Pou4f3* expressed in the inner ear?



Search results (1) Showing results for: **pou4f3** - POU domain, class 4, transcription factor 3

Exact match Single-gene Display Multi-gene Display

**pou4f3**

External Resource Links: UCSC, UniParc, ENSEMBL, PubMed, HomoloGene, SHIELD, DVD

Functional annotation

Scoring method: Gene scope

P1, mouse, scRNA-seq, cochlear epithelium (Kelley)

Pou4f3

tSNE\_2

tSNE\_1

P0, mouse, RNA-seq, hair cells vs epithelial non-hair cells (Hertzano)

Pou4f3-level expression: 20, 843, 1,666, 2,490

P0, mouse, RNA-seq, cochlea, hair cells compared with rest of cochlear duct (Groves)

Pou4f3-level expression: 10, 14,433, 28,857, 43,280

P2, mouse, sc-qRT-PCR, cochlea (Heller)

Pou4f3-level expression: 0, 4, 7, 11

Deafness Gene Annotation

1. Where is Pou4f3 expressed in the inner ear?

39

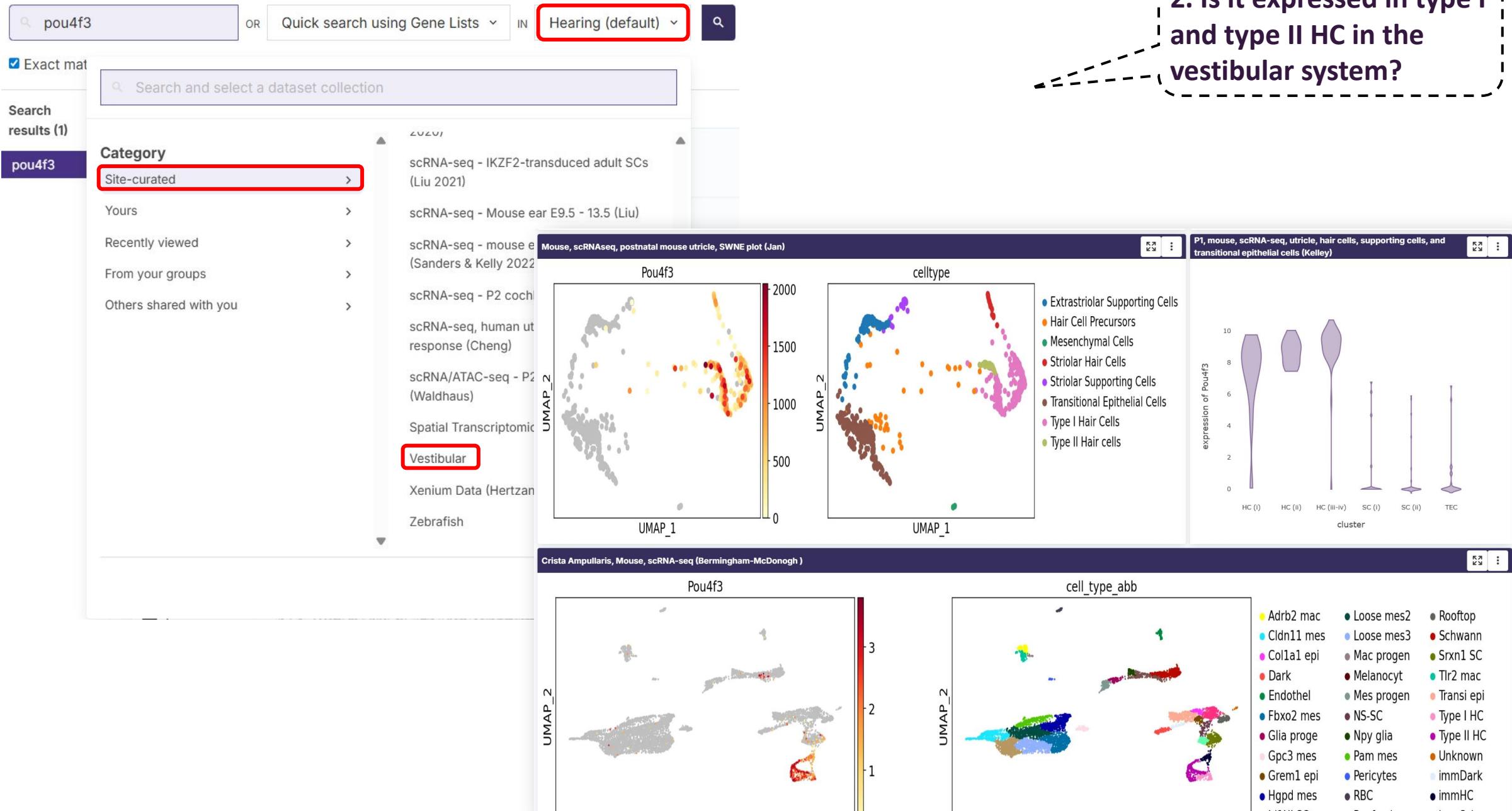
# 1. Lookup expression of a gene



You just joined a lab that studies the role of the transcription factor POU4F3. You are interested to find out:

1. Where is *Pou4f3* expressed in the inner ear?
2. Is it expressed in type I and type II HC in the vestibular system?
3. Do mutations in *Pou4f3* cause hearing loss in human or in mouse?
4. You want to see the expression of *Pou4f3* in the following dataset from your lab: P8, mouse, scRNA-seq, hair cells, *Anc80-Lkzf2* transduced and control (Hertzano)

**2. Is it expressed in type I and type II HC in the vestibular system?**



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## Citation

# 1. Lookup expression of a gene



You just joined a lab that studies the role of the transcription factor POU4F3. You are interested to find out:

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### 3. Do mutations in *Pou4f3* cause hearing loss in human or in mouse?

Search results (1)

pou4f3

Showing results for: **pou4f3 - POU domain, class 4, transcription factor 3**

External Resource Links ▾

UCSC UniParc ENSEMBL PubMed HomoloGene SHIELD DVD

Functional annotation ▾

Scoring method: Gene scope ▾

**P1, mouse, scRNA-seq, cochlear epithelium (Kelley)**

Deafness Gene Annotation

Deafness gene info

Phenotypes

behavior growth/size/body hearing/vestibular/ear  
nervous system

Deafness resource links

MGD

# 1. Lookup expression of a gene



You just joined a lab that studies the role of the transcription factor POU4F3. You are interested to find out:

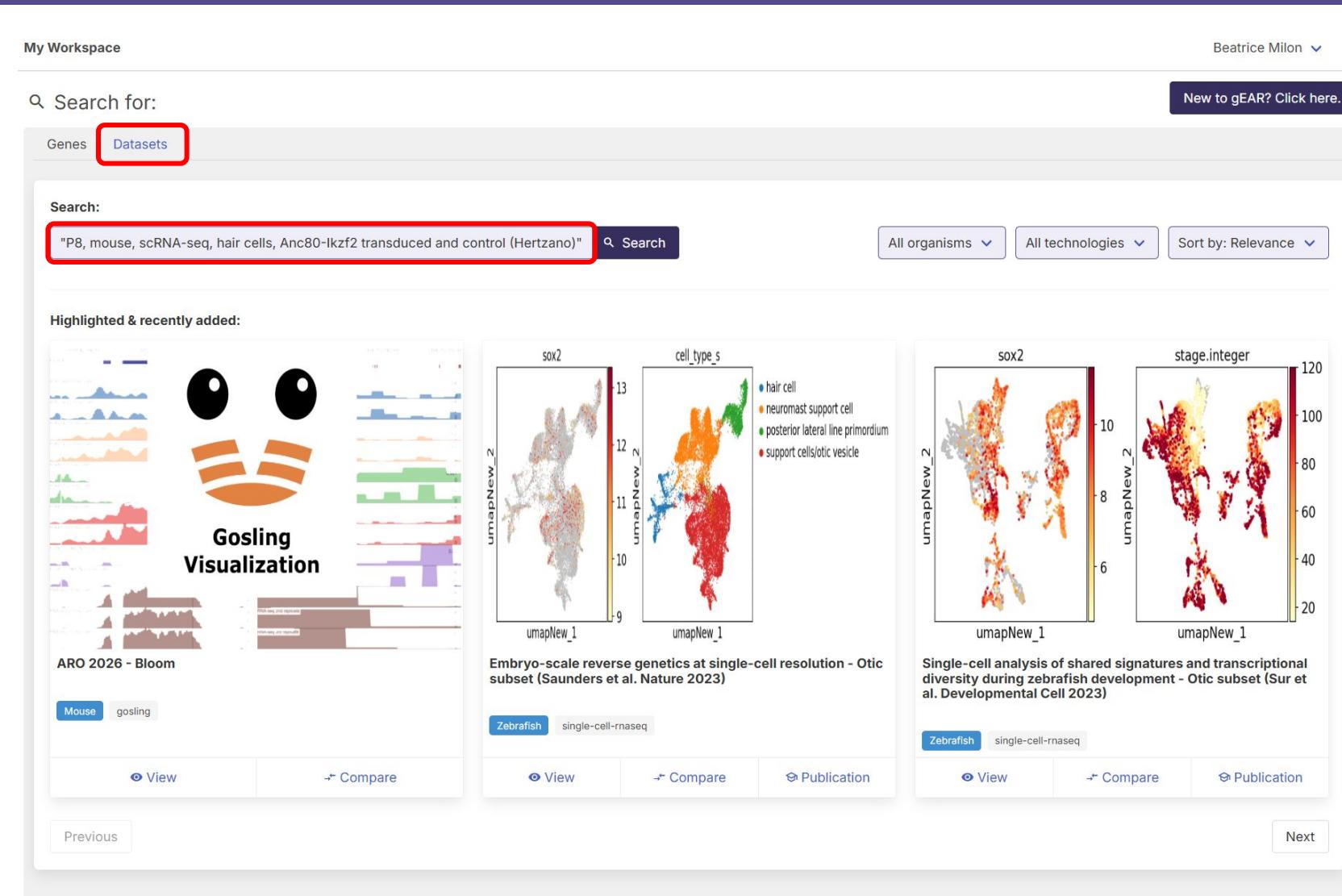
1. Where is *Pou4f3* expressed in the inner ear?
2. Is it expressed in type I and type II HC in the vestibular system?
3. Do mutations in *Pou4f3* cause hearing loss in human or in mouse?
4. You want to see the expression of *Pou4f3* in the following dataset from your lab: P8, mouse, scRNA-seq, hair cells, *Anc80-Lkzf2* transduced and control (Hertzano)

**Menu**

- My Workspace
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**Citation**

gEAR: Gene Expression Analysis Resource portal for community-driven, multi-omic data exploration.  
Orvis J, et al. Nat Methods. 2021 Jun 25.  
doi: 10.1038/s41592-021-01200-9  
PMID: 34172972



4. You want to see the expression of *Pou4f3* in the following dataset from your lab: P8, mouse, scRNA-seq, hair cells, Anc80-Ikzf2 transduced and control (Hertzano)

**Dataset Explorer**

Beatrice Milon

Collection management - View: Sort by: Relevance Showing 1 - 1 of 1 result 1

Hearing (default) Title Access Organism Owner Type Date added

P8, mouse, scRNA-seq, hair cells, Anc80-Ikzf2 transduced and control (Hertzano) Public Mouse Ronna Hertzano single-cell-rnaseq 2019-02-01

**Filter controls**

Search by keyword "P8, mouse, scRNA-seq, h" Show from this collection only No

Ownership All Your datasets Group-affiliated datasets Datasets shared with you Public datasets

Organism All Chicken Human

**P8, mouse, scRNA-seq, hair cells, Anc80-Ikzf2 transduced and control (Hertzano)**

Organism: Mouse Owner: Ronna Hertzano Type: single-cell-rnaseq Added: Thu Jan 31 2019  
 Annotation source: Ensemble ID Source version: 93 Pubmed ID: 30464345 GEO ID: GSE120462

**Analysis tools**

**Gene Expression Search**

Pou4f3 OR Use Gene Lists IN Choose a Dataset Collection

Exact match  Single-gene Display  Multi-gene Display

Search results (1) Showing results for: pou4f3 - POU domain, class 4, transcription factor 3

**pou4f3**

External Resource Links UCSC UniParc ENSEMBL PubMed HomoloGene SHIELD DVD

Functional annotation

Scoring method: Gene scope

**P8, mouse, scRNA-seq, hair cells, Anc80-Ikzf2 transduced and control (Hertzano)**

expression of Pou4f3

cell\_type

IHC OHC

vik- vik+

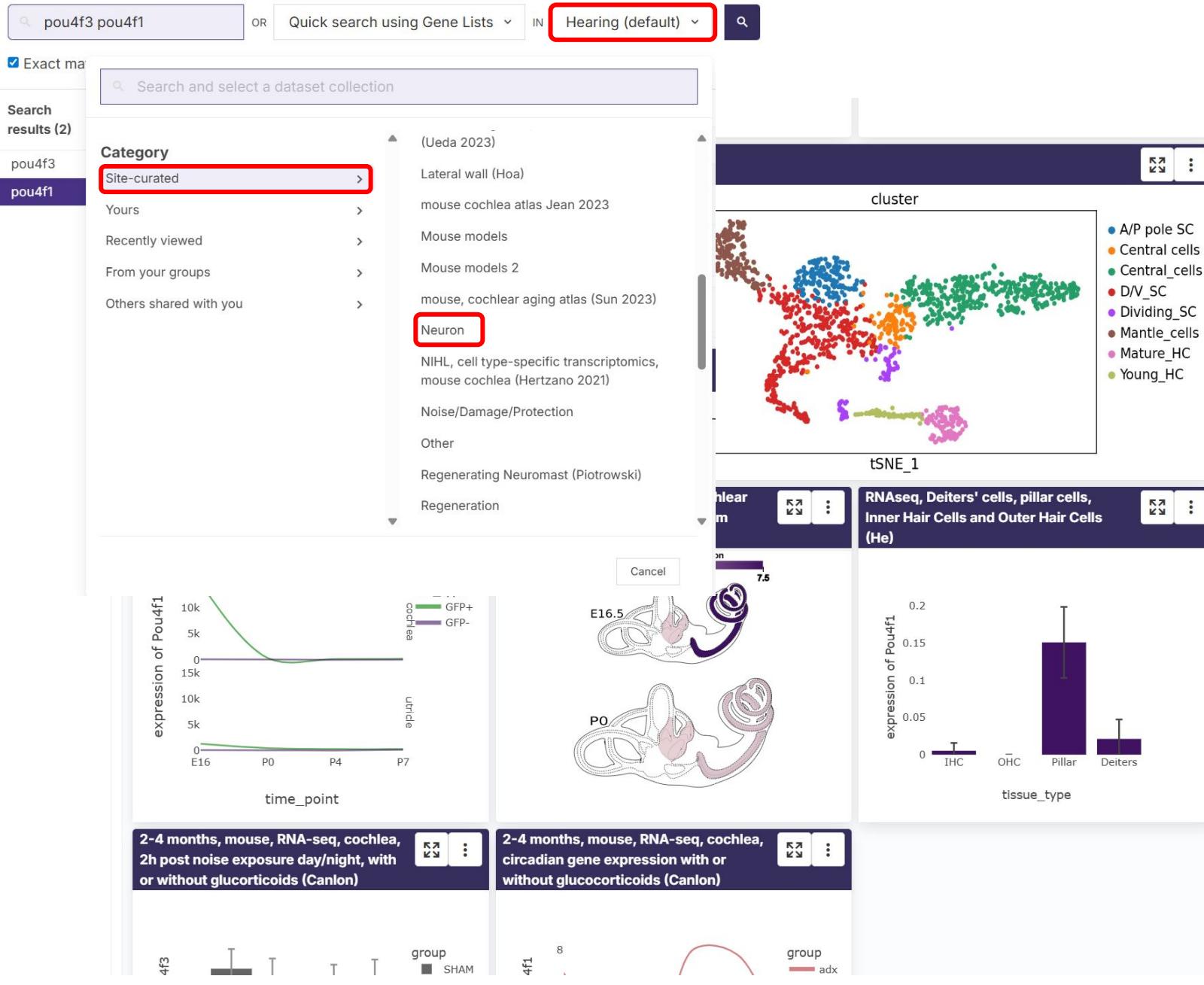
**4. You want to see the expression of Pou4f3 in the following dataset from your lab: P8, mouse, scRNA-seq, hair cells, Anc80-Ikzf2 transduced and control (Hertzano)**



## 2. Lookup expression of multiple genes

You now wonder if:

1. *Pou4f1* is also expressed in the ear and would like to easily look at *Pou4f1* and *Pou4f3*.
2. Are there other members of the POU4F family you are not aware of that are expressed in the ear?
3. Can you look at all these members together rather than looking at genes one at a time?



1. **Pou4f1** is also expressed in the ear and would like to easily look at **Pou4f1** and **Pou4f3**.



pou4f3 pou4f1 OR Quick search using Gene Lists IN **Neuron**

Exact match  Single-gene Display  Multi-gene Display

Search results (2)

pou4f3

**pou4f1**

Showing results for: pou4f1 - POU domain, class 4, transcription factor 1

External Resource Links

CDDS UCSC UniParc Uniprot/SWISSPROT ENSEMBL PubMed HomoloGene SHIELD PhosphoSite

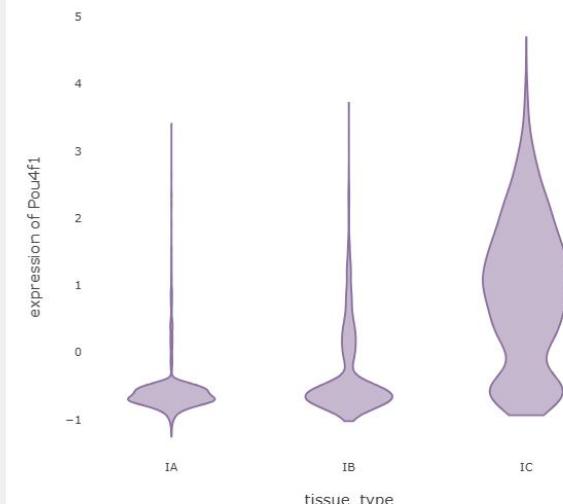
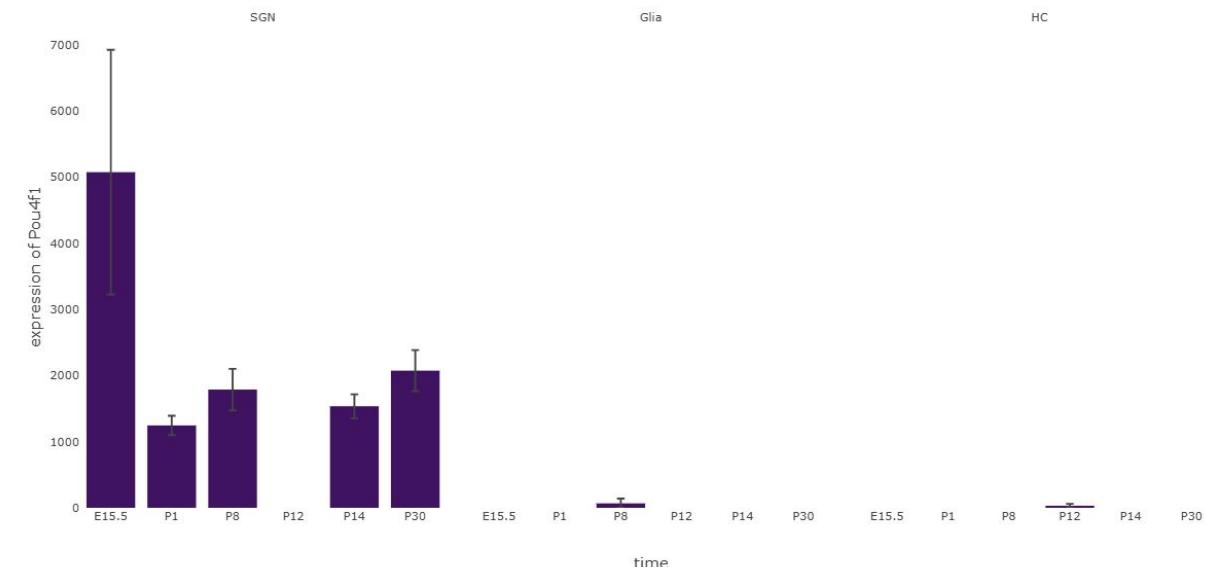
Functional annotation

Scoring method: Gene scope

E15.5, P1, P8, P14, P30, mouse, RNA-Seq, cochlea, spiral ganglion neurons (Liu)



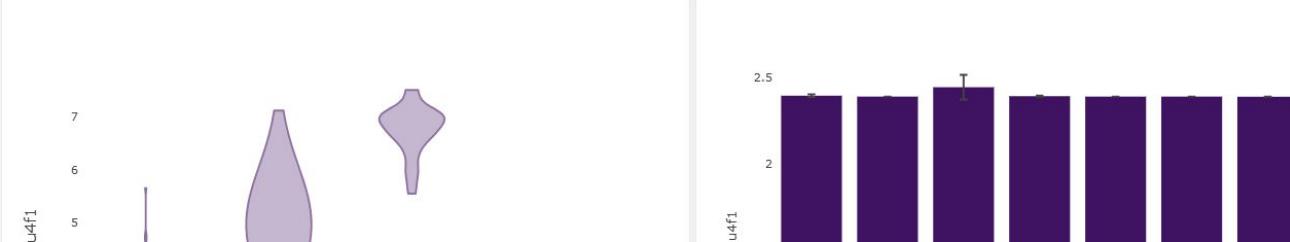
9 wko, mouse, scRNA-seq, cochlea, spiral ganglion neurons (Decibel Tx)



P25-P27, mouse, scRNA-seq, cochlear sensory neurons (Goodrich)



P24-P43, mouse, microarray, molecular profiling of seven types of medial vestibular nucleus (MVN) neurons as identified by electrophysiology (du Lac)



1. **Pou4f1** is also expressed in the ear and would like to easily look at **Pou4f1** and **Pou4f3**.



## 2. Lookup expression of multiple genes

You now wonder if:

1. *Pou4f1* is also expressed in the ear and would like to easily look at *Pou4f1* and *Pou4f3*.
2. Are there other members of the POU4F family you are not aware of that are expressed in the ear?
3. Can you look at all these members together rather than looking at genes one at a time?

pou4f

OR Quick search using Gene Lists IN Neuron

Exact match  Single-gene Display  Multi-gene Display

Search results (3)

Showing results for: pou4f1 - POU domain, class 4, transcription factor 1

**pou4f1**

pou4f2

pou4f3

External Resource Links

CCDS UCSC UniParc Uniprot/SWISSPROT ENSEMBL PubMed HomoloGene SHIEI  
PhosphoSite

Functional annotation

2. Are there other members of the POU4F family you are not aware of that are expressed in the ear?



## 2. Lookup expression of multiple genes

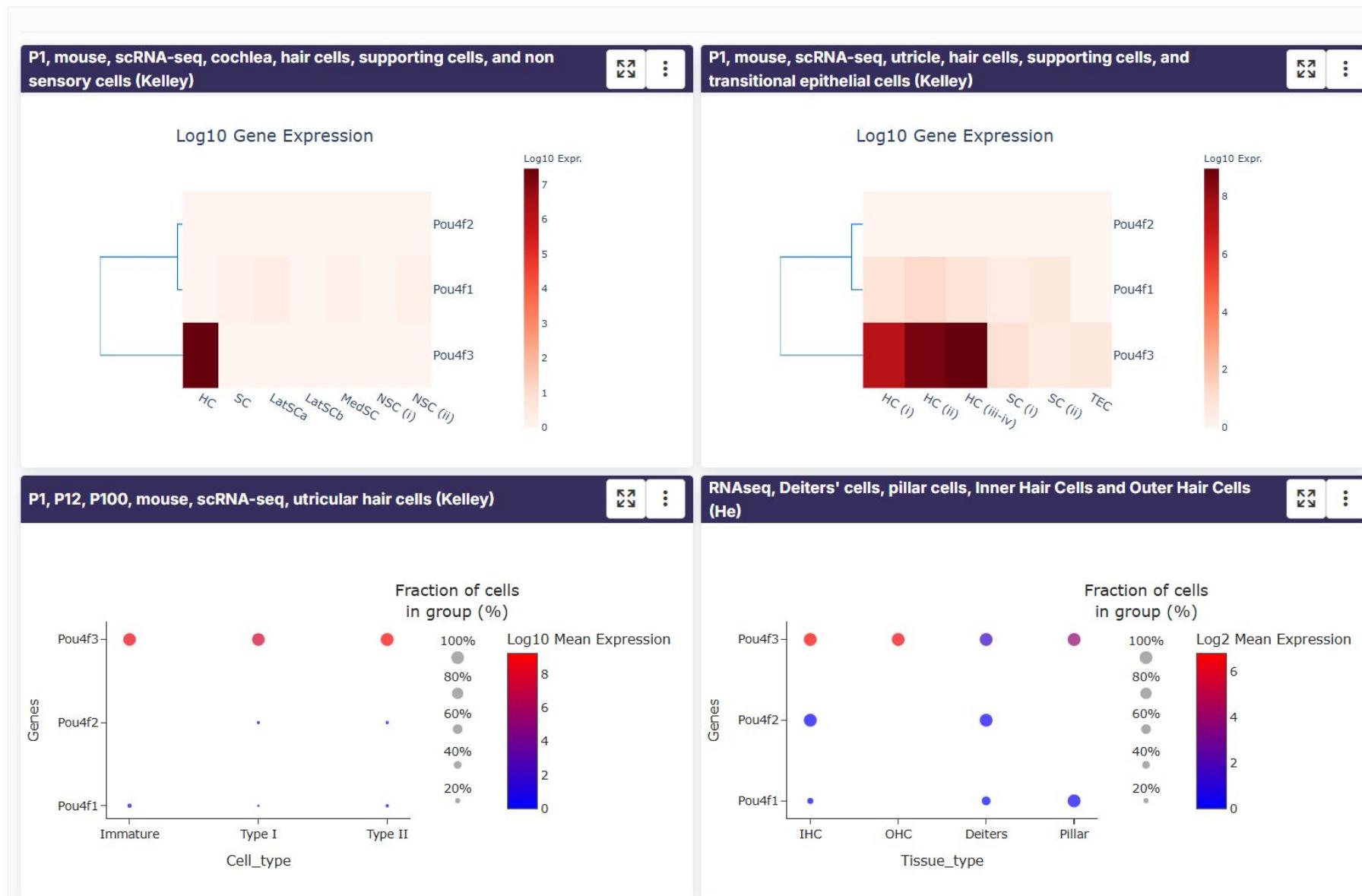
You now wonder if:

1. *Pou4f1* is also expressed in the ear and would like to easily look at *Pou4f1* and *Pou4f3*.
2. Are there other members of the POU4F family you are not aware of that are expressed in the ear?
3. Can you look at all these members together rather than looking at genes one at a time?

pou4f1 pou4f2 pou4f3

OR Quick search using Gene Lists

IN Hair cell

 Exact match  Single-gene Display Multi-gene Display

3. Can you look at all these members together rather than looking at genes one at a time?

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# Gene Expression

1. Using the default profile find the expression of *Atoh1* in the inner ear
2. RFX3 is an important transcription factor in hair cell development. Find out how many other *Rfx* genes there are by eliminating ‘exact match’ from your search.
3. Type the names of all *Rfx* genes in the search box and using the multi-gene search, look at their expression in the hair cell profile. What other *Rfx* genes are significantly expressed in hair cells?

## Citation



gEAR: Gene Expression Analysis Resource portal for community-driven, multi-omic data exploration.

Orvis J, et al. Nat Methods. 2021

Jun 25.

doi: 10.1038/s41592-021-01200-9

PMID: 34172972



Search

Gene Expression Explore Datasets

Atoh1 OR Quick search using Gene Lists IN Hearing (default)

Exact  Single-gene Display  Multi-gene Display

Search results (1)  
atoh1

Showing results for: atoh1 - atonal bHLH transcription factor 1

External Resource Links: CCDS, UCSC, UniParc, Uniprot/SWISSPROT, ENSEMBL, PubMed, HomoloGene, SHIELD  
PhosphoSite

Deafness Gene Annotation

Functional annotation

Scoring method: Gene scope

P1, mouse, scRNA-seq, cochlear epithelium (Kelley)

Atoh1

tsNE\_2

tsNE\_1

cell\_type

DC1/2, DC3, Hensen, IHC, IPC, iPhC, IS, IdC, LGER1, LGER2, LGER3, MGER, OHC, OPC, OS, Oc90, eIHC, eOHC

P0, mouse, RNA-seq, hair cells vs epithelial non-hair cells (Hertzano)

Atoh1-level expression: 20, 282, 543, 806

P0, mouse, RNA-seq, cochlea, hair cells compared with rest of cochlear duct (Groves)

Atoh1-level expression: 10, 9,042, 18,075, 27,108

P2, mouse, sc-qRT-PCR, cochlea (Heller)

Atoh1-level expression: 0, 4, 8, 12

time to practice

alarm clock

OR

IN



Exact match  Single-gene Display  Multi-gene Display

Search results (16)

- rfx1**
- rfx1a
- rfx1b
- rfx2
- rfx3
- rfx3-as1
- rfx4
- rfx5
- rfx6
- rfx7
- rfx7a
- rfx7b
- rfx8
- rfxank
- rfxap
- rfxapl1

Showing results for: rfx1 - regulatory factor X, 1 (influences HLA class II expression)

#### External Resource Links

[CCDS](#) [UCSC](#) [UniParc](#) [Uniprot/SWISSPROT](#) [ENSEMBL](#) [PubMed](#) [HomoloGene](#) [SHIELD](#)

[PhosphoSite](#)

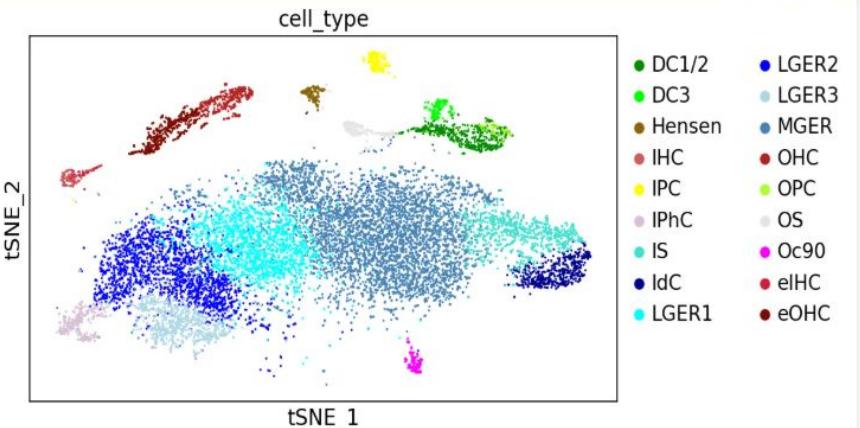
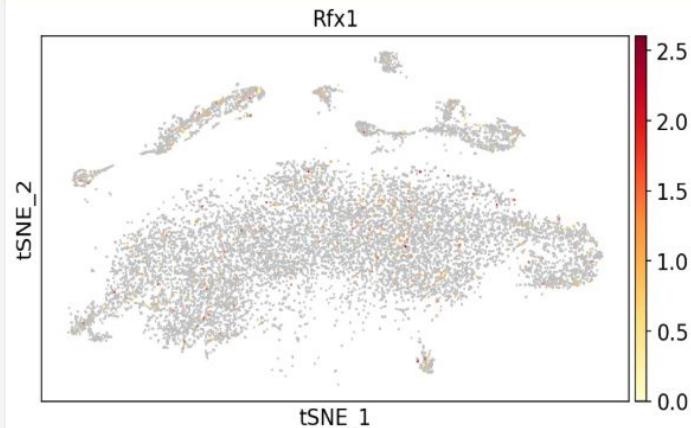
#### Deafness Gene Annotation



#### Functional annotation

Scoring method: [Gene scope](#)

P1, mouse, scRNA-seq, cochlear epithelium (Kelley)



P0, mouse, RNA-seq, hair cells vs epithelial non-hair cells (Hertzano)

Rfx1-level expression  
35 55 75 95

P0, mouse, RNA-seq, cochlea, hair cells compared with rest of cochlear duct (Groves)

Rfx1-level expression  
0 1,727 3,453 5,179

2. RFX3 is an important transcription factor in hair cell development. Find out how many other *Rfx* genes there are by eliminating 'exact match' from your search'.

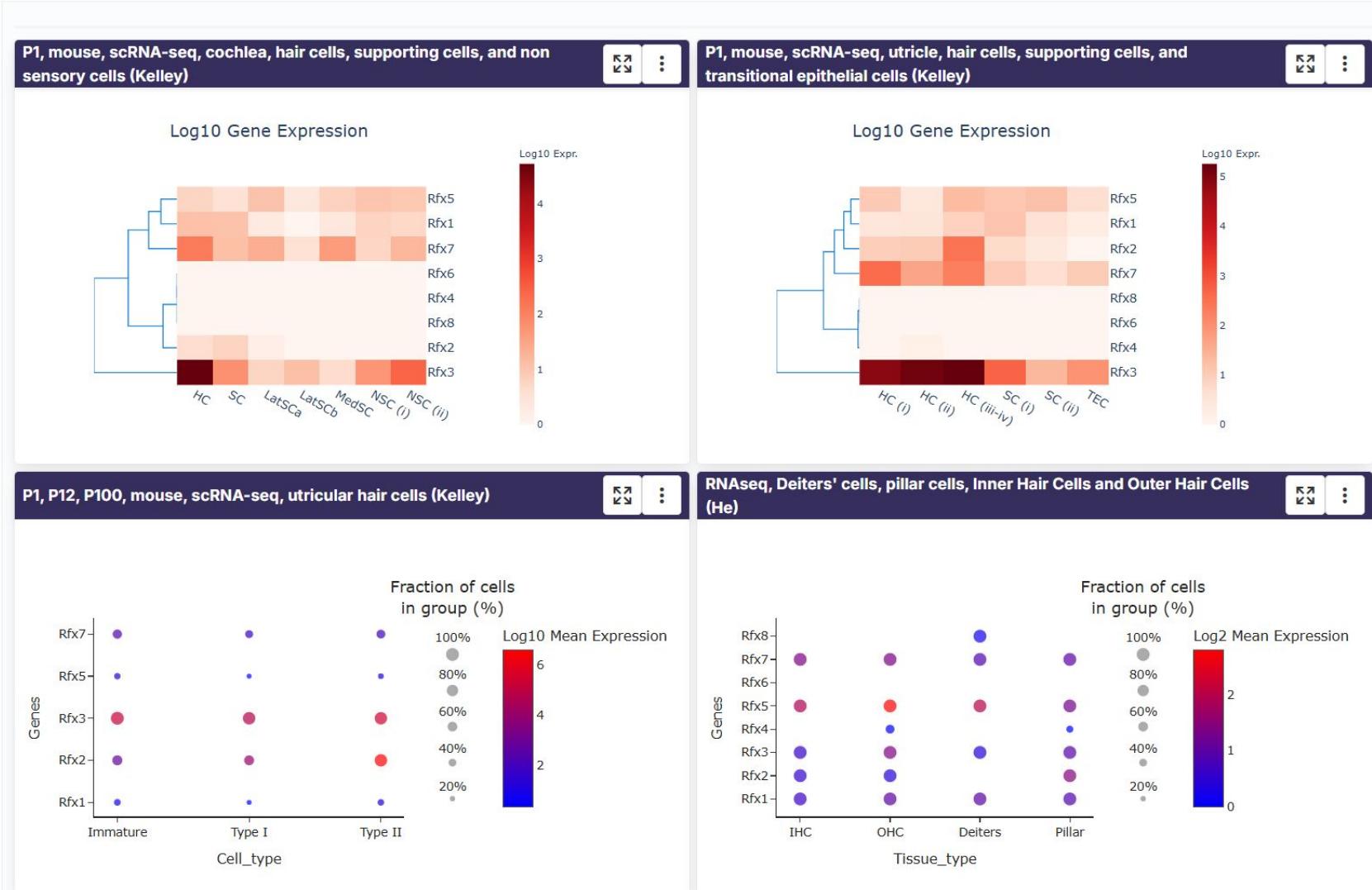




OR  IN

Exact match  Single-gene Display  Multi-gene Display

3. Type the names of all *Rfx* genes in the search box and using the multi-gene search, look at their expression in the hair cell profile. What other *Rfx* genes are significantly expressed in hair cells?





gene Expression Analysis Resource

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**Citation**



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doi: 10.1038/s41592-021-01200-9

PMID: 34172972

# Beatrice Milon

## Menu



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doi: 10.1038/s41592-021-01200-9

PMID: 34172972

### 3. Visualize epigenomics data



Transcriptomics data is essential to determine the expression of a gene. However, to discover regulatory networks, epigenomics data is also needed.

1. *Pou4f3* is expressed in HC at P1. What are the corresponding chromatin modifications around the gene?
2. What about the chromatin more distal from *Pou4f3*?
3. *Slc26a5*'s expression starts at P4. What does the chromatin looks like compared to *Pou4f3*?
4. Some data from my lab are on the UCSC Genome Browser. Can I view the epigenomic data from gEAR in UCSC?

Collection management - View: Sort by: Date uploaded Showing 1 - 16 of 16 results 1

Hearing (default)

**Filter controls**

Search by keyword

Show from this collection only  No

Ownership  All  Your datasets  Group-affiliated datasets  Datasets shared with you  Public datasets

Organism  All  Chicken  Human  Marmoset  Mouse  Rat  Zebrafish

Dataset type  All  Bulk RNASeq  Epigenetic  Microarray  Single-cell RNASeq  Spatial Transcriptomics

Date added  Any time  Within last week  Within last month  Within last year

Title	Access	Organism	Owner	Type	Date added
P1HC Regulatory Elements - Neils Lab2	Public	Mouse	Shaun Adkins	gosling	2026-05-03
<b>P1HC Regulatory Elements - Neils Lab2</b>	<b>Organism</b> Mouse	<b>Owner</b> curator	<b>Type</b> gosling	<b>Added</b> Mon May 03 2021	
	<b>Annotation source</b> Not given	<b>Source version</b> Not given	<b>Pubmed ID</b> Not available	<b>GEO ID</b> Not available	
<input type="button" value="Analysis tools"/> <input type="button" value=""/>					
<b>Public dataset</b>					
<b>Not downloadable</b>					
Supporting cells trans differentiation - ATAC, P1SC_responsive, nonresponsive, control - Neils Lab2	Public	Mouse	curator	gosling	2021-05-03
Cochlear support cells - cSC and uSC - Neils Lab2	Public	Mouse	curator	gosling	2021-05-03
P1SC Supporting cells - Neils Lab2	Public	Mouse	curator	gosling	2021-05-03
<b>P1HC Regulatory Elements - Neils Lab2</b>	<b>Public</b>	<b>Mouse</b>	<b>curator</b>	<b>gosling</b>	<b>2021-05-03</b>
Karen Avraham Dataset	Public	Mouse	curator	gosling	2021-04-07
ATAC-seq, Mouse Cochlea, P2, Epithelial (CD326+) vs Non-Epithelial (CD326-), V3 (Hertzano)	Public	Mouse	curator	gosling	2021-02-08
ATAC-seq, Mouse Cochlea, P2, Epithelial (CD326+) vs Non-Epithelial (CD326-), Reupload (Hertzano)	Public	Mouse	curator	gosling	2021-02-06
P1 HCs and induced-HCs, mouse, ATAC-seq and ChIP-seq (Segil)	Public	Mouse	Jayaram	gosling	2020-07-31

**1. Pou4f3 is expressed in HC at P1. What are the corresponding chromatin modifications around the gene?**

## Gene Expression Search

Beatrice Milon ▾

 OR  IN   Exact match  Single-gene Display  Multi-gene Display

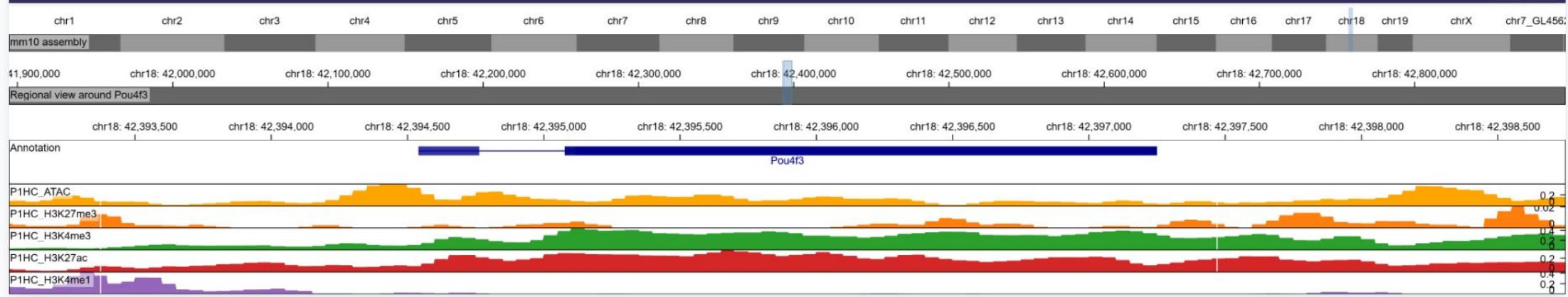
Search results (1)

Showing results for: pou4f3 - POU domain, class 4, transcription factor 3

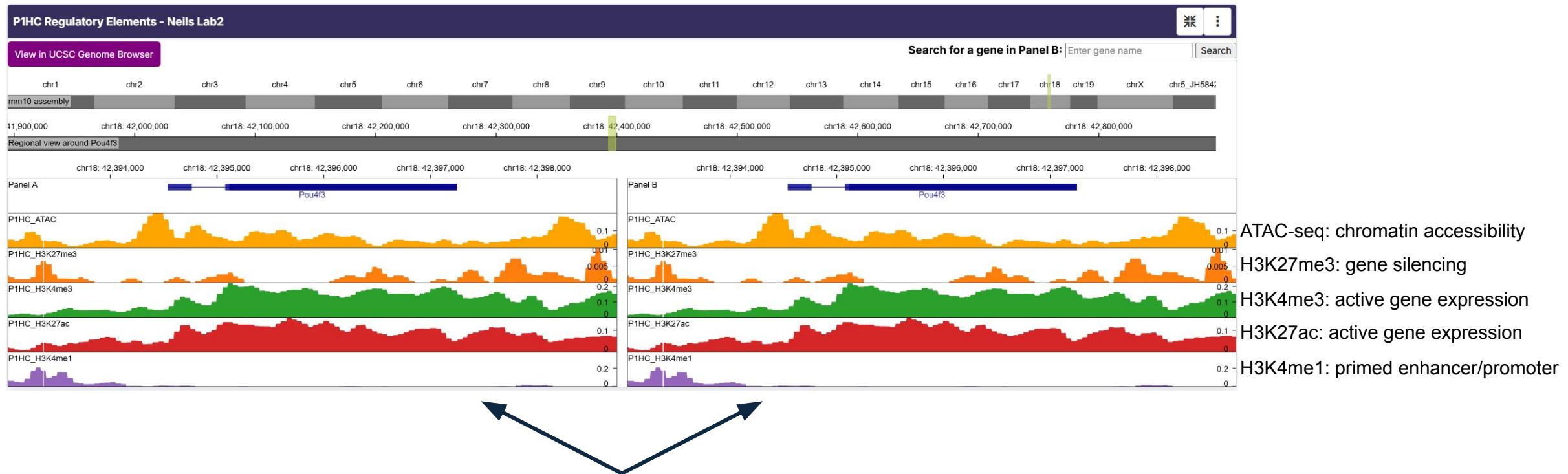
pou4f3

External Resource Links [UCSC](#) [UniParc](#) [ENSEMBL](#) [PubMed](#) [HomoloGene](#) [SHIELD](#) [DVD](#)Functional annotation Scoring method:  

## P1HC Regulatory Elements - Neils Lab2



1. *Pou4f3* is expressed in HC at P1. What are the corresponding chromatin modifications around the gene?



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## Citation



gEAR: Gene Expression Analysis Resource portal for community-driven, multi-omic data exploration.

Orvis J, et al. Nat Methods. 2021 Jun 25.

doi: 10.1038/s41592-021-01200-9

PMID: 34172972

### 3. Visualize epigenomics data

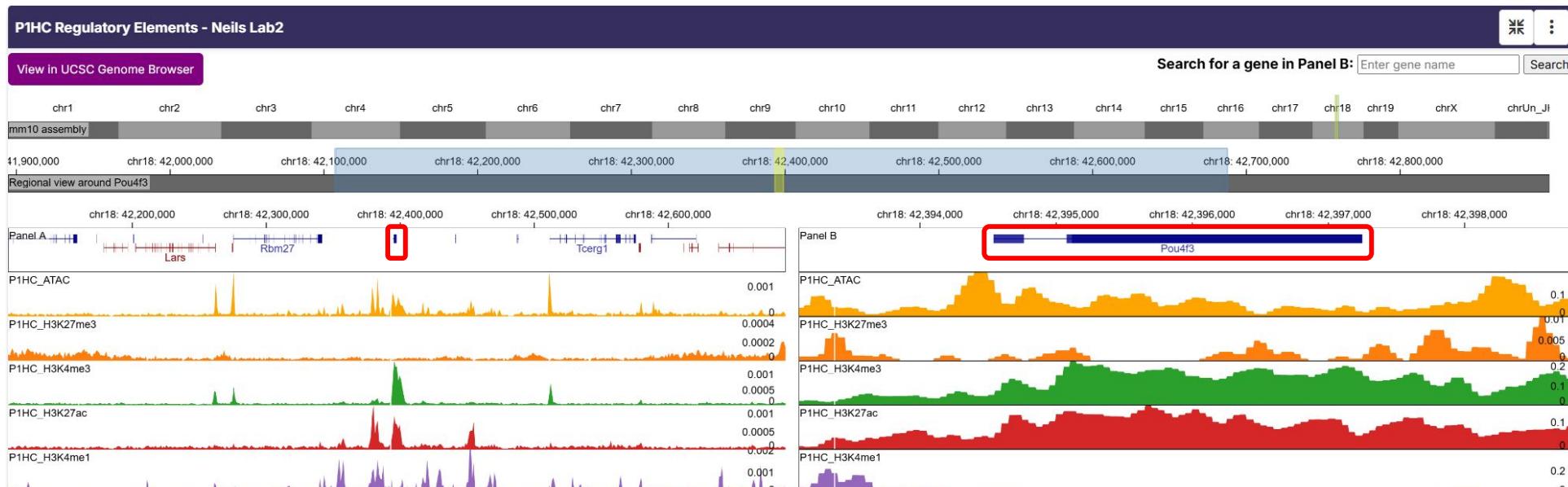


Transcriptomics data is essential to determine the expression of a gene. However, to discover regulatory networks, epigenomics data is also needed.

1. *Pou4f3* is expressed in HC at P1. What are the corresponding chromatin modifications around the gene?
2. What about the chromatin more distal from *Pou4f3*?
3. *Slc26a5*'s expression starts at P4. What does the chromatin looks like compared to *Pou4f3*?
4. Some data from my lab are on the UCSC Genome Browser. Can I view the epigenomic data from gEAR in UCSC?



## 2. What about the chromatin more distal from *Pou4f3*?



Zoomed Out panel

Zoomed In panel

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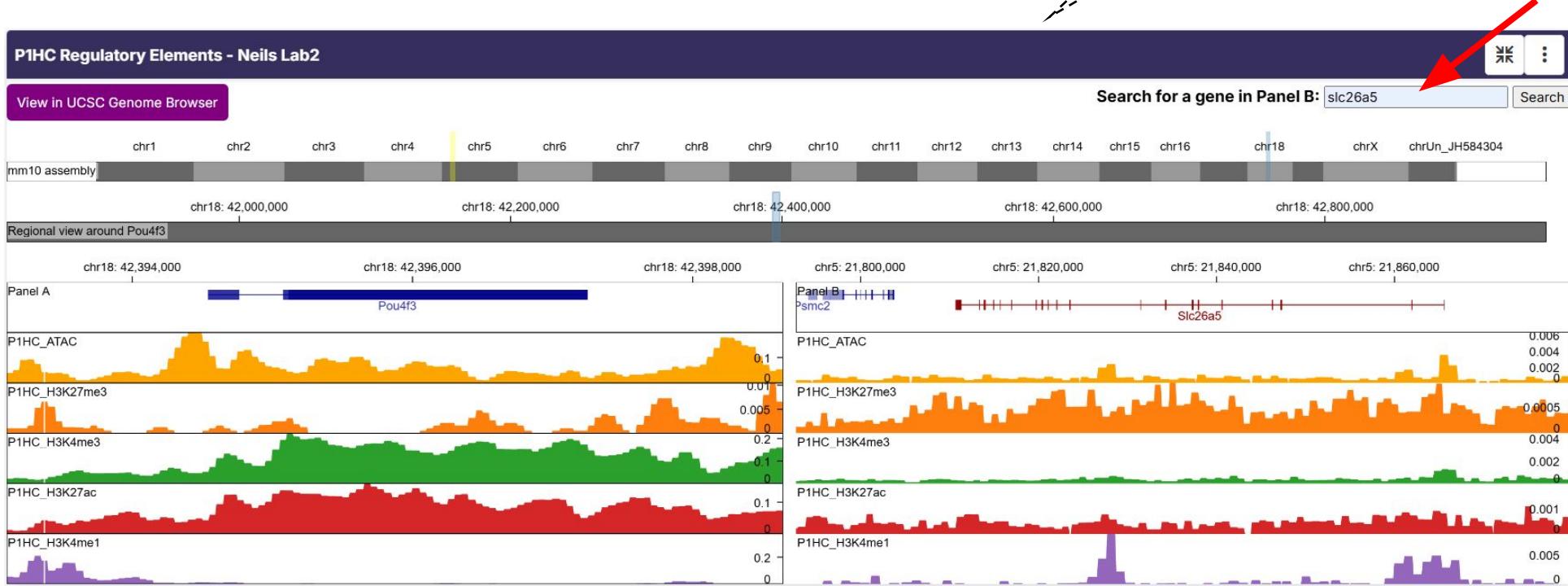
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**Menu**[My Workspace](#)**Explore**[Gene Expression](#)[Projection Tool](#)[Datasets](#)**Analyze**[Single Cell Workbench](#)[Comparison Tool](#)[Single-gene Displays](#)[Multi-gene Displays](#)**Manage**[Dataset Collections](#)[Gene Lists](#)[Dataset Uploader](#)**Support**[Help](#)[Feedback](#)**Citation**

gEAR: Gene Expression Analysis Resource portal for community-driven, multi-omic data exploration.

Orvis J, et al. Nat Methods. 2021 Jun 25.

doi: 10.1038/s41592-021-01200-9

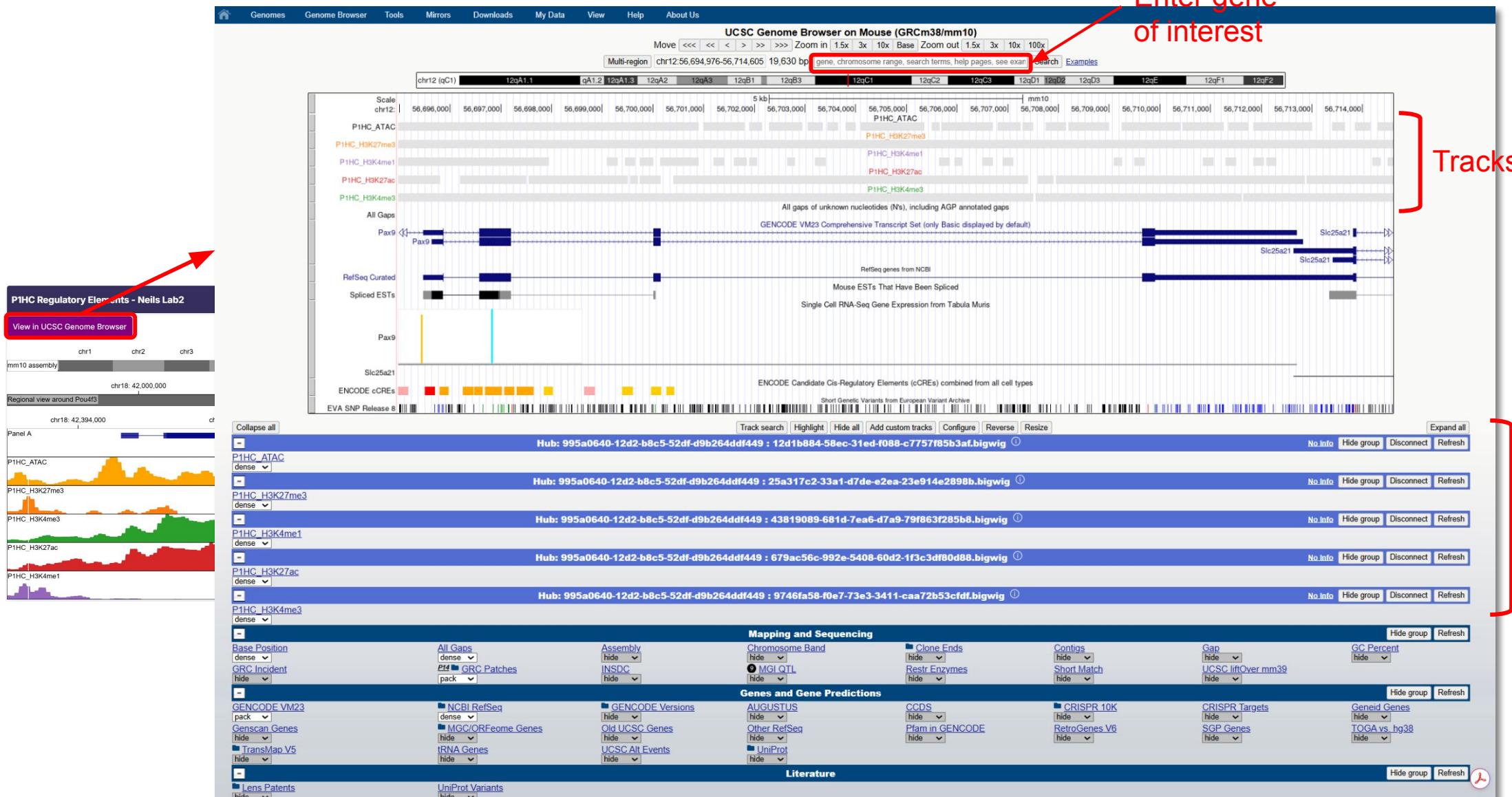
PMID: 34172972

### 3. Visualize epigenomics data

**Vecteezy**

**Transcriptomics data is essential to determine the expression of a gene. However, to discover regulatory networks, epigenomics data is also needed.**

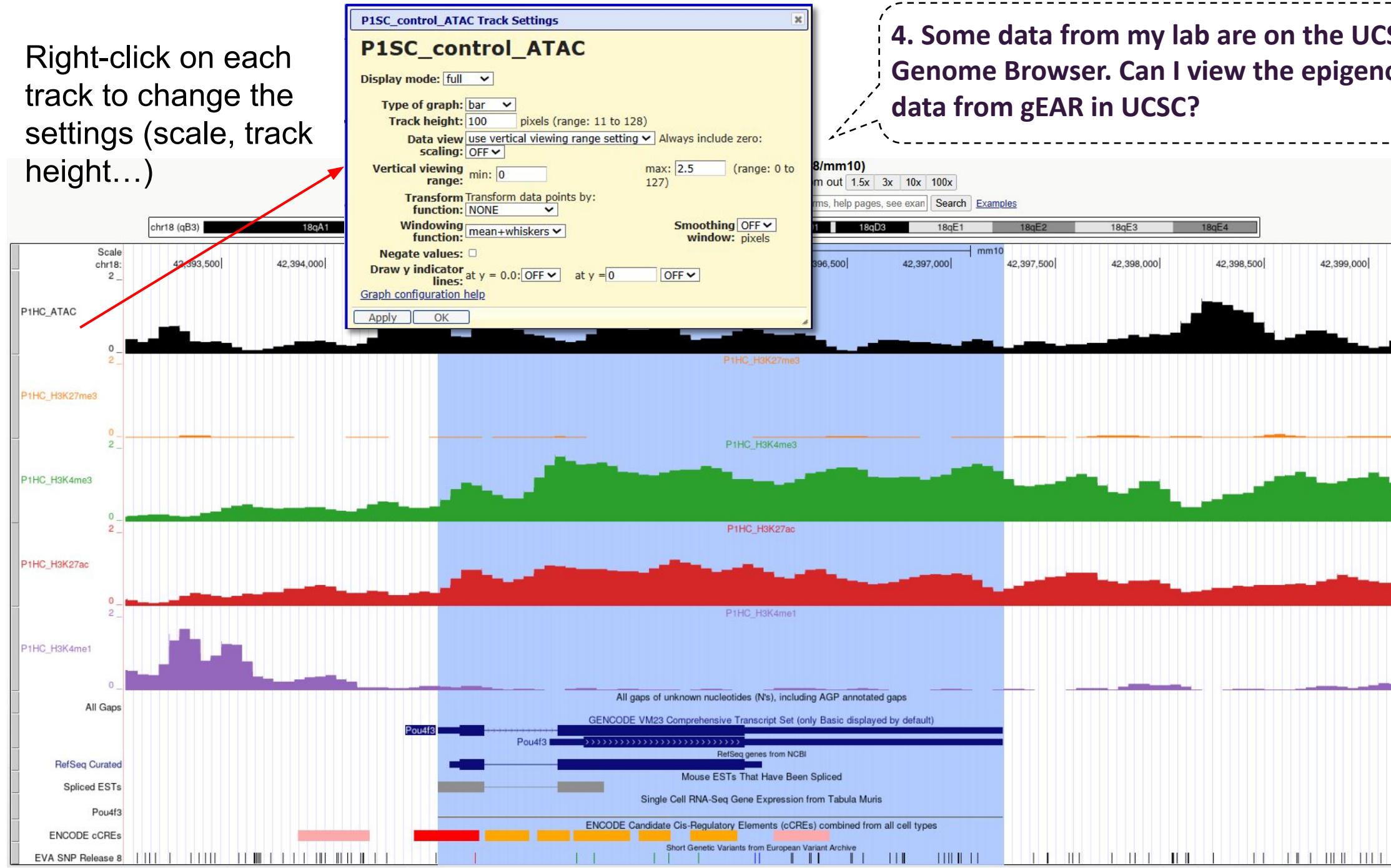
1. *Pou4f3* is expressed in HC at P1. What are the corresponding chromatin modifications around the gene?
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#### 4. Some data from my lab are on the UCSC Genome Browser. Can I view the epigenomic data from gEAR in UCSC?

Right-click on each track to change the settings (scale, track height...)



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# Epigenomics Data

1. Using the “Supporting cells trans differentiation - ATAC, P1SC\_responsive, nonresponsive, control - Neils Lab2” profile, check the proximal and distal chromatin around *Pou4f3* in the 3 cell types.
2. Open the tracks in UCSC and customize the tracks.

Collection management - View: Sort by: Date uploaded Showing 1 - 16 of 16 results 1

**Filter controls**

Search by keyword Keyword search Show from this collection only No

Ownership All Your datasets Group-affiliated datasets Datasets shared with you Public datasets

Organism All Chicken Human Marmoset Mouse Rat Zebrafish

Dataset type All Bulk RNASeq Epigenetic Microarray Single-cell RNASeq Spatial Transcriptomics

Date added Any time Within last week Within last month Within last year

Title Access Organism Owner Type Date added

ARO 2026 - Bloom	Public	Mouse	Shaun Adkins	gosling	2026-01-12
Litao Bigwigs - Gosling test	Public	Mouse	Shaun Adkins	gosling	2025-08-21
ear enhancers	Public	Mouse	Jonathan Ting	gosling	2023-06-20
K4PUYU4K	Public	Mouse	Wkkww	gosling	2022-06-05
ATAC-seq of Sox2+, Atoh1+ and Lgr5+ P2 mouse cochlear cells, in comparison to Lgr5+ derived cochlear organoids 0-10 days in culture	Public	Mouse	Gurmannah Kalra	gosling	2021-08-24
P2, mouse, scATAC-seq, Chromatin Accessibility (Waldhaus)	Public	Mouse	curator	gosling	2021-05-20
Atoh1 binding Hair cells - Neils Lab2	Public	Mouse	curator	gosling	2021-05-03
perinatal maturation of SC - E17, P1 and P6 SC - Neils Lab2	Public	Mouse	curator	gosling	2021-05-03
<b>Supporting cells trans differentiation - ATAC, P1SC_responsive, nonresponsive, control - Neils Lab2</b>	Public	Mouse	curator	gosling	2021-05-03
Cochlear support cells - cSC and uSC - Neils Lab2	Public	Mouse	curator	gosling	2021-05-03
P1SC Supporting cells - Neils Lab2	Public	Mouse	curator	gosling	2021-05-03
P1HC Re	Public	Mouse	curator	gosling	2021-05-03
Karen Av	Public	Mouse	curator	gosling	2021-05-03
ATAC-se (CD326-)	Public	Mouse	curator	gosling	2021-05-03
ATAC-se (CD326-)	Public	Mouse	curator	gosling	2021-05-03
P1 HCs a	Public	Mouse	curator	gosling	2021-05-03

time to practice

1. Using the “Supporting cells trans differentiation - ATAC, P1SC\_responsive, nonresponsive, control - Neils Lab2” profile, check the proximal and distal chromatin around *Pou4f3* in the 3 cell types.

**Supporting cells trans differentiation - ATAC, P1SC\_responsive, nonresponsive, control - Neils Lab2**

Organism: Mouse      Owner: curator      Type: gosling      Added: Mon May 03 2021

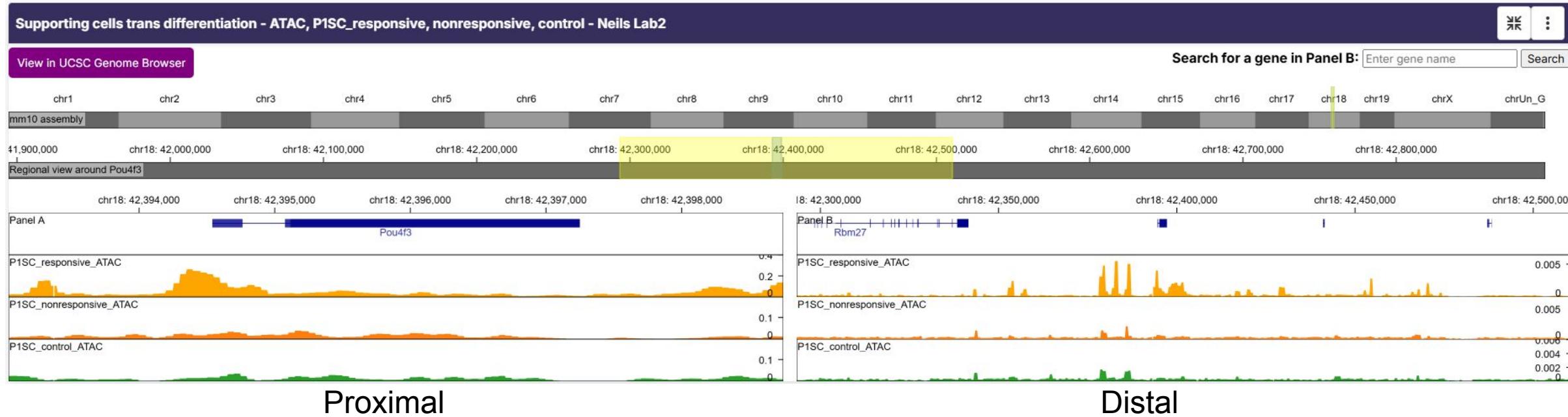
Annotation source: Not given      Source version: Not given      Pubmed ID: Not available      GEO ID: Not available

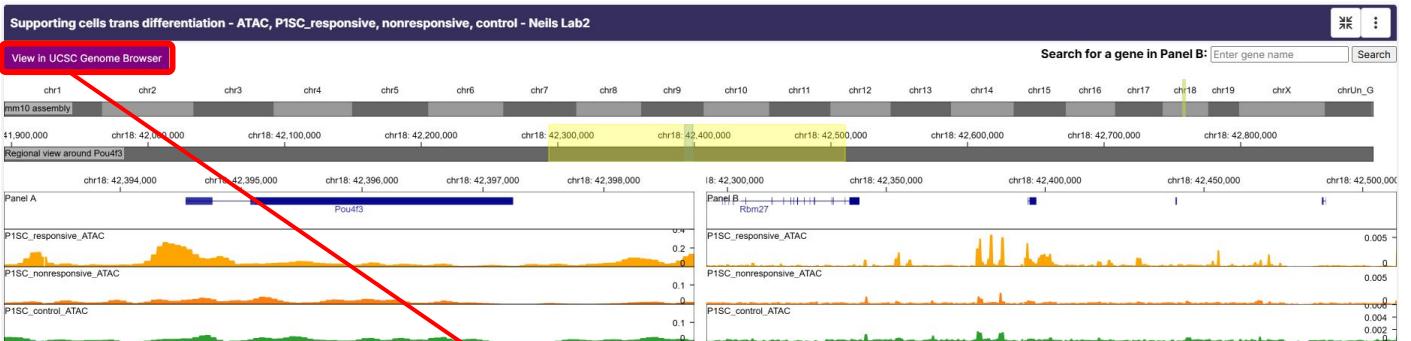
Analysis tools:

Not downloadable



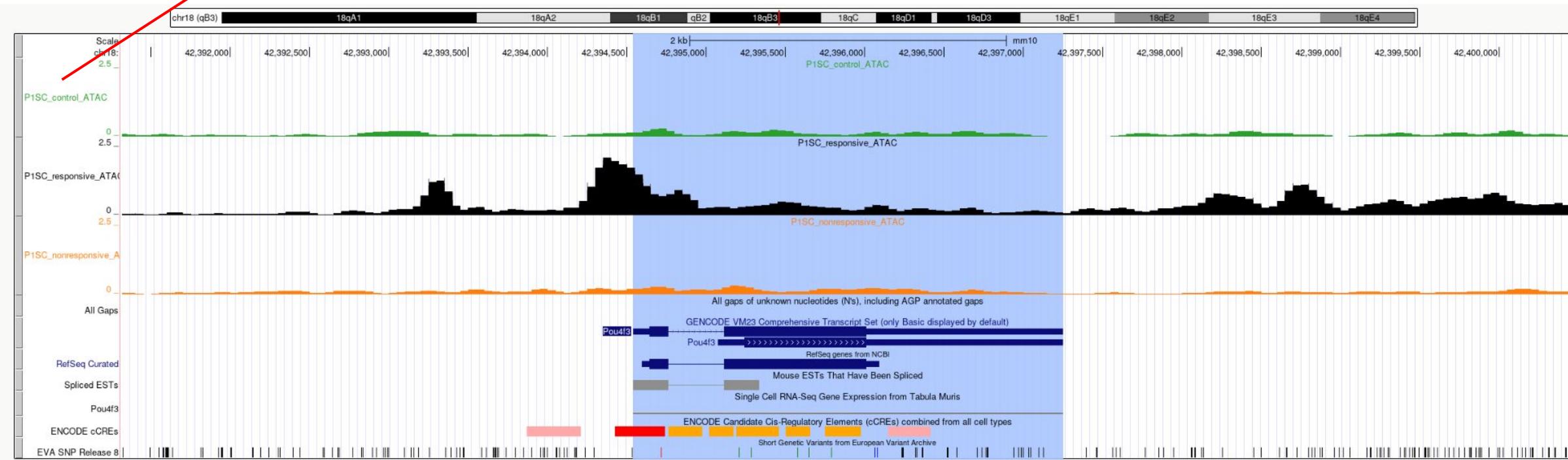
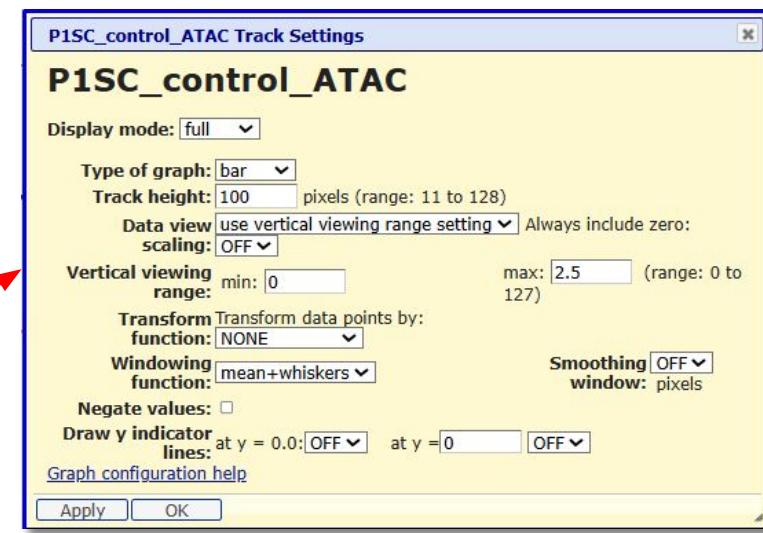
1. Using the “Supporting cells trans differentiation - ATAC, P1SC\_responsive, nonresponsive, control - Neils Lab2” profile, check the proximal and distal chromatin around *Pou4f3* in the 3 cell types.





2. Open the tracks in UCSC and customize the tracks.





2. Open the tracks in UCSC and customize the tracks.



## 4. Compare expression between two conditions



Cochlear hair cells (the sensory cells) are divided into two types: inner and outer hair cells. You are interested in the molecular differences between the two cell types.

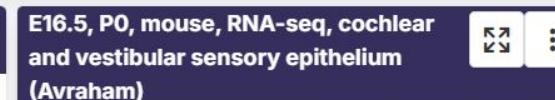
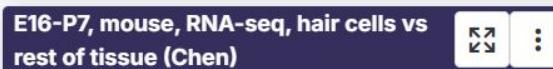
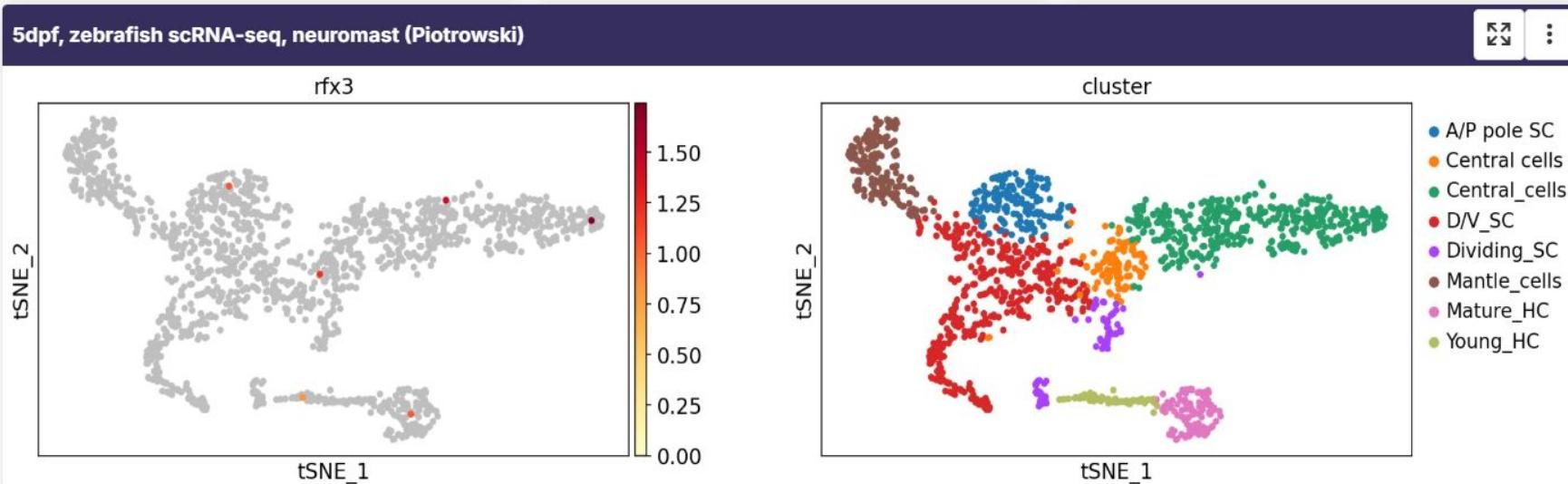
1. Are there genes that are more specific for outer hair cells when compared to inner hair cells?
2. Are some of the canonical hair cell markers differentially expressed between inner and outer HCs?
3. How can I remember the genes that I saw when hovering-over?
4. Can I see the genes I selected in other datasets?

OR

IN

🔍

Exact match  Single-gene Display  Multi-gene Display



- Choose Display
- Dataset Information
- Dataset publication
- GEO Information
- Take Notes
- Single Cell Workbench
- Comparison Tool →
- Single-gene Curator
- Multi-gene Displays
- Download Bundle
- Download H5AD

1. Are there genes that are more specific for outer hair cells when compared to inner hair cells?



## 1 Select a dataset ✓

Current dataset: RNAseq, Deiters' cells, pillar cells, Inner Hair Cells and Outer Hair Cells (He)

## 2 Select conditions you want to compare ^

Series to compare

Required

X-axis (query) condition

Required

Y-axis (reference) condition

Required

- Deiters
- IHC
- OHC
- Pillar

- Deiters
- IHC
- OHC
- Pillar

Number of selected observations: 22

Selected filters:

### Extra filters to apply to both conditions

Useful for doing X vs Y comparison on subsets of data beyond the main series to compare.

## 3 Select comparison parameters [Optional] ^

Significance test

Select test

Wilcoxon rank-sum

Data filters

Log2

P-value cutoff

0.05

Report output as

2.0

Cutoff filter

Colorize

Fold Change Cutoff (>=N)

No filter

Standard Deviation

Plot

1. Are there genes that are more specific for outer hair cells when compared to inner hair cells?



Selected Dataset

RNAseq, Deiters' cells, pillar cells, Inner Hair Cells and Outer Hair Cells (He)

Comparison conditions

X-axis

tissue\_type  
OHC

Y-axis

tissue\_type  
IHC

Selected filters

All

Plot configuration

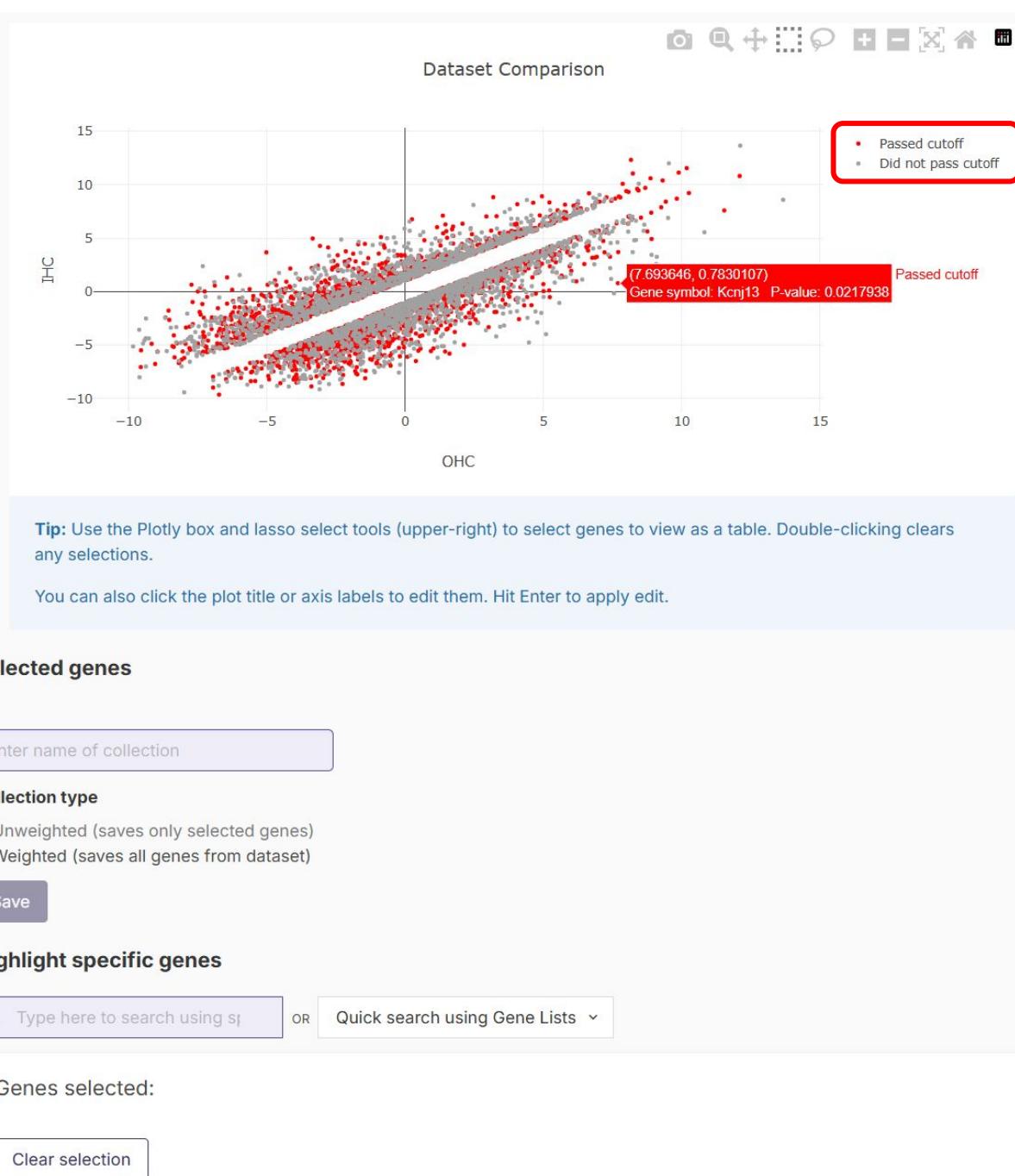
Significance test

Test: wilcoxon  
P-value cutoff: 0.05  
Cutoff filter: colorize

Data filters

Report output as: log2  
Fold Change Cutoff: 2.0  
Standard Deviation: 0

Edit Parameters



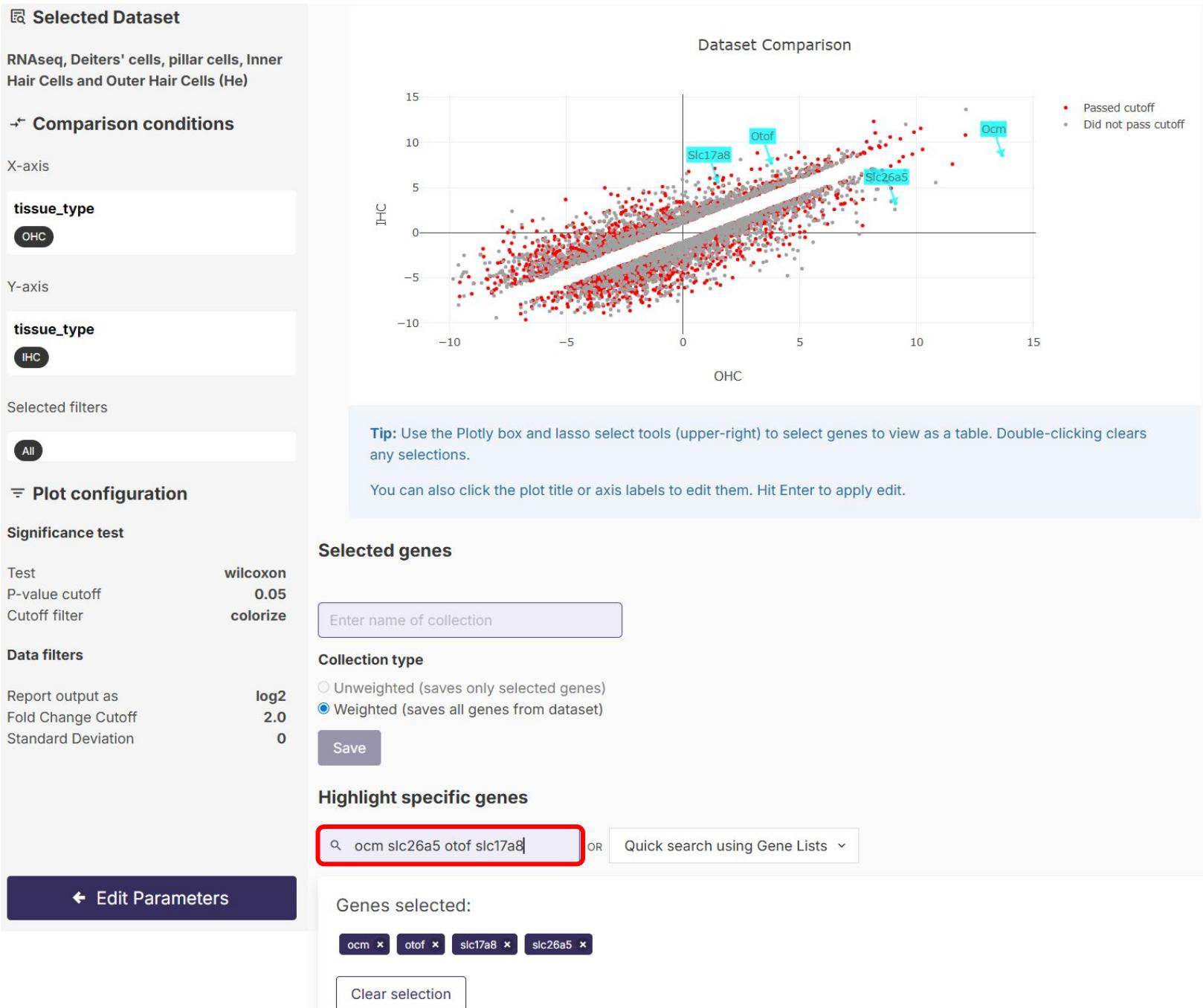
2. Are some of the canonical hair cell markers differentially expressed between inner and outer HCs



## 4. Compare expression between two conditions

Cochlear hair cells (the sensory cells) are divided into two types: inner and outer hair cells. You are interested in the molecular differences between the two cell types.

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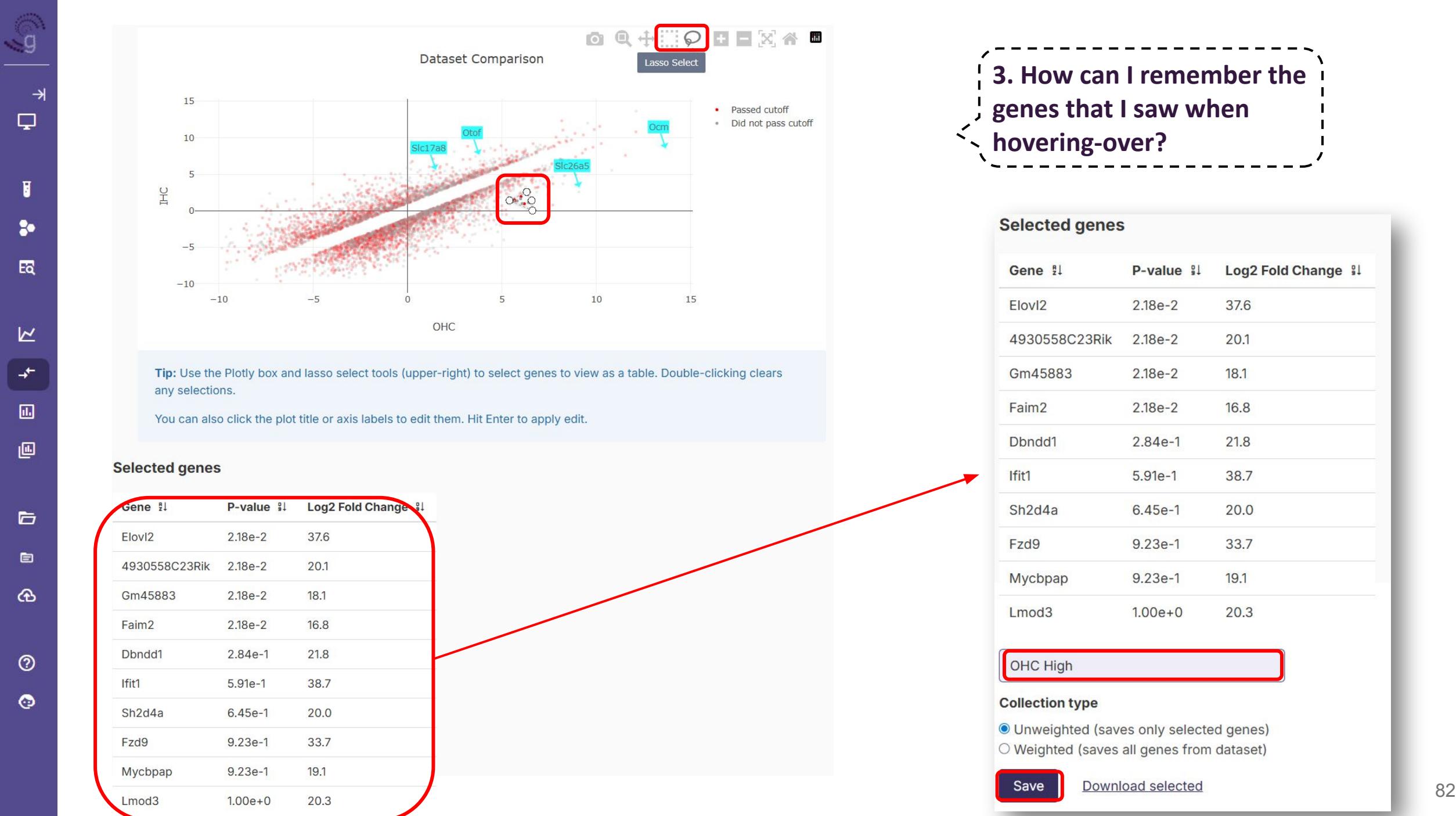
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4. Can I see the genes I selected in other datasets?



Type here to search using sp OR Quick search using Gene Lists IN Hearing (default)

Exact  Single-gene Display  Multi-gene Display

Resume

Category
Gene search
Multigene search
Multigene search
Gene search
Multigene search

Saved Items

- Favorites >
- Recent >
- Saved gene lists >**
- Shared gene lists >

Gene Lists

- + Cochlear HC July >
- + Decibel/Muller SGN markers >
- + Demo for ZF for MBHD >
- + Exercise 3 >
- + He IHC markers >
- + IHC Feb19 >
- + Monday >
- ✓ OHC High >**
- + Pillar/Deiter P0-P2 >
- + Type 1a >
- + Type 1b >
- + Type 1c >

Genes

- ✓ 4930558C23Rik
- ✓ Dbndd1
- ✓ Elovl2
- ✓ Faim2
- ✓ Fzd9
- ✓ Gm45883
- ✓ Ifit1
- ✓ Lmod3
- ✓ Mycbpap
- ✓ Sh2d4a

#### 4. Can I see the genes I selected in other datasets?

Type here to search using sp OR **OHC High** IN Hearing (default)

Exact  Single-gene Display  Multi-gene Display



## Expression Comparison

1. Find the Adult, Zebrafish, RNA-seq, sorted inner ear HCs vs non-sensory cells (He).
2. Compare the expression between the two conditions (Hair Cell vs Non-Sensory Surrounding Cell).  
Filter out any genes using a t-test with p-value less than 0.001.
3. Use either the box-select or lasso select to select a few genes from the plot. Save as an unweighted gene list.



1. Find the Adult, Zebrafish, RNA-seq, sorted inner ear HCs vs non-sensory cells (He).

Collection management + View: Sort by: Date uploaded Showing 1 - 4 of 4 results 1

### Filter controls

Search by keyword Keyword search

Show from this collection only No

Ownership All Your datasets Group-affiliated datasets Datasets shared with you Public datasets

Organism All Chicken Human Marmoset Mouse Rat Zebrafish

Dataset type All Bulk RNASeq Epigenetic (Epiviz) Microarray Single-cell RNASeq Spatial Transcriptomics

Title	Access	Organism	Owner	Type	Date added
Adult, Zebrafish, RNA-seq, sorted inner ear HCs vs non-sensory cells (He)	Public	Zebrafish	curator	bulk-rnaseq	2020-04-30
<b>Adult, Zebrafish, RNA-seq, sorted inner ear HCs vs non-sensory cells (He)</b>	<b>Organism</b> Zebrafish <b>Annotation source</b> Ensembl	<b>Owner</b> curator <b>Source version</b> 84	<b>Type</b> bulk-rnaseq <b>Added</b> Wed Apr 29 2020	<b>Pubmed ID</b> 29406519 <b>GEO ID</b> GSE101693	
		<b>Analysis tools</b> ▾	Single-gene curator Multi-gene curator Comparison tool Single-cell analysis workbench		
RNASEQ, hair cell , zebrafish late	Public	Zebrafish	Ronna Hertzano	bulk-rnaseq	2019-01-18
U-tagged HC mRNA and whole larvae input, RNA-seq	Public	Zebrafish	Joshua Orvis	bulk-rnaseq	2018-10-22
4dpf, zebrafish, RNA-seq, TU-tagged hair cells mRNA and whole larvae input (Nicolson)	Public	Zebrafish	Ronna Hertzano	bulk-rnaseq	2018-10-22



2. Compare the expression between the two conditions (Hair Cell vs Non-Sensory Surrounding Cell). Filter out any genes using a t-test with p-value less than 0.001.



**1 Select a dataset**

Current dataset: Adult, Zebrafish, RNA-seq, sorted inner ear HCs vs non-sensory cells (He)

**2 Select conditions you want to compare**

**Series to compare** Required

condition

**X-axis (query) condition** Required **Y-axis (reference) condition** Required

Hair cell

non-sensory surrounding cell

Hair cell

non-sensory surrounding cell

Number of selected observations: 6

Selected filters:

**Extra filters to apply to both conditions**  
Useful for doing X vs Y comparison on subsets of data beyond the main se

**3 Select comparison parameters [Optional]**

**Significance test**

Select test: T-test

P-value cutoff: 0.001

Cutoff filter: Filter out

**Data filters**

Report output as: Log2

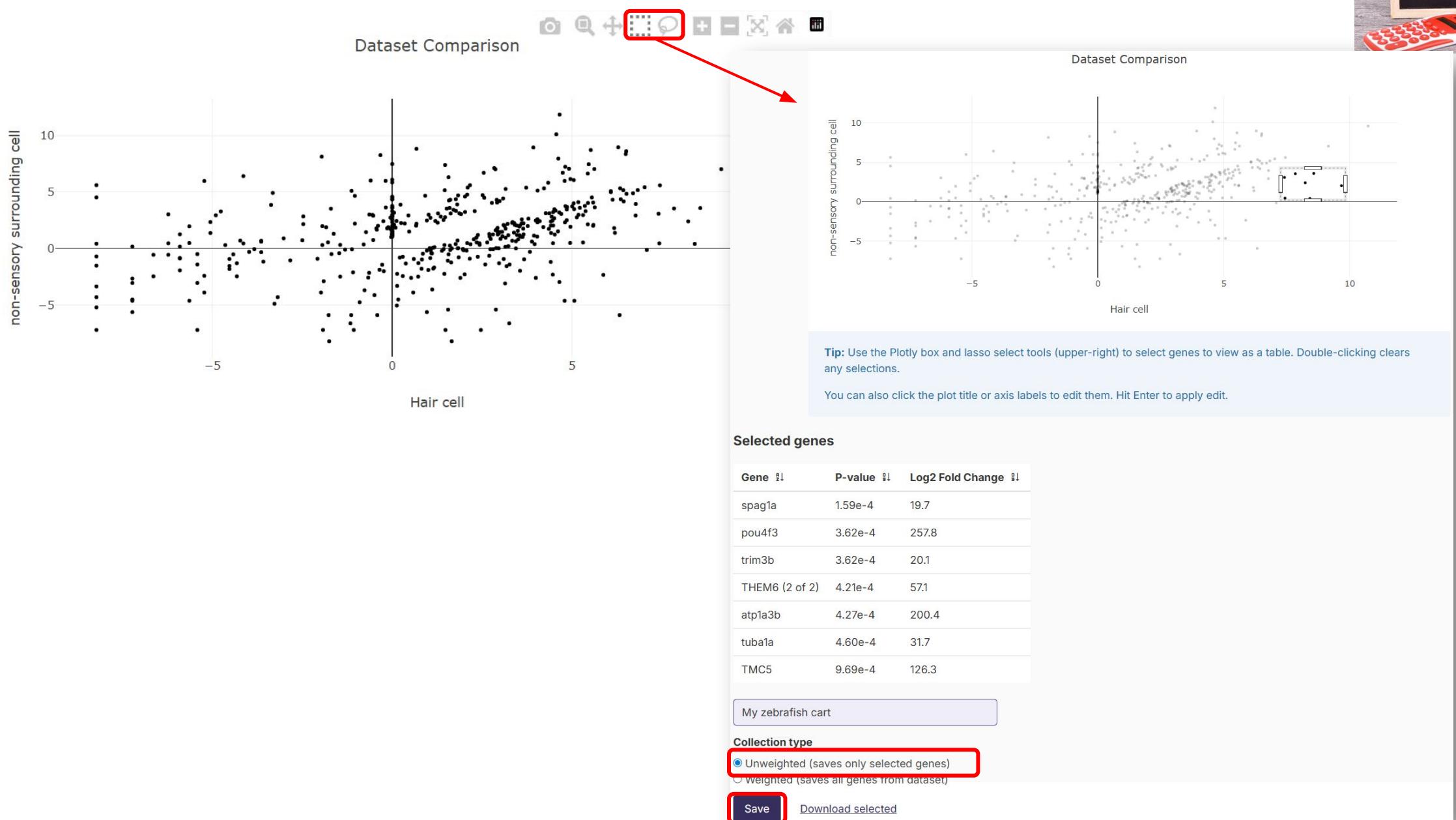
Fold Change Cutoff (>=N): 2.0

Standard Deviation: No filter

**Plot**



3. Use either the box-select or lasso select to select a few genes from the plot. Save as an unweighted gene list.



## 5. Explore scRNA-seq datasets - Primary Analysis



**Single cell RNA-seq has revolutionized our ability to understand the molecular identity of cells. Every cell in the tissue has its entire transcriptome recorded allowing a wealth of information to be captured.**

**However, for people with no informatics background, scRNA-seq datasets can be intimidating.**

- 1. You want to analyze clusters that you saw in a publication, but you're not sure where to start.**
- 2. What are the top markers for each cluster and how do I find their expression?**
- 3. I am really interested in the molecular differences between Hensen cells and OHCs.**



► Nat Commun. 2020 May 13;11:2389. doi: [10.1038/s41467-020-16113-y](https://doi.org/10.1038/s41467-020-16113-y)

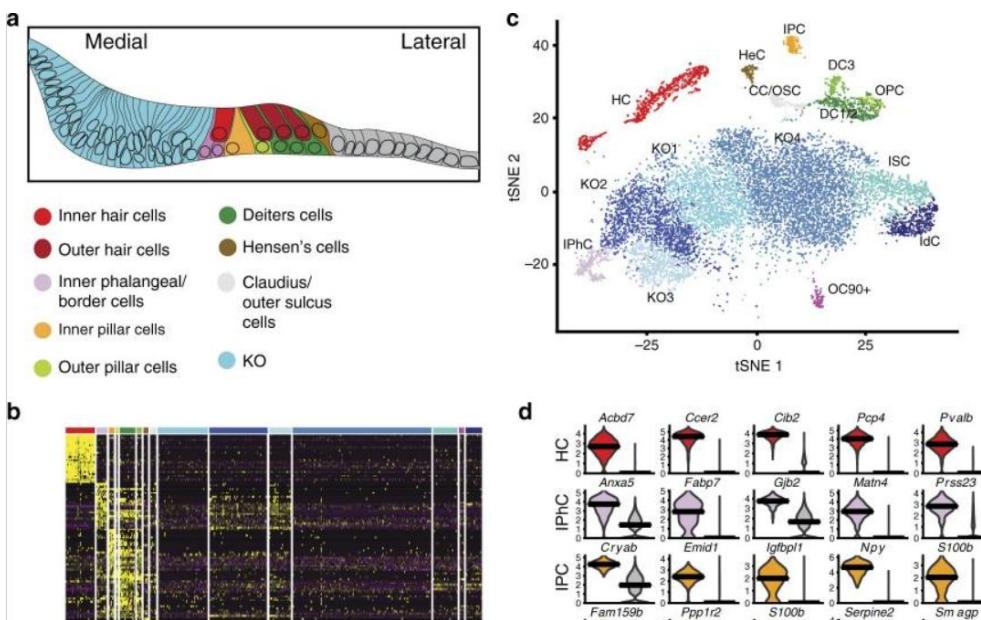
1. You want to analyze clusters that you saw in a publication, but you're not sure where to start.

## Characterization of the development of the mouse cochlear epithelium at the single cell level

Likhitha Kolla<sup>1, #</sup>, Michael C Kelly<sup>1, #</sup>, Zoe F Mann<sup>2</sup>, Alejandro Anaya-Rocha<sup>1</sup>, Kathryn Ellis<sup>1</sup>, Abigail Lemons<sup>1</sup>, Adam T Palermo<sup>3</sup>, Kathy S So<sup>3</sup>, Joseph C Mays<sup>1</sup>, Joshua Orvis<sup>4</sup>, Joseph C Burns<sup>3</sup>, Ronna Hertzano<sup>4, 5</sup>, Elizabeth C Driver<sup>1</sup>, Matthew W Kelley<sup>1, □</sup>

► Author information ► Article notes ► Copyright and License information

PMCID: PMC7221106 PMID: [32404924](https://pubmed.ncbi.nlm.nih.gov/32404924/)



points, similar examinations of many other cell types and developmental transitions are clearly possible. The entire data set is available through the gEAR Portal (

<https://umgear.org/p?l=f7baf4ea>

Inner and outer HCs were known to be transcriptionally distinct by E16 (ref. <sup>23</sup>). In contrast, the timing and degree of transcriptomic differences between SC types was less obvious. The



Pou4f3 OR Quick search using Gene Lists IN Kelley lab datasets

Exact match  Single-gene Display  Multi-gene Display

Search results (1) pou4f3

Showing results for: pou4f3 - POU domain, class 4, transcription factor 3

External Resource Links: UCSC, UniParc, ENSEMBL, PubMed, HomoloGene, SHIELD, DVD

Functional annotation

E16, mouse, scRNA-seq, cochlear epithelium (Kelley)

Pou4f3

tSNE\_2

tSNE\_1

cell\_type

tSNE\_2

tSNE\_1

GER Hensen IHC IPC IPhC IS IdC LER/Bmp4 LER/Fst

LGER LPro MPro OHC\_1 OHC\_2 OS Oc90/Otoa Oc90/Sparc1 Ube2c+

P1, mouse, scRNA-seq, cochlear epithelium (Kelley)

Pou4f3

tSNE\_2

tSNE\_1

cell\_type

tSNE\_2

tSNE\_1

Choose Display

Dataset Information

Dataset publication

GEO Information

Take Notes

Single Cell Workbench

Comparison Tool

Single-gene Curator

Multi-gene Displays

Download Bundle

Download H5AD

Download Image

P7, mouse, scRNA-seq, cochlear epithelium (Kelley)

1. You want to analyze clusters that you saw in a publication, but you're not sure where to start.



## 1 Select a dataset ✓

Current dataset: P1, mouse, scRNA-seq, cochlear epithelium (Kelley)

Expand dataset selection tool

## 2 Select new or saved analysis

Current analysis: None selected

Select an analysis

Select an analysis

New

**Imported analysis**

**Primary analysis**

Imported analysis is highlighted with a red box and a red arrow points from it to the analysis selection section below.

Public saved analyses

sadkins test

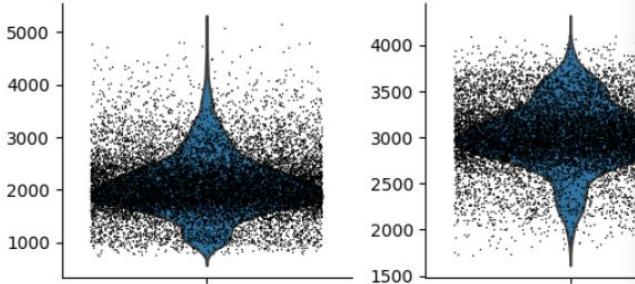
Unlabeled 2021-3-7 13:7:44

Your saved analyses

None found

Your recent unsaved analyses

None found



Current dataset: P1, mouse, scRNA-seq, cochlear epithelium (Kelley)  
Current analysis: Primary analysis



Toggle icon guide

### Primary analysis selected

You have selected an analysis bundled with the dataset itself, usually created by the dataset author outside of this workbench. You can use the workbench to perform actions below provided by the analyses the authors have uploaded, but all other "de novo" analysis steps will be disabled until you create an entirely new analysis.

#### 3 Create a labeled t-SNE

Enter a gene of interest to see its t-SNE colored both by expression and cluster / cell type.

Gene symbol

Search

#### 4 Find marker genes ▾

#### ★ Compare genes and clusters ▾

1. You want to analyze clusters that you saw in a publication, but you're not sure where to start.

## 5. Explore scRNA-seq datasets - Primary Analysis



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Current dataset: P1, mouse, scRNA-seq, cochlear epithelium (Kelley)  
Current analysis: Primary analysis

1 - Dataset selection      2 - Analysis selection      3 - Labeled t-SNE      4 - Marker genes      5 - Compare genes

**Primary analysis selected**

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**3 Create a labeled t-SNE**

Enter a gene of interest to see its t-SNE colored both by expression and cluster / cell type.

**Gene symbol**

**Search**

**4 Find marker genes ^**

This analysis step will show you the marker genes within each group of cells as defined by the clustering method used. You can adjust the number of genes you would like to see for each cluster by adjusting the 'N genes' value.

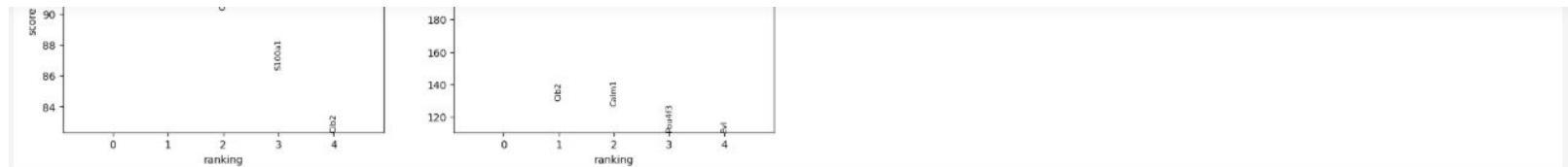
**N genes**

A red box highlights the 'N genes' input field.

**Compute**

**2. What are the top markers for each cluster and how do I find their expression?**

## 2. What are the top markers for each cluster and how do I find their expression?



### Top ranked genes per cluster

Click to select genes of interest. You can select individual genes as well as entire rows and columns.

	DC1/2	DC3	Hensen	IHC	IPC	IPhC	IS	IdC	LGER1	LGER2	LGER3	MGER	OHC	OPC	OS	Oc90	eIHC	eOHC	
0	Socs2	Prss23	Fkbp1a	Cib2	Cryab	Gjb2	Igf1		Ptgds	Pdia6	<b>Fkbp9</b>	Tsen15	Epyc	Cib2	Ppp1r2	Hs3st1	Oc90	Evl	Coc
1	S100a1	Tectb	Fst	<b>Pvalb</b>	Npy	S100a1	Epyc		Cdkn1c	Clu	Tectb	Cst3	Crabp1	<b>Pcp4</b>	S100a1	Bmp4	Vmo1	Calm1	Cic
2	Ppp1r2	Socs2	Itih5	Pcp4	Tectb	Socs2	Cnmd		1500015010Rik	Ddost	Cpxm2	Fstl1	Calb1	Evl	Fzd9	Igfbp4	Krt18	Ccer2	Cac
3	Fkbp1a	S100a1	App	Ccer2	Emid1	Skp1a	Meg3		Otoa	Ppib	Col9a1	Igfbp3	Slc12a2	Calm1	Socs2	Gata2			
4	Igfbp3	Lfng	Socs2	Mlf1	Uchl1	Matn4	1500015010Rik		Smoc2		Col9a1	Fstl1	Gjb2	Itm2a	Tpm1	Fkbp1a	Fst		

Download table

### Marker gene visualization

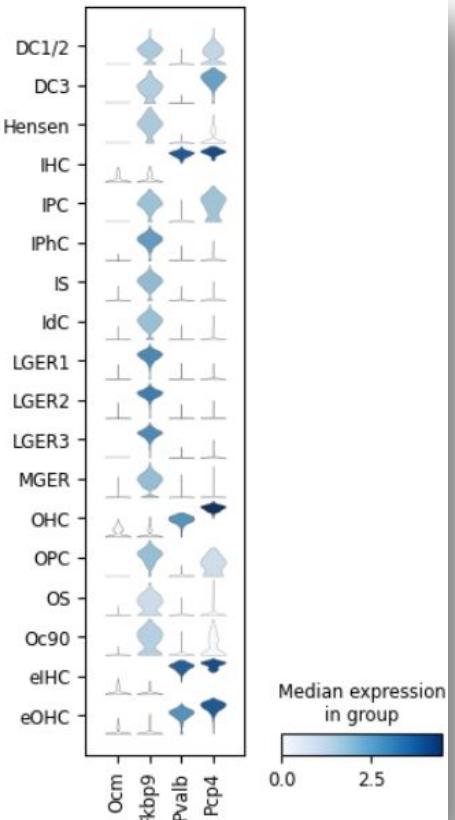
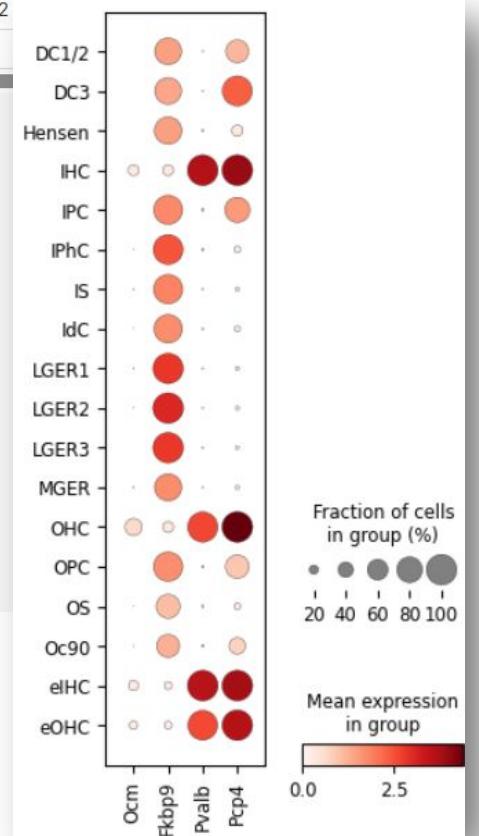
Select desired marker genes in the table above and/or type gene symbols in the field below to visualize

Enter gene symbols (comma-separated)

Ocm

- Unique marker genes selected in table: 3
- Unique marker genes manually entered: 1
- Total unique genes selected: 4

Visualize



## 5. Explore scRNA-seq datasets - Primary Analysis



**Single cell RNA-seq has revolutionized our ability to understand the molecular identity of cells. Every cell in the tissue has its entire transcriptome recorded allowing a wealth of information to be captured.**

**However, for people with no informatics background, scRNA-seq datasets can be intimidating.**

1. You want to analyze clusters that you saw in a publication, but you're not sure where to start.
2. What are the top markers for each cluster and how do I find their expression?
3. I am really interested in the molecular differences between Hensen cells and OHCs.



#### 4 Find marker genes ✓

##### ★ Compare genes and clusters ^

The method dropdown menu lists the available statistical tests for your comparison. The "t-test overestimated variance" option may help in situations where clusters contain few cells and variance is difficult to estimate directly, otherwise for robust clusters choose "t-test" (Assumes normally distributed data). The "Wilcoxon-Rank-Sum" option is a non-parametric test and may be helpful when a dataset includes a few genes with very high expression (i.e., outliers). P-value testing correction can be performed either by Benjamini-Hochberg or Bonferroni methods, where Bonferroni is more conservative.

N genes

5

Query cluster

Hensen

Reference (comparison) cluster

OHC

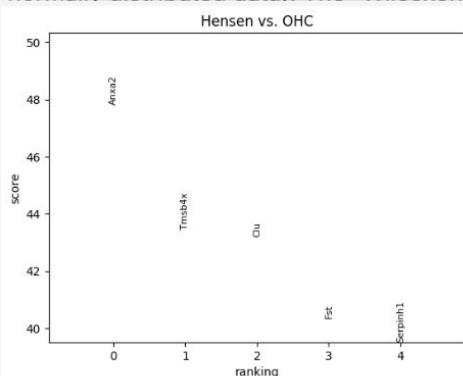
Method

T-test (overestimated variance)

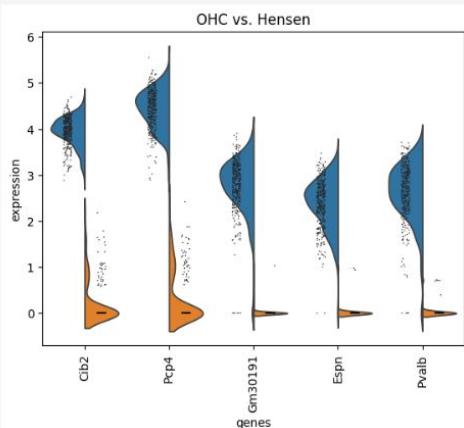
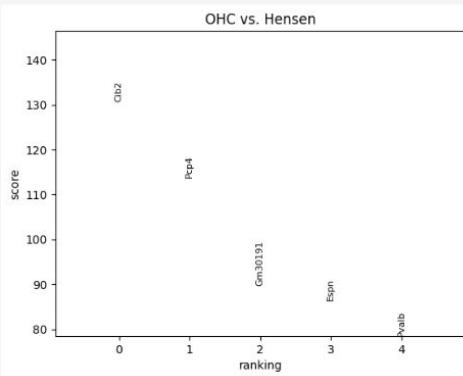
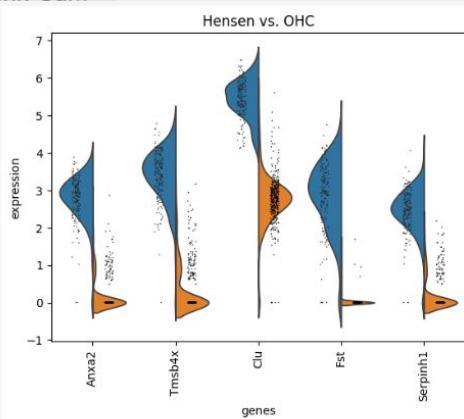
P-value correction method

Benjamini-Hochberg

Run



Show table Download table



3. I am really interested in the molecular differences between Hensen cells and OHCs.



## scRNA-seq Primary Analysis

1. Find the Lateral wall (Hoa) profile.
2. There are 4 snRNA-seq datasets that were processed using different methods. Do the methods have an influence on the top 10 marker genes of the different cell types?
3. You notice that Spindle and Root cells are clustered separately only with snRNA-seq. Do they overlap in their gene expression?



Gene Expression Explore Datasets

Kcnj10 OR Quick search using Gene Lists IN Hearing (default)

Exact

Search and select a dataset collection

Category

- Site-curated > Lateral wall (Hoa) (highlighted with a red box)
- Yours
- Recently viewed
- From your groups
- Others shared with you

Human inner ear & inner ear Organoid (van der Valk 2023)

IHC/OHC demo

Inner ear organoid, differentiation d20-d60 (Ueda 2023)

mouse cochlea atlas Jean 2023

Mouse models

Mouse models 2

mouse, cochlear aging atlas (Sun 2023)

Neuron

NIHL, cell type-specific transcriptomics, mouse cochlea (Hertzano 2021)

Noise/Damage/Protection

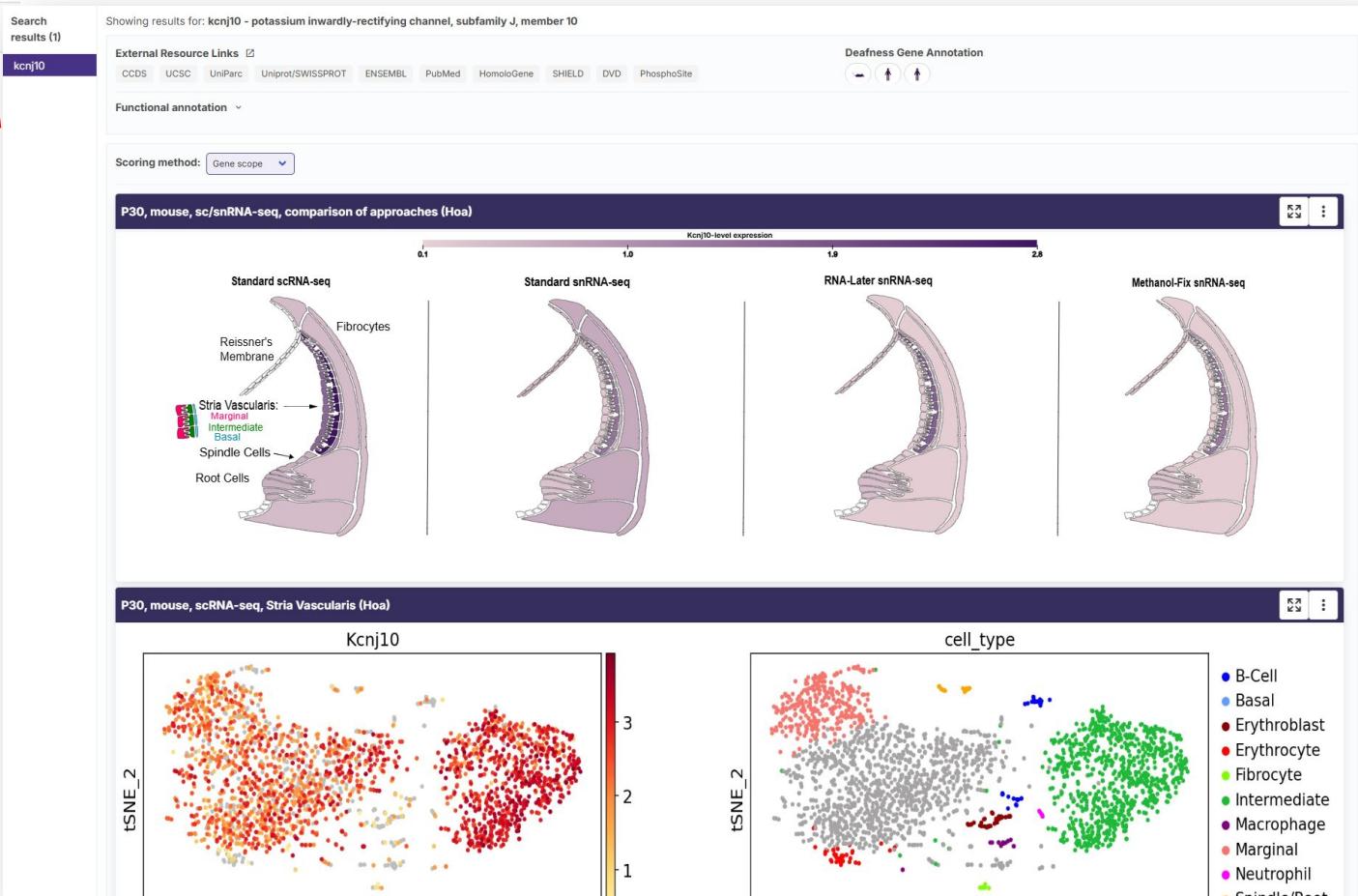
Other

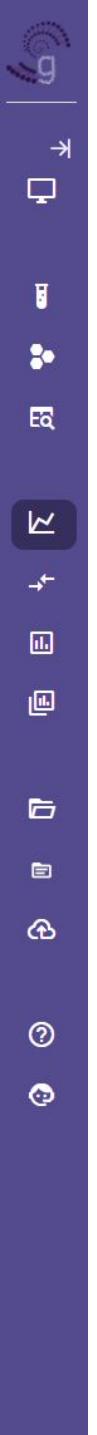
Regenerating Neuromast (Piotrowski)

Regeneration

Cancel

1. Find the Lateral wall (Hoa) profile.





P30, mouse, sc/snRNA-seq, comparison of approaches (Hoa)

P30, mouse, scRNA-seq, Stria Vascularis (Hoa)

P30, mouse, snRNA-seq, Stria Vascularis (Hoa)

Adult, Mouse, snRNA-seq, Standard Processing (Hoa)

Adult, Mouse, snRNA-seq, RNA-Later (Hoa)

Adult, Mouse, snRNA-seq, methanol-fix (Hoa)



Choose Display

Dataset Information

Dataset publication

GEO Information

Take Notes

Single Cell Workbench

Comparison Tool

Single-gene Curator

Multi-gene Displays

Download Bundle

Download H5AD

Download Image

	Basal	Fibrocyte	Intermediate	Macrophage	Marginal	Reissner	Root	Spindle	Unknown
0	Ebf1	Ebf1	Dct	Elmo1	Cacnb2	Stim2	Trpm3	Camk2d	Nrxn3
1	Actn1	Pid1	Dlc1	Dock8	Ank3	Gm29266	Pde4b	Lect1	Tenm2
2	Apod	Cald1	Tyr	1700112E06Rik	Cdh18	Ppp2r2b	Eya4	Chst9	Prkg1
3	Prkca	Cped1	Met	Arhgap15	Iqgap2	Plxdc2	Grb14	Rbms3	Meg3
4	Neb1	Auts2	Atp1b1	Inpp5d	Kcnq1	Sulf1	Msi2	Gm29266	Cntn4
5	Enah	Trpm3	Hpsse	Myo1f	Dclk1	Meis1	Chst9	Adgrl3	mt-Cytb
6	Ablim3	Coch	Pde1c	Slc8a1	Lrp2	Sntb1	Veph1	Trpm3	9430076C15Rik
7	Add3	Phactr1	Mob3b	Cacna1a	Slit3	Nkain2	Auts2	Plxdc2	Pcdh9
8	Cldn11	Cntn4	Bnc2	Ldlrad4	Gas2	Grid2	Pbx1	Eya4	Hdac9
9	Nudt4	Ptpkr	Nrcam	Hpgds	Cacna1d	Plcb4	Setbp1	BC006965	Kcnb2

2. There are 4 snRNA-seq datasets that were processed using different methods. Do the methods have an influence on the top 10 marker genes of the different cell types?



1 Select a dataset ✓

Current dataset: Adult, Mouse, snRNA-seq, methanol-fix (Hoa)

Expand dataset selection tool

2 Select new or saved analysis ✓

Current analysis: Primary analysis

Primary analysis

3 Find marker genes ^

This analysis step will for each cluster by ad

N genes

10

Compute

**Perform the steps for the 4 datasets and compare the genes in the tables**



3 Find marker genes ✓

★ Compare genes and clusters ^

N genes  
10

Query cluster  
Spindle

Reference (comparison) cluster  
Root

Method  
Wilcoxon rank-sum

P-value correction method  
Benjamini-Hochberg

Show table   Download table

Run

Root vs. Spindle

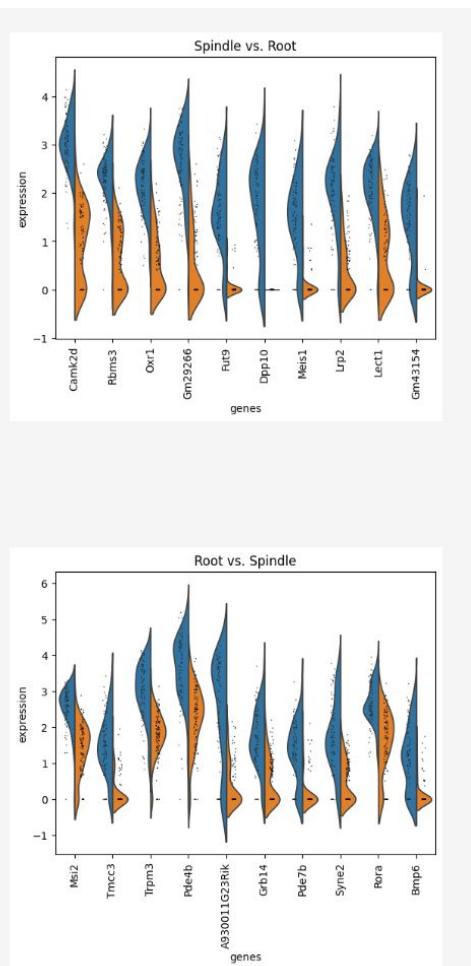
score

ranking

genes

Trpm3  
Tmc2  
Pde7b  
A930011G23Rik  
Grb4  
Pde7b  
Synet2  
Rora  
Bmp6

Show table   Download table



3. You notice that Spindle and Root cells are clustered separately only with snRNA-seq. Do they overlap in their gene expression?





gene Expression Analysis Resource

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gEAR: Gene Expression Analysis Resource portal for community-driven, multi-omic data exploration.

Orvis J, et al. Nat Methods. 2021 Jun 25.

doi: 10.1038/s41592-021-01200-9

PMID: 34172972

# Chris Shults

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## 6. Explore the dataset content of gEAR

You joined a lab that focuses on scRNA-seq of the ear in chicken.

1. You want to find what datasets are already available.
2. You now want to be able to see some of these datasets side-by-side. A new profile therefore should be created.
3. You would like to customize the new profile to better fit your needs.
4. Search for gene expression in your new profile.





Hearing (default)

**Filter controls****Search by keyword**

Keyword search

Show from this collection only



No

**Ownership**

All

Your datasets  
Group-affiliated datasets  
Datasets shared with you  
Public datasets**Organism**

All

Chicken

Human

Marmoset  
Mouse  
Rat  
Zebrafish**Dataset type**

All

Bulk RNASeq

Epigenetic

Microarray

Single-cell RNASeq

Spatial Transcriptomics

**Date added**

Any time

Within last week

Within last month

Within last year

Title	Access	Organism	Owner	Type	Date added
scRNA-seq analysis of early responding supporting cells post sisomicin infusion in P7 chicken (UMAP, Benkafadar 2023)	Public	Chicken	curator	single-cell-rnaseq	2023-07-28
scRNA-seq analysis of early responding supporting cells post sisomicin infusion in P7 chicken (violin, Benkafadar 2023)	Public	Chicken	curator	single-cell-rnaseq	2023-07-28
scRNA-seq analysis of early responding supporting cells post sisomicin infusion in P7 chicken (UMAP, Benkafadar 2023)	Public	Chicken	curator	single-cell-rnaseq	2023-07-28
Dying Short HCs, chicken - trajectory colored by cell type (Heller)	Public	Chicken	curator	single-cell-rnaseq	2021-05-05
Dying Short HCs, chicken - trajectory colored by expression (Heller)	Public	Chicken	curator	single-cell-rnaseq	2021-05-05
Dying Short HCs, chicken - violin plot (Heller)	Public	Chicken	curator	single-cell-rnaseq	2021-05-05
Dying Tall HCs, chicken - trajectory colored by cell type (Heller)	Public	Chicken	curator	single-cell-rnaseq	2021-05-05
Dying Tall HCs, chicken - trajectory colored by expression (Heller)	Public	Chicken	curator	single-cell-rnaseq	2021-05-05
Dying Tall HCs, chicken - violin plot (Heller)	Public	Chicken	curator	single-cell-rnaseq	2021-05-05
Dying Tall and Short HCs, chicken (Heller)	Public	Chicken	curator	single-cell-rnaseq	2021-05-05
HC Tonotopy Dynamic Expression Plot, P7, short HC, scRNA-seq (Janesick), geneID	Public	Chicken	curator	single-cell-rnaseq	2021-05-04
HC Tonotopy Dynamic Expression Plot, P7, Tall HC Trajectory, scRNA-seq (Janesick), updated, geneID	Public	Chicken	curator	single-cell-rnaseq	2021-05-01
HC Tonotopy Dynamic Expression Plot, P7, HC States, scRNA-seq (Janesick), geneID	Public	Chicken	curator	single-cell-rnaseq	2021-04-30
Chicken Basilar Papilla Baseline, P7, violin plot, scRNA-seq (Janesick), geneID	Public	Chicken	curator	single-cell-rnaseq	2021-04-30
Chicken Basilar Papilla Baseline, P7, svg, scRNA-seq (Janesick), geneID	Public	Chicken	curator	single-cell-rnaseq	2021-04-30
Chicken Basilar Papilla Baseline, P7, tSNE plot, scRNA-seq (Janesick), geneID	Public	Chicken	curator	single-cell-rnaseq	2021-04-29
Molecular anatomy of the chicken utricle (P7) - Trajectory Striola I, States, entrezID	Public	Chicken	curator	single-cell-rnaseq	2021-04-23
Molecular anatomy of the chicken utricle (P7) - Trajectory Striola I, Gene	Public	Chicken	curator	single-cell-rnaseq	2021-04-

1. You want to find what datasets are already available.

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4. Search for gene expression in your new profile.



2. You now want to be able to see some of these datasets side-by-side. A new profile therefore should be created.

The screenshot shows the 'Collection management' interface. At the top, there are buttons for 'View' (grid, list, card) and 'Sort by' (Date uploaded). Below this, a dropdown menu is set to 'Hearing (default)'. On the left, there's a sidebar with various icons. In the main area, a 'New collection' section is open, prompting for a name: 'My Chicken Profile'. A red box highlights the 'Add' button. To the right, a 'Share' icon is also highlighted with a red box.

This screenshot shows the main dataset list after the new collection has been added. The 'Collection management' header is at the top. Below it, the 'My Chicken Profile' collection is listed. It includes a 'Share' icon (highlighted with a red box), a 'Private collection' toggle switch (highlighted with a red box), and a 'Toggle collection access' button. The main content area displays three datasets: 'NA-seq analysis of early responding' (with a violin plot), 'Dying Tall HCcs, chicken - violin plot (Heller)' (with a violin plot), and 'Dying Tall and Short HCcs, chicken (Heller)' (with a t-SNE plot). Each dataset has its own 'Analysis tools' section with a share icon highlighted with a red box.

This screenshot shows the 'Collection management' interface again, but this time focusing on the 'My Chicken Profile' collection. It lists the datasets added to the collection: 'NA-seq analysis of early responding' (with a violin plot), 'Dying Tall HCcs, chicken - violin plot (Heller)' (with a violin plot), and 'Dying Tall and Short HCcs, chicken (Heller)' (with a t-SNE plot). Each dataset has its own 'Analysis tools' section with a share icon highlighted with a red box.



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Collection management

View: grid icon Sort by: Date uploaded

**Collection arrangement view**

Title

scRNA-seq analysis of early responding support...sisomicin infusion in P7 chicken (UMAP, Benkaf...

My Chicken Profile

Toggle collection access

Private collection

Single-gene view

Dying Tall HCs, chicken - violin plot (Heller)

expression of OCM cell\_type: CT, D1T, D2T

HC Tonotopy Dynamic Expression Plot, P7, short HC, scRNA-seq (Janesick), geneID

expression of OSMR2 Proximal <-> Distal

Dying Tall and Short HCs, chicken (Heller)

tsNE\_2 tsNE\_1

expression of OSMR2

Legend: CS (yellow), CT (red), D1S (green), D1T (blue), D2S (dark green), D2T (purple)

Multi-gene view

There are no multi-gene displays saved for this collection. You can add some by clicking the "View, add or remove displays from current collection" button (+/- icon) on any dataset.

3. You would like to customize the new profile to better fit your needs.

**Collection arrangement**

Single-gene view

Dying Tall and Short HCs, chicken (Heller)

tsNE\_2 tsNE\_1

expression of OSMR2

Legend: CS (yellow), CT (red), D1S (green), D1T (blue), D2S (dark green), D2T (purple)

Dying Tall HCs, chicken - violin plot (Heller)

expression of OCM cell\_type: CT, D1T, D2T

HC Tonotopy Dynamic Expression Plot, P7, short HC, scRNA-seq (Janesick), geneID

expression of OSMR2 Proximal <-> Distal

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## 6. Explore the dataset content of gEAR

You joined a lab that focuses on scRNA-seq of the ear in chicken.

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3. You would like to customize the new profile to better fit your needs.
4. Search for gene expression in your new profile.





Search bar: pou4f3 sox2 OR Quick search using Gene Lists IN My Chicken Profile

Exact  Similar

Resume

Category

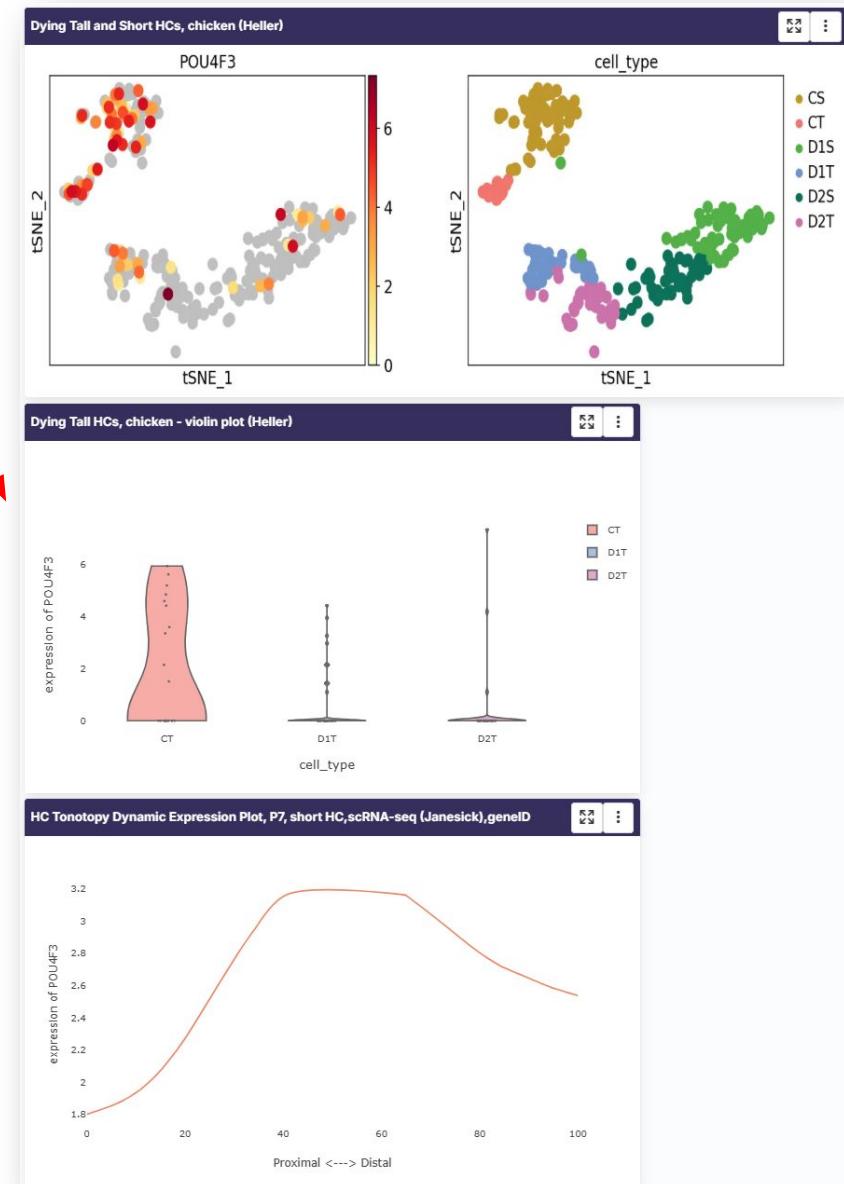
- Site-curated >
- Yours >** (highlighted with red box)
- Recently viewed >
- From your groups >
- Others shared with you >

Dataset Collection

- DOD
- DOD PTS-TTS
- Epiriz
- Exercise 2
- gEAR Manuscript
- IHC/OHC demo
- Male-Female-Noise-Metformin
- Mouse Mutants
- Mouse Wildtype
- My Chicken Profile >** (highlighted with red box)
- Noise
- RFX

Cancel

4. Search for gene expression in your new profile.

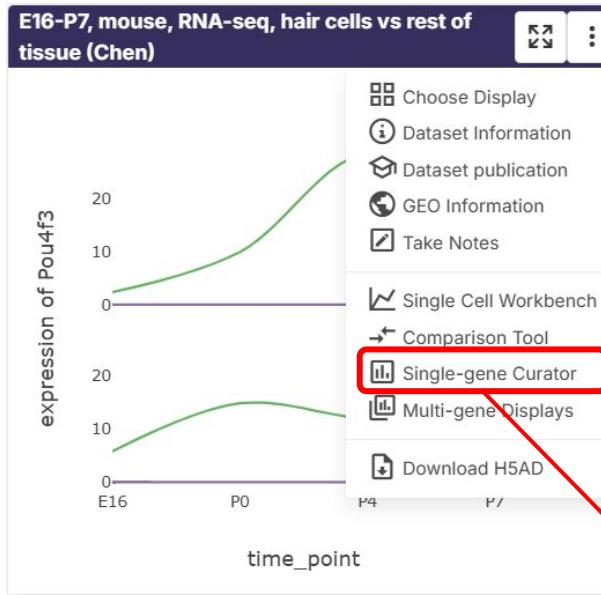




## 7. Dataset Curation: Single-Gene and Multi-Gene Displays

Displays can be customized to best fit datasets.

1. You want to customize a single-gene view.
2. You want to customize a multi-gene view.

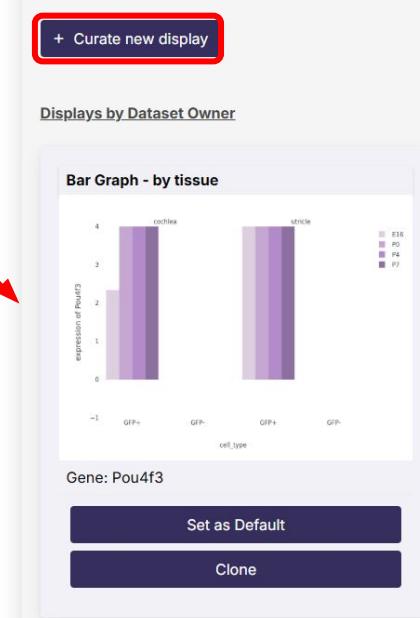


1 Select a dataset ✓

Current dataset: E16-P7, mouse, RNA-seq, hair cells vs rest of tissue (Chen)

2 Create new or load existing curation ^

+ Curate new display



3 Select dataset plot type and analysis type ✓

Current plot type: line  
Current analysis: Primary analysis

Plot type **Required** Line

Select plot type

Interactive

Bar

Line

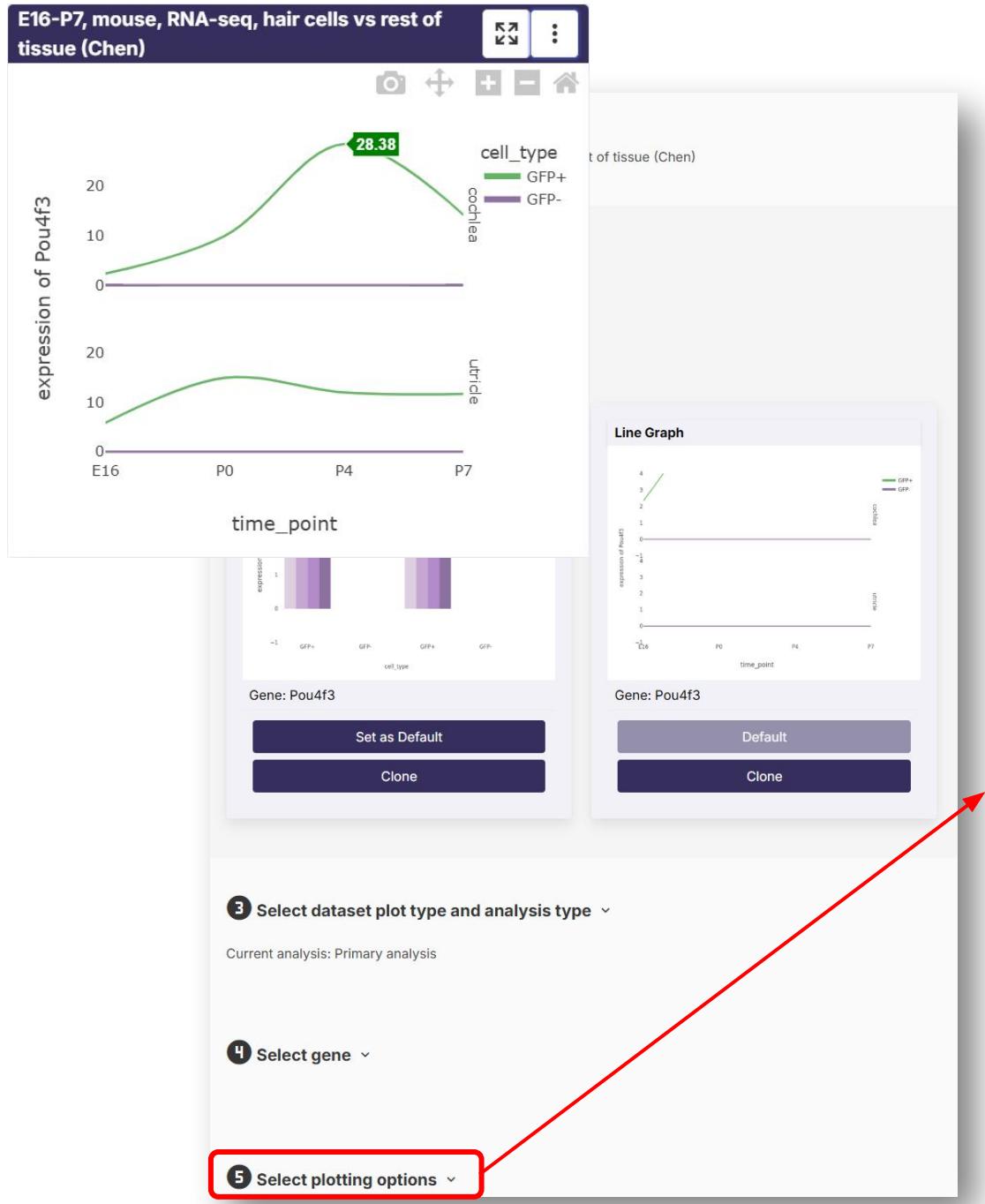
Scatter

4 Select gene ^

Pou4f3  
Required

5 Select plotting options ▾

1. You want to customize a single-gene view.



## 5 Select plotting options

More customization options will be available once the plot has been created.

### X-axis

time\_point

Required

### Y-axis

expression

Required

### Color

cell\_type

▼

If series is categorical, each group is a different color. If series is continuous, color will be a gradient.

### Marker size

▼

### Annotation label

expression

▼

Series values to display when hovering over a data point

### Subplots by row

tissue

▼

### Categorical data

cell\_type

louvain

time\_point

tissue

Plot



Dataset: E16-P7, mouse, RNA-seq, hair cells vs rest of tissue (Chen)

Analysis: Primary analysis

Number of selected observations: 16

Gene: Pou4f3

Dataset filters

Plot configuration

Change sort order

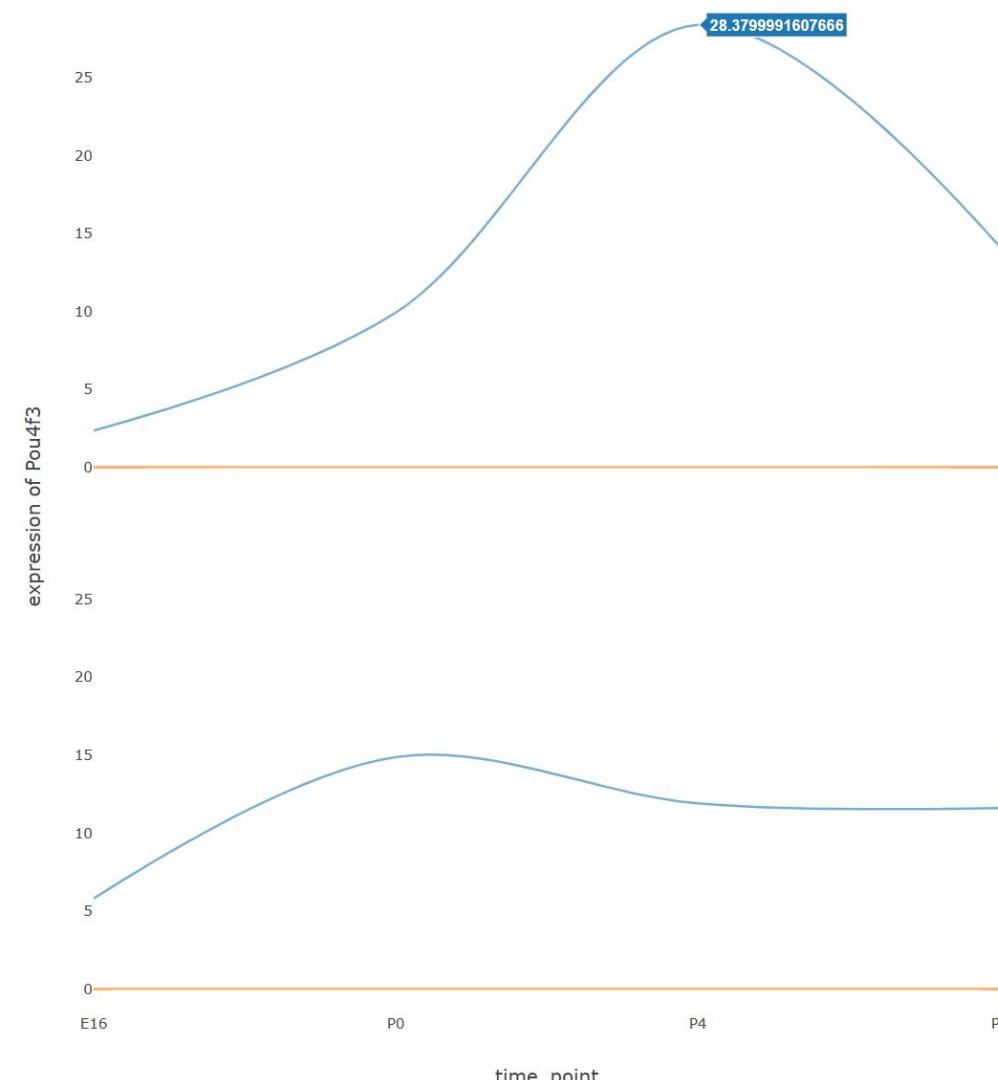
Change colors

Selected conditions:

All



cell\_type  
GFP+  
GFP-



Update Plot

← Go Back

Enter name of display

Overwrite existing display instead

Make this my default display

Save as new display

Download config (JSON)



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Jun 25.

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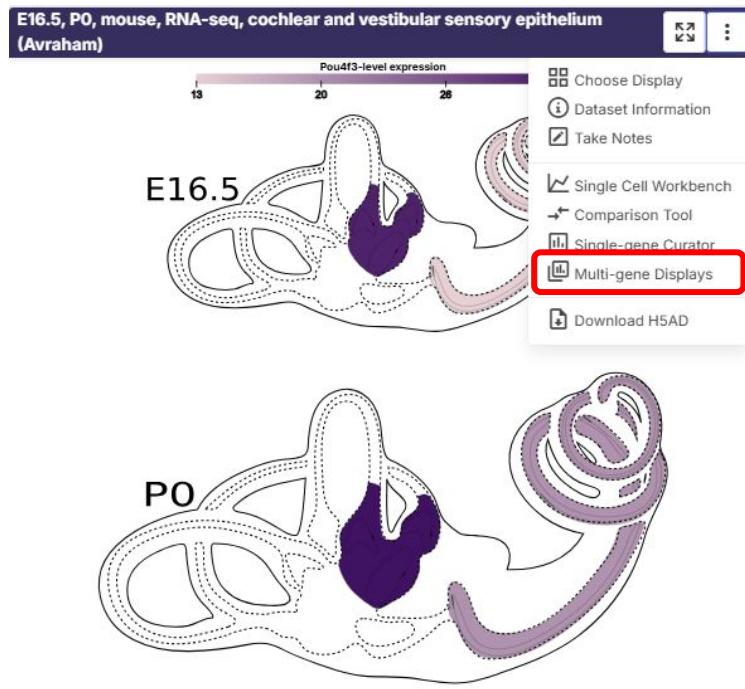
PMID: 34172972

## 7. Dataset Curation: Single-Gene and Multi-Gene Displays



Displays can be customized to best fit datasets.

1. You want to customize a single-gene view.
2. You want to customize a multi-gene view.



2. You want to customize a multi-gene view.

1 Select a dataset

Current dataset: E16.5, P0, mouse, RNA-seq, cochlear and vestibular sensory epithelium (Avraham)

2 Create new or load existing curation

+ Curate new display

Displays by Dataset Owner

DotPlot\_All

Plot type \* Required

Select plot type

Select plot type

Genes as axis labels

Dotplot

Heatmap Heatmap

Violin

Genes as data points

Quadrant

Volcano

Number of genes: 2

Default

Clone

3 Select dataset plot type and analysis type

Current analysis: Primary analysis

Plot type \* Required

Select plot type

Analysis (optional) ✓

Primary analysis (default)

4 Select genes

Number of selected genes: 3

Genes entered manually or chosen from an existing gene list that are found in this dataset will be added to the group of selected genes to plot.

pou4f3 sox2 tubb3 OR Quick search using Gene Lists

At least 2 found genes required

5 Select plotting options

**1 Select a dataset** ✓

Current dataset: E16.5, P0, mouse, RNA-seq, cochlear and vestibular sensory epithelium (Avraham)

**2 Create new or load existing curation** ^

+ Curate new display

Displays by Dataset Owner

**DotPlot\_All**

Fraction of cells in group (%)

Log2 Mean Expression

Genes: Sox2, Gr1

Cell\_type and time\_point: E16.5, P0, Cochlea, Vestibule

Number of genes: 2

Default

Clone

**3 Select dataset plot type and analysis type** ^

Current analysis: Primary analysis

**4 Select genes** ^

**5 Select plotting options** ^

**5 Select plotting options** ^

More customization options will be available once the plot has been created.

**Primary grouping** Required

cell\_type

**Secondary grouping**

time\_point

**Add clusterbar groups**

cell\_type  
 louvain  
 time\_point

Adds a bar for each selected data series to the top of the plot.

**Create matrixplot**

Aggregate mean expression based on selected primary and secondary groups. Highly recommended to keep checked unless the number of samples is small.

44

**Plot**



Dataset: E16.5, P0, mouse, RNA-seq, cochlear and vestibular sensory epithelium (Avraham)

Analysis: Primary analysis

Number of selected observations: 4

Number of selected genes: 3

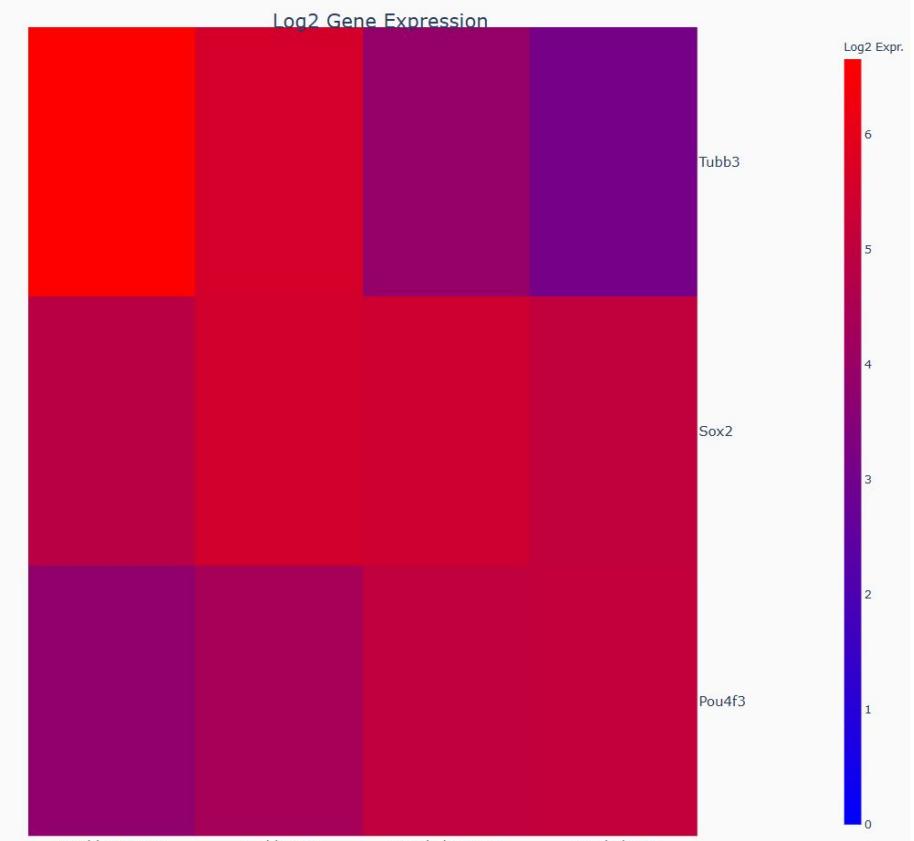
#### Dataset filters

#### Plot configuration

#### Change sort order

Selected conditions:

All



Update Plot

← Go Back

Enter name of display

Overwrite existing display instead

Make this my default display

Save as new display

Download config (JSON)



Dataset: E16.5, P0, mouse, RNA-seq, cochlear and vestibular sensory epithelium (Avraham)

Analysis: Primary analysis

Number of selected observations: 4

Number of selected genes: 3

### Dataset filters

#### Plot configuration

Primary grouping

cell\_type

Secondary grouping

time\_point

Color palette

Red-Yell...

Reverse palette



Select parameters to edit

Plot title

Enter title of plot

If left blank, plot will have a default title or no title.

Legend title

Enter title of legend

If left blank, legend will have a default title.

#### Change sort order

Drag-and-drop to determine order of plotting

cell\_type

Vestibule

Cochlea

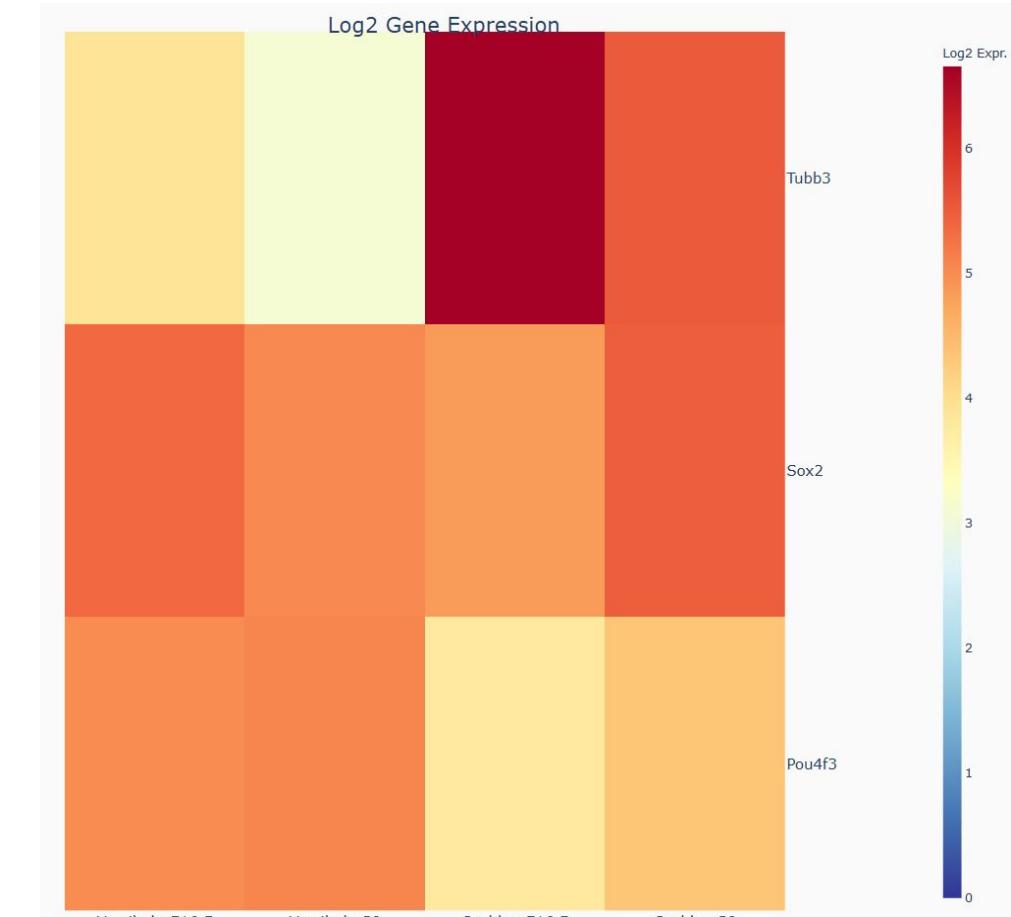
time\_point

E16.5

P0

Select

All



Update Plot

## 8. Explore gene expression spatially



You've spent hours analyzing expression data based on cell clustering, but you've recently heard there is a new spatial transcriptomics dataset collection on gEAR...

1. You want to visualize the gene expression of *Kcne1* using a spatial transcriptomics dataset.
2. You've identified a list of marker genes for cells in the organ of Corti, however, you wonder if any of these genes exhibit base-to-apex expression patterns.
3. After analyzing your single-cell dataset, you realize there is a cluster of cells that you are having difficulty identifying. You speculate that using the projection tool might help annotate this cluster.

**Menu**

- My Workspace

**Explore**

- Gene Expression** (selected)
- Projection Tool

**Datasets**

**Analyze**

- Single Cell Workbench
- Comparison Tool
- Single-gene Displays
- Multi-gene Displays

**Manage**

- Dataset Collections
- Gene Lists
- Dataset Uploader

**Support**

- Help
- Feedback

**Citation**

gEAR: Gene Expression Analysis Resource portal for community-driven, multi-omic data exploration.  
Orvis J, et al. Nat Methods. 2021 Jun 25.  
doi: 10.1038/s41592-021-01200-9  
PMID: 34172972

## 1. Navigate to Gene Expression

Kcne1

Exact gene symbols only

**2. Search for Kcne1 gene**

**1. Where is Kcne1 expressed in the cochlea?**

1. Enter gene symbols
OR Use Gene Lists ▾

2. Choose a dataset collection
3. Choose display type
4. Go!

Spatial Transcriptomics ▾
 Single-gene Display     Multi-gene Display
**Search**

**Category**

- Site-curated >
- Yours >
- Recently viewed >
- From your groups >
- Others shared with you >

**Search and select a dataset collection**

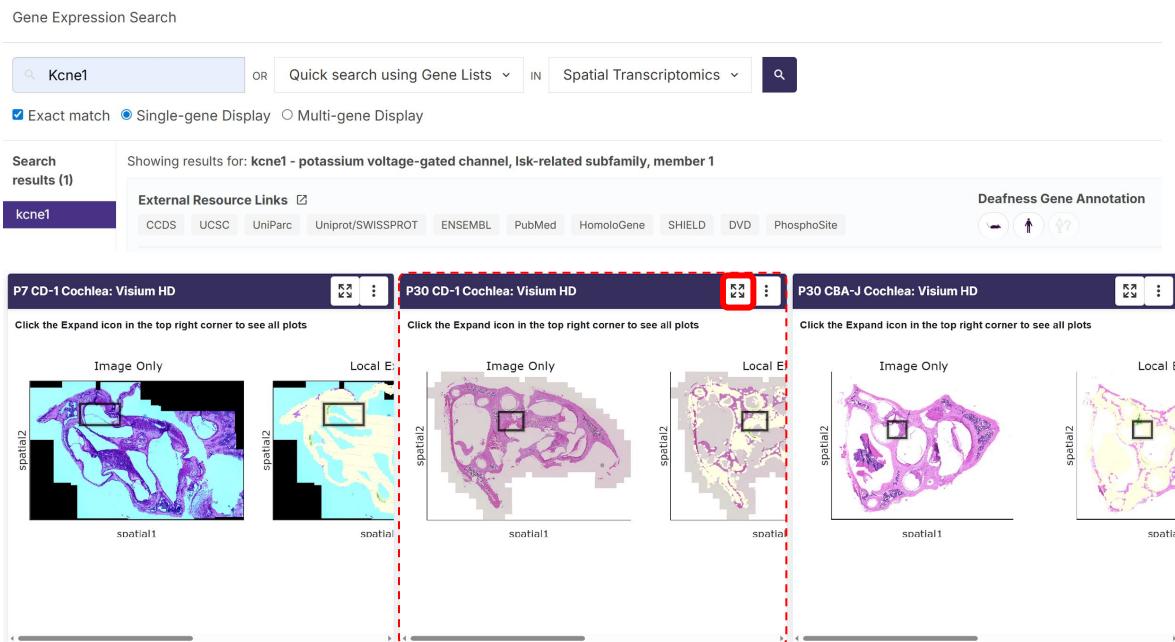
- Spatial Transcriptomics > **Spatial Transcriptomics**
- Vestibular
- Xenium Data (Hertzano)
- Zebrafish

Date
2026-01-09 17:19:48
2026-01-09 17:19:34
2026-01-09 16:04:59
2026-01-09 16:04:55
2026-01-09 16:04:43

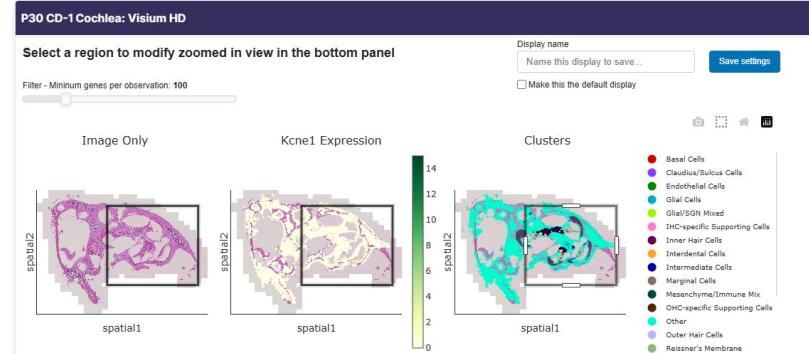
**3. Be sure to choose “Spatial Transcriptomics” in the dataset collection box**

3. After expanding the “P30 CD-1 Cochlea: Visium HD” dataset, you can Kcne1 expression depicted in 4 different panels.

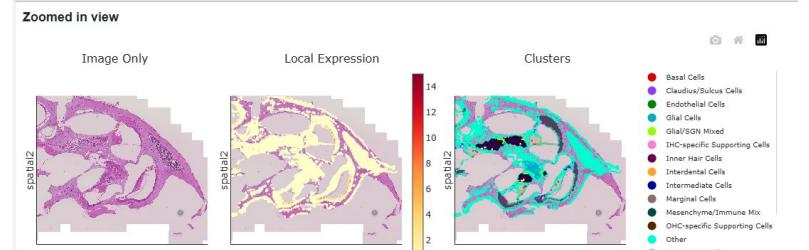
## 1. Where is Kcne1 expressed in the cochlea?



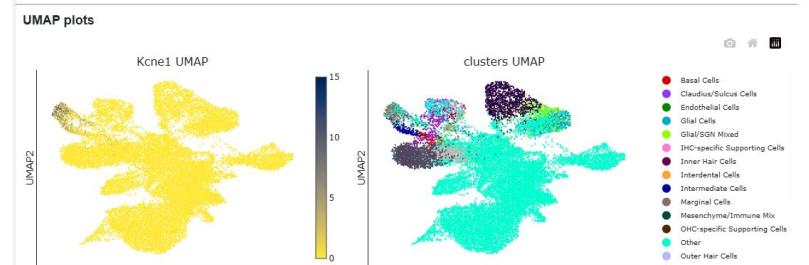
Full Image



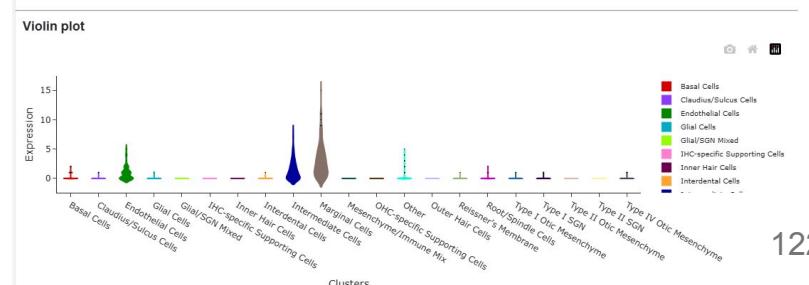
ROI Zoom



UMAP Projection

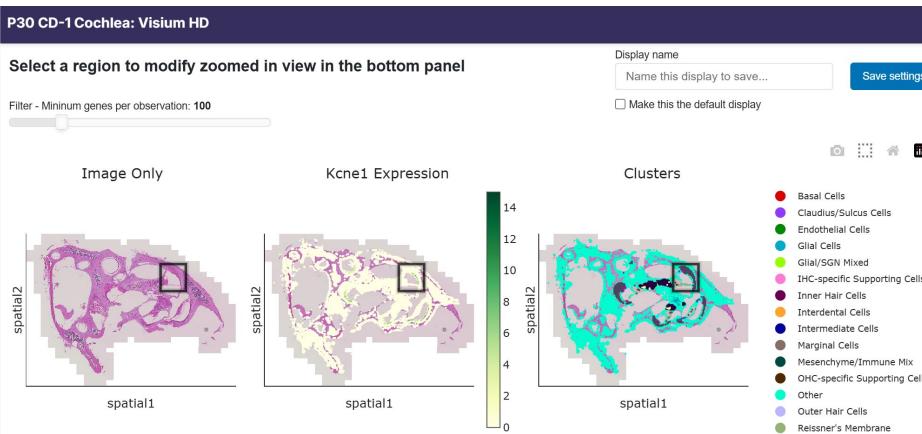


Violin Plot



4. After zooming in to one of the cochlear turns, you've identified that **Kcne1** is expressed primarily in the marginal cells of the stria vascularis!

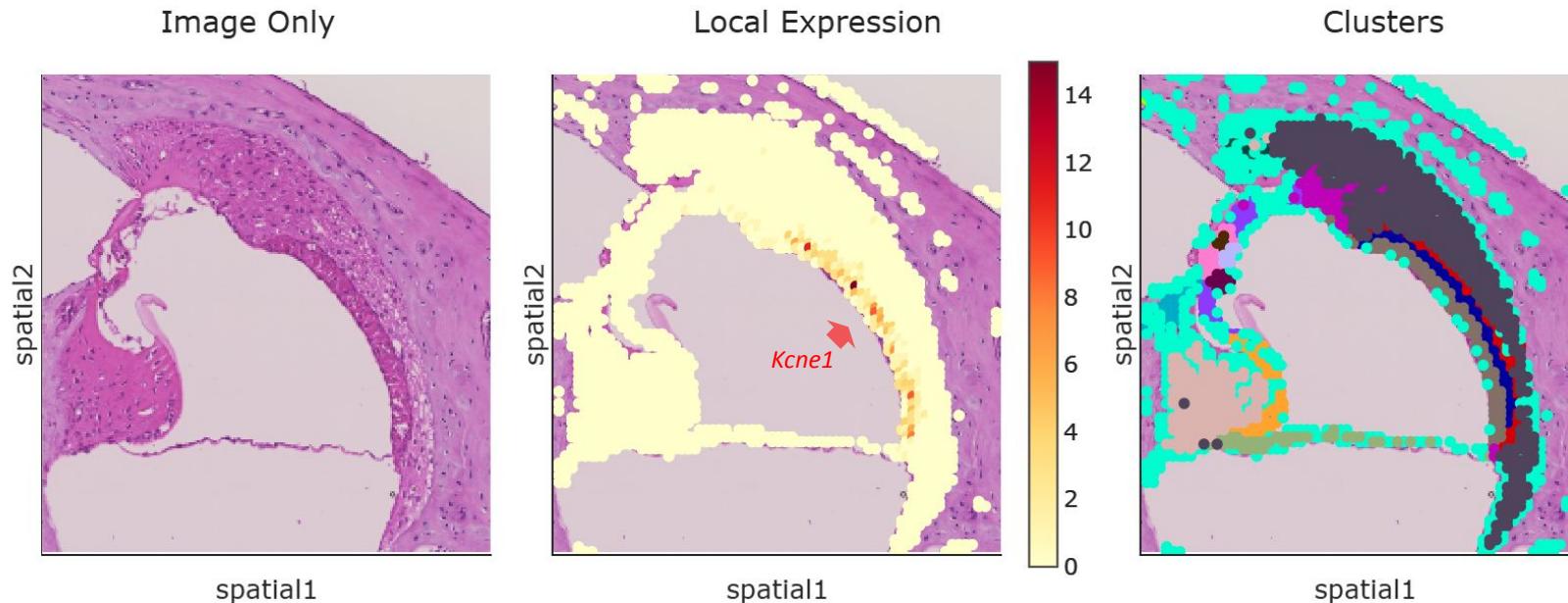
1. Where is *Kcne1* expressed in the cochlea?



Select region of interest for zoomed in view



Zoomed in view



Menu 

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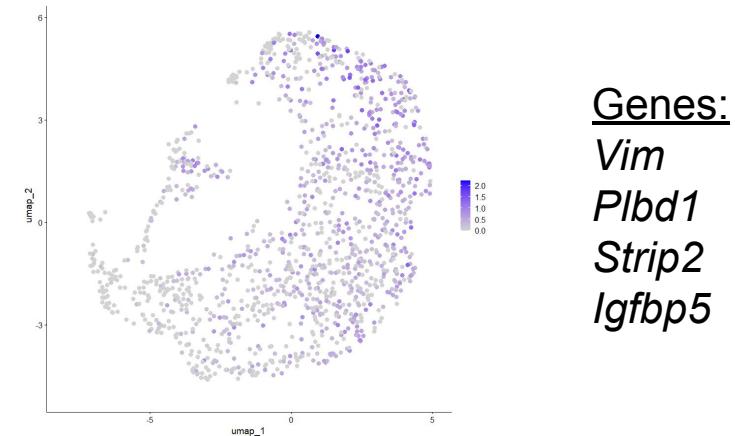
## 8. Explore gene expression spatially



You've spent hours analyzing expression data based on cell clustering, but you've recently heard there is a new spatial transcriptomics dataset collection on gEAR...

1. You want to visualize the gene expression of *Kcne1* using a spatial transcriptomics dataset.
2. You've identified a list of marker genes for cells in the organ of Corti, however, you wonder if any of these genes exhibit base-to-apex expression patterns.
3. After analyzing your single-cell dataset, you realize there is a cluster of cells that you are having difficulty identifying. You speculate that using the projection tool might help annotate this cluster.

1. You've generated a list of genes that seem to have a gradient of expression that you believe follows a base-to-apex expression pattern.



2. Do any of my genes show a base-to-apex gradient of expression?

2. Next, you enter in your gene list to see their expression patterns.

Gene Expression Search

OR  IN

Exact match

Showing results for:

External Resources	Category	(Liu 2021)
	Site-curated	scRNA-seq - Mouse ear E9.5 - 13.5 (Liu)
Functional annotations	Yours	scRNA-seq - mouse embryonic, SGN (Sanders & Kelly 2022)
	Recently viewed	scRNA-seq - P2 cochlea (Heller 2021)
Scoring method:	From your groups	scRNA-seq, human utricle regenerative response (Cheng)
	Others shared with you	scRNA/ATAC-seq - P2, mouse cochlea (Waldhaus)

3. Here, you've identified that your gene list does indeed show an increase in gene expression from base to apex within the organ of Corti!

2. Do any of my genes show a base-to-apex gradient of expression?

P30 CD-1 Cochlea: Visium HD

Zoomed in view

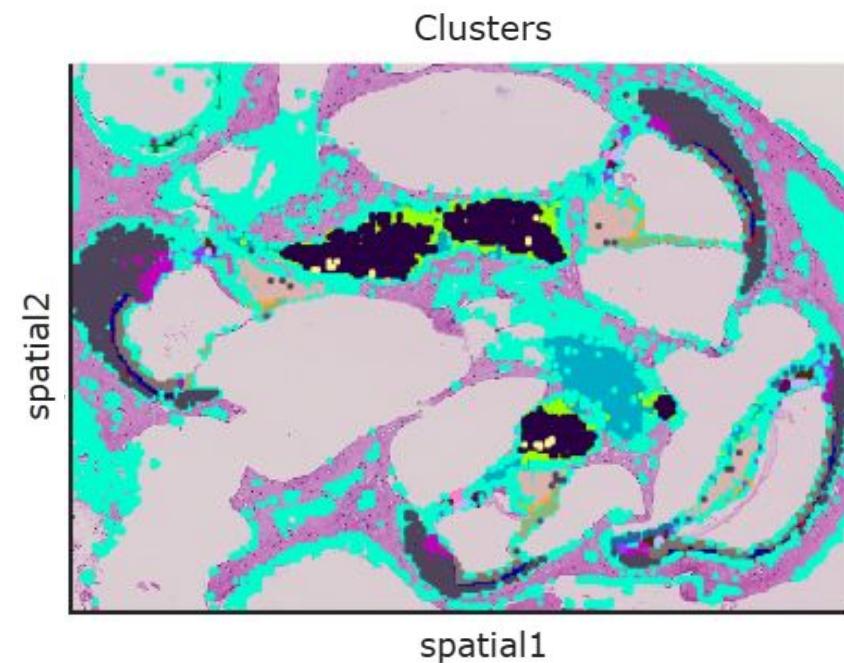
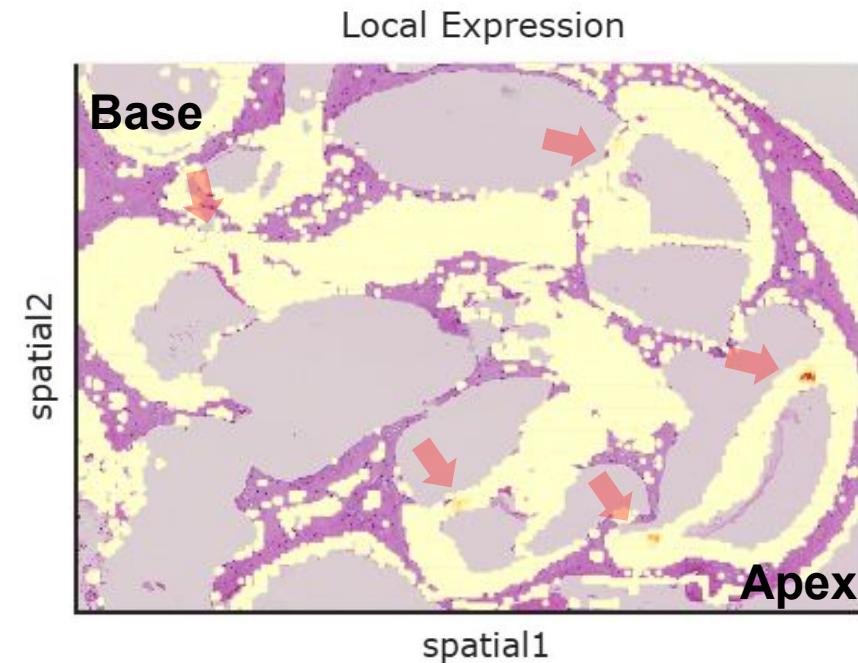
Search results (4)

vim

plbd1

strip2

igfbp5



## 8. Explore gene expression spatially



You've spent hours analyzing expression data based on cell clustering, but you've recently heard there is a new spatial transcriptomics dataset collection on gEAR...

1. You want to visualize the gene expression of *Kcne1* using a spatial transcriptomics dataset.
2. You've identified a list of marker genes for cells in the organ of Corti, however, you wonder if any of these genes exhibit base-to-apex expression patterns.
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## Menu

K

My Workspace

## Explore

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## 1. Navigate to the Projection Tool

## Projection Search

Unknown Cluster

AND

Spatial Transcriptomics

 Single-pattern Display  Multi-pattern Display

## Select algorithm

Principal Component Analysis (PCA)

 Z-score normalize gene expression

If enabled, can increase noise in dataset if too many low-expression genes are present.

 Set negative coefficient weight outputs to zero

This will be applied at the time of plotting and not saved in projection output.

Scoring method: Pattern scope

To explore projections in various datasets, please choose a pattern and a dataset collection above and click the magnifying glass

## 3. How can I use spatial transcriptomics to identify an unknown cell cluster?

Example 1

Beatrice Milon

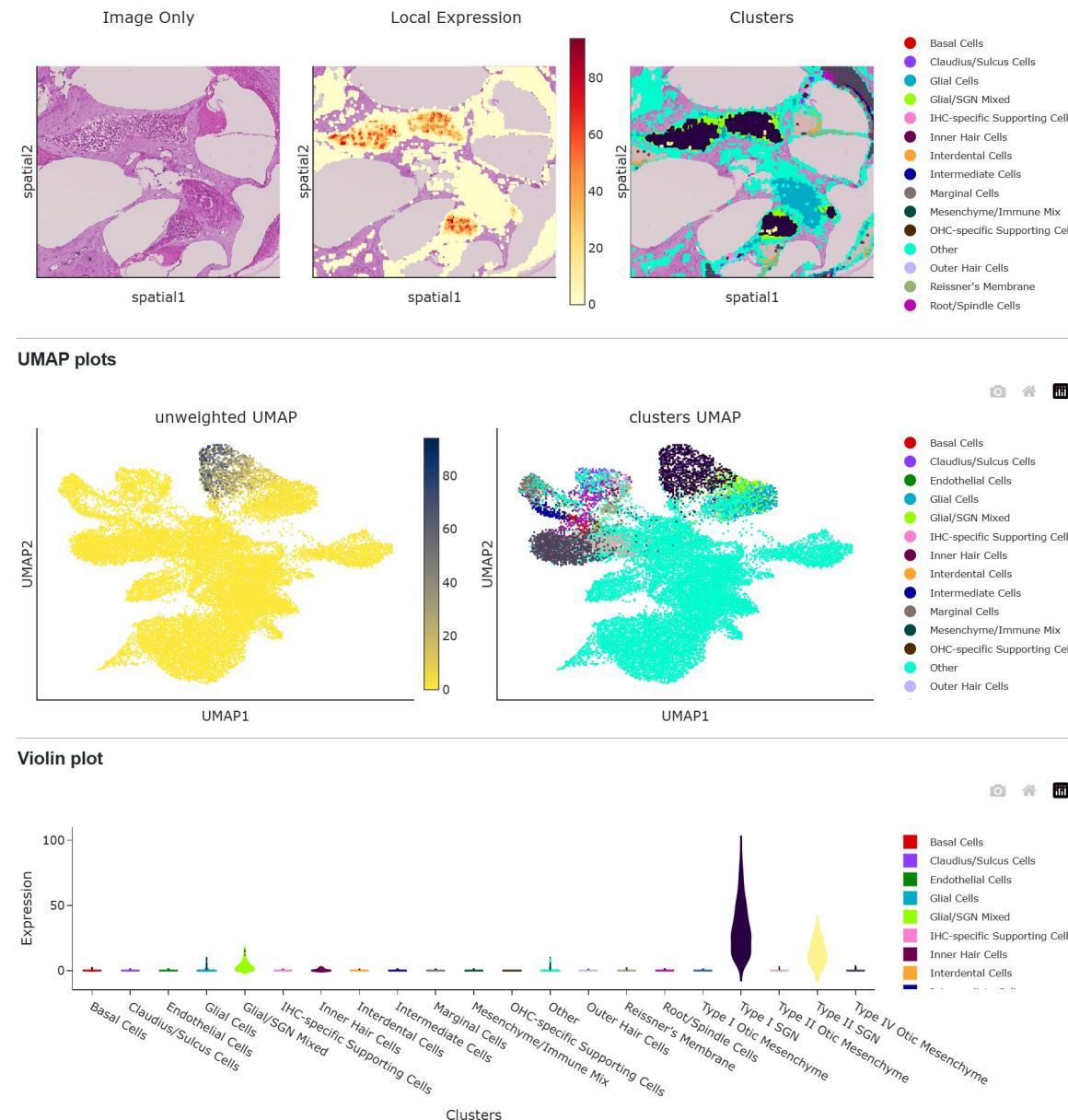
The projection tool allows you to project a pattern onto a dataset and visualize the dynamics across studies, samples, cells, etc. You can select a pattern from the collection, a dataset, and an algorithm to use for the projection. The projection is applied against each sample within each dataset in the collection, where the color or value of the plot (dependent on type) represents the strength of the pattern in that dataset.

## 2. Choose your gene list of marker genes specific to the unknown cluster and spatial dataset collection

3. Using the projection tool, you see that your unknown cells are spiral ganglia neurons!

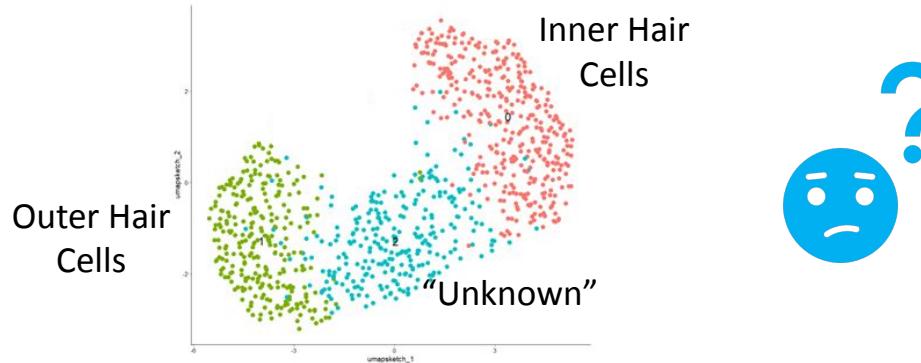
3. How can I use spatial transcriptomics to identify an unknown cell cluster?

### Example 1



## Menu

1. While analyzing your single-cell dataset, you realize that you have 3 clusters after filtering hair cells – inner, outer, and “unknown” hair cells.



3. How can I use spatial transcriptomics to identify an unknown cell cluster?

### Example 2

2. Navigate back to the projection tool and choose your marker genes specific to the unknown cluster and spatial transcriptomics dataset collection

Projection Search

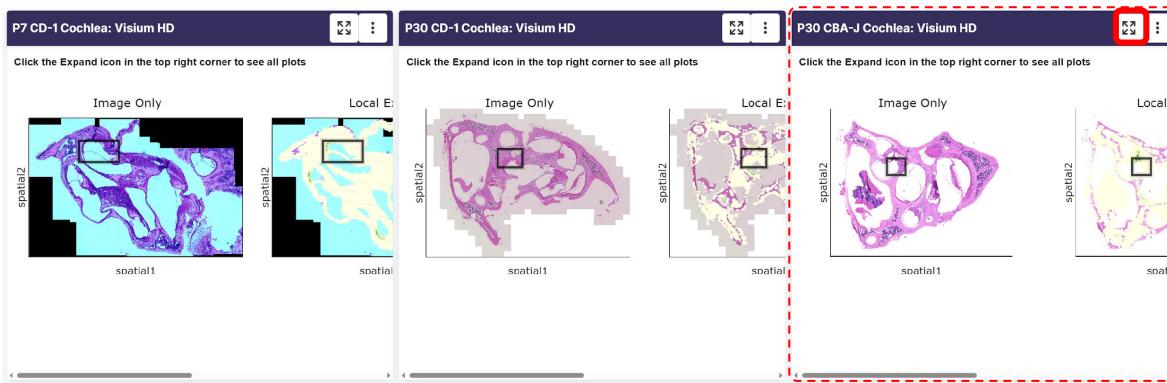
Unknown Cluster AND Spatial

Single-pattern Display

Select algorithm

Z-score normalize gene expression  
If enabled, can increase noise in dataset if too many low-expression genes are present.

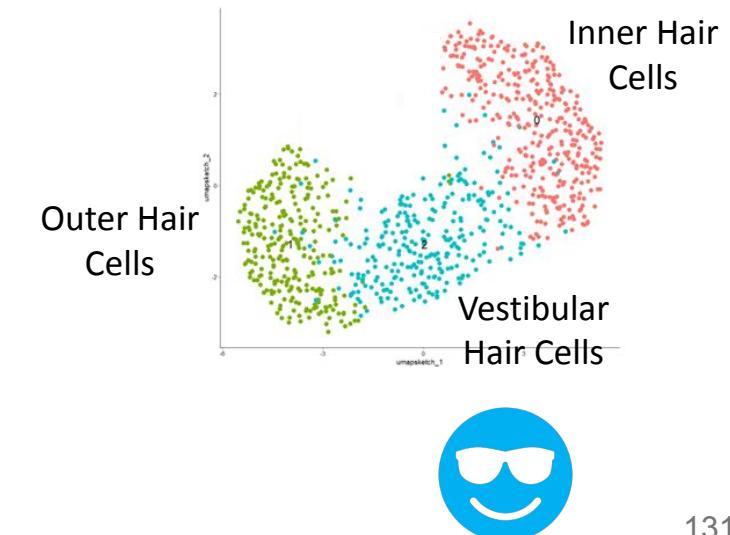
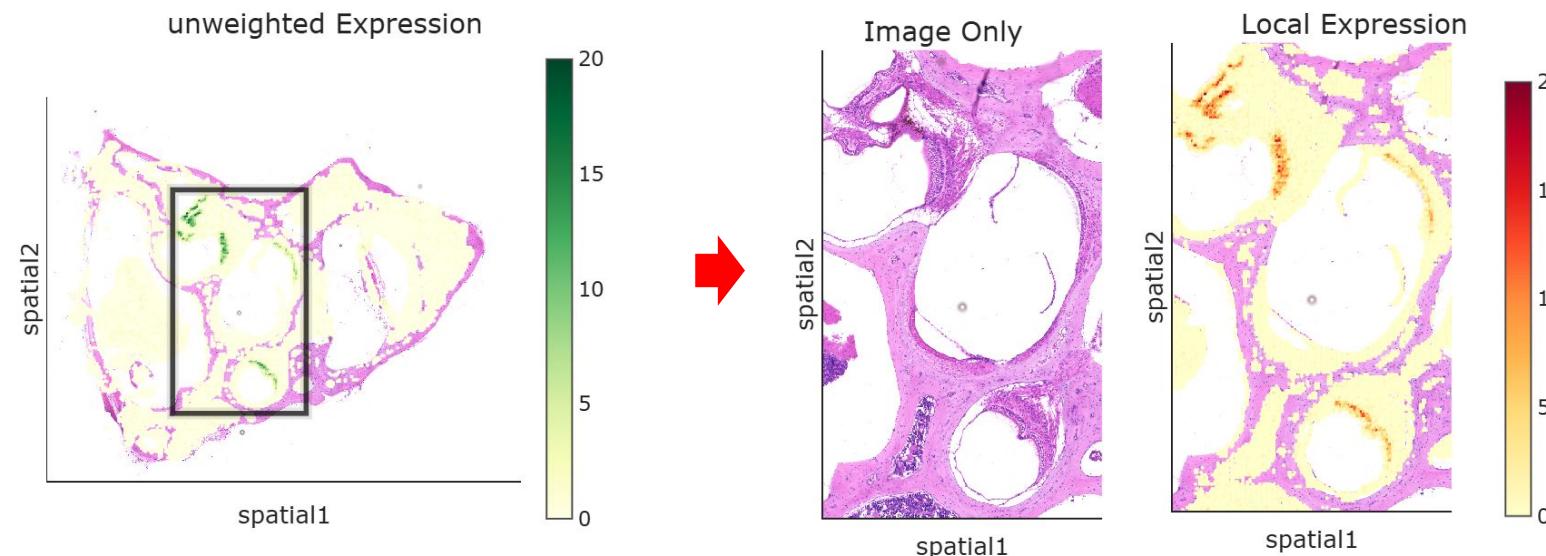
3. This time, you wonder if you accidentally captured hair cells from a different part of the ear while dissecting...



3. How can I use spatial transcriptomics to identify an unknown cell cluster?

### Example 2

4. After projecting your gene list on a spatial dataset that also has the vestibular regions of the ear, you realize the third cluster are actually **hair cells found in the vestibular system!**



Help gEAR by taking our survey!



**Menu**[My Workspace](#)**Explore**[Gene Expression](#)[Projection Tool](#)[Datasets](#)**Analyze**[Single Cell Workbench](#)[Comparison Tool](#)[Single-gene Displays](#)[Multi-gene Displays](#)**Manage**[Dataset Collections](#)[Gene Lists](#)[Dataset Uploader](#)**Support**[Help](#)[Feedback](#)**Citation**

gEAR: Gene Expression Analysis Resource portal for community-driven, multi-omic data exploration.

Orvis J, et al. Nat Methods. 2021

Jun 25.

doi: 10.1038/s41592-021-01200-9

PMID: 34172972



# Spatial Transcriptomics

1. Using a spatial transcriptomics dataset, what cell types express *Calb2*?
2. Using the Projection Tool, project the “Type I SGNs” gene list found under the “Favorites” tab on a spatial transcriptomics dataset. Does the gene list map where you would expect?
3. Now using the same Projection Tool, project the gene list titled “Unknown Spatial Example” found under the “Favorites” tab on a spatial transcriptomics dataset. What is the most likely cell type that corresponds to this unknown cluster?



## Gene Expression Search

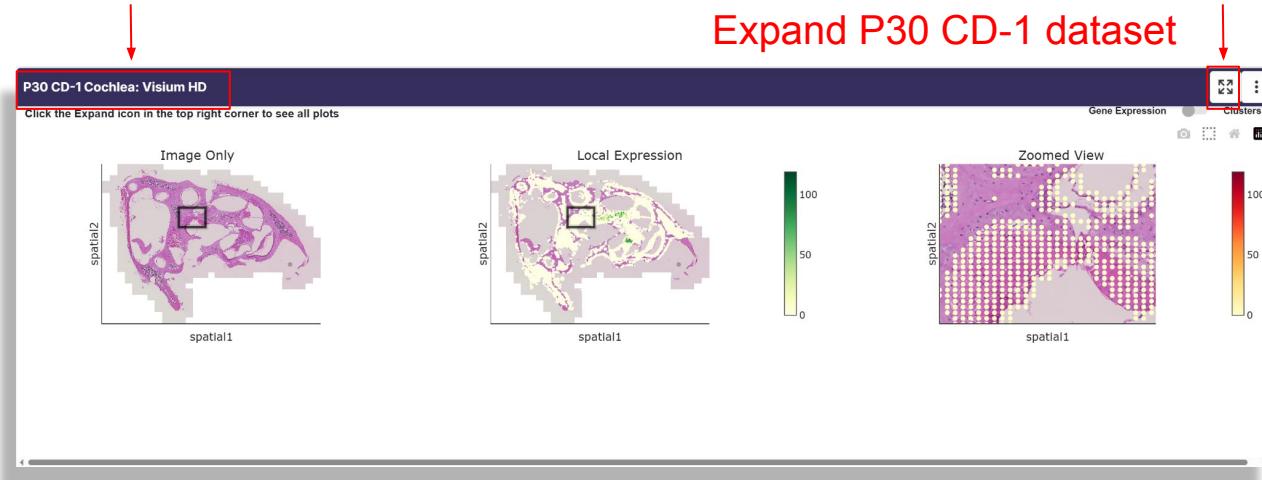
Calb2 OR Quick search using Gene Lists IN Spatial Transcriptomics

Exact match  Single-gene Display  Multi-gene Display

Search results (1) Showing results for: **calb2 - calbindin 2**

External Resource Links  CCDS  UCSC  UniParc  Uniprot/SWISSPROT  ENSEMBL  PubMed  HomoloGene  SHIELD  PhosphoSite

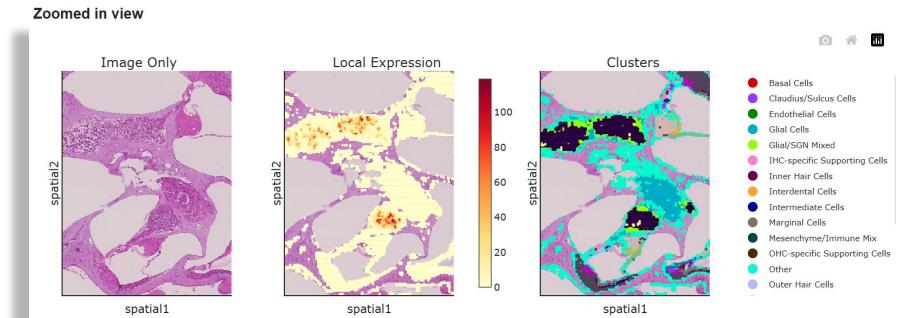
calb2



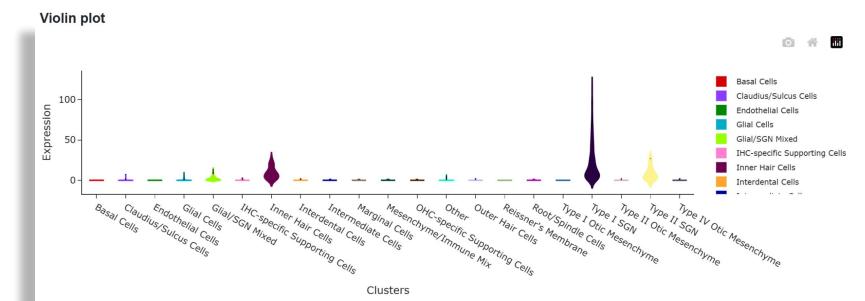
1. Using a spatial transcriptomics dataset, what cell types express *Calb2*?

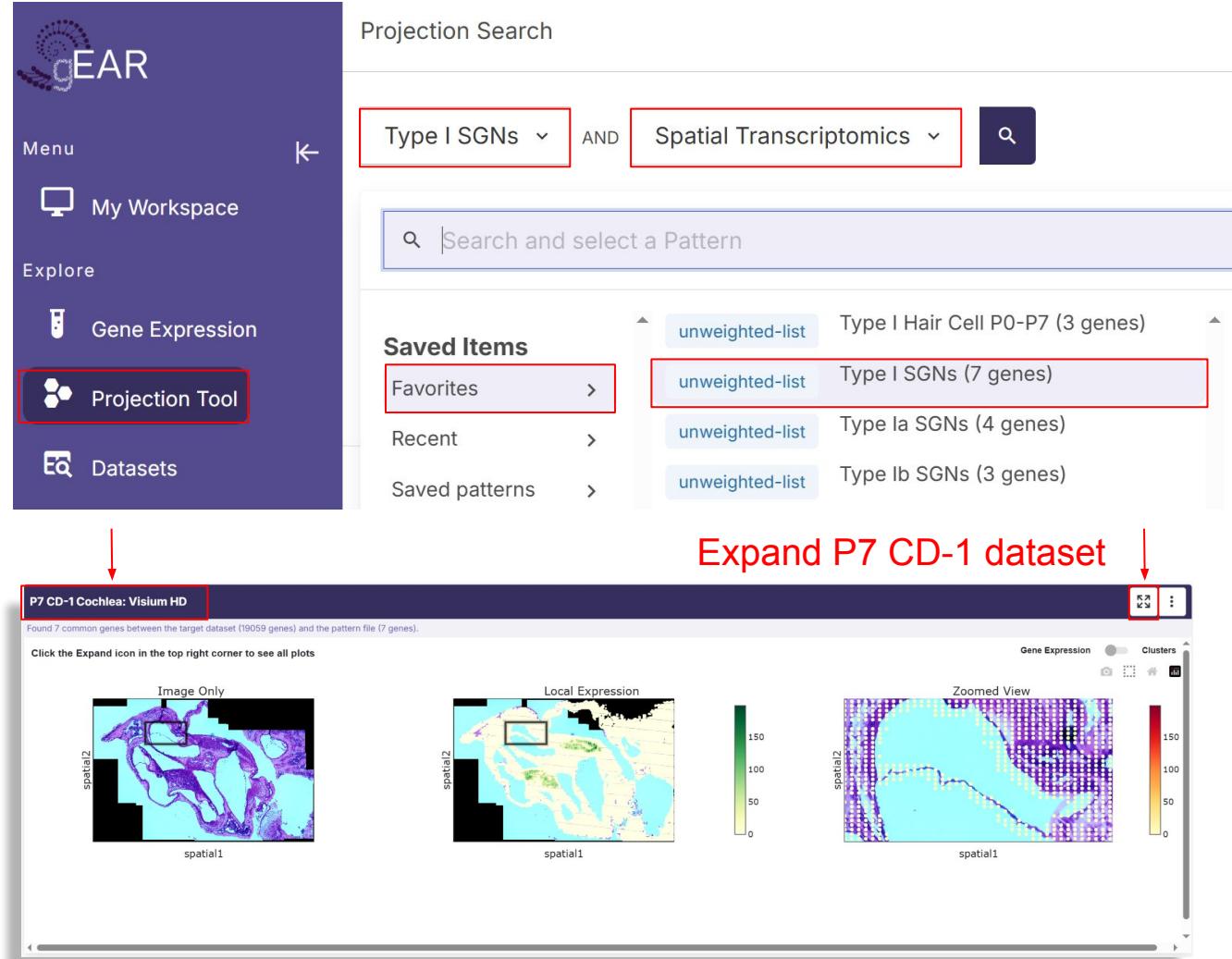


Zoom in to view your region of interest



Scroll down to the violin plot to help identify the cells that express *Calb2*:



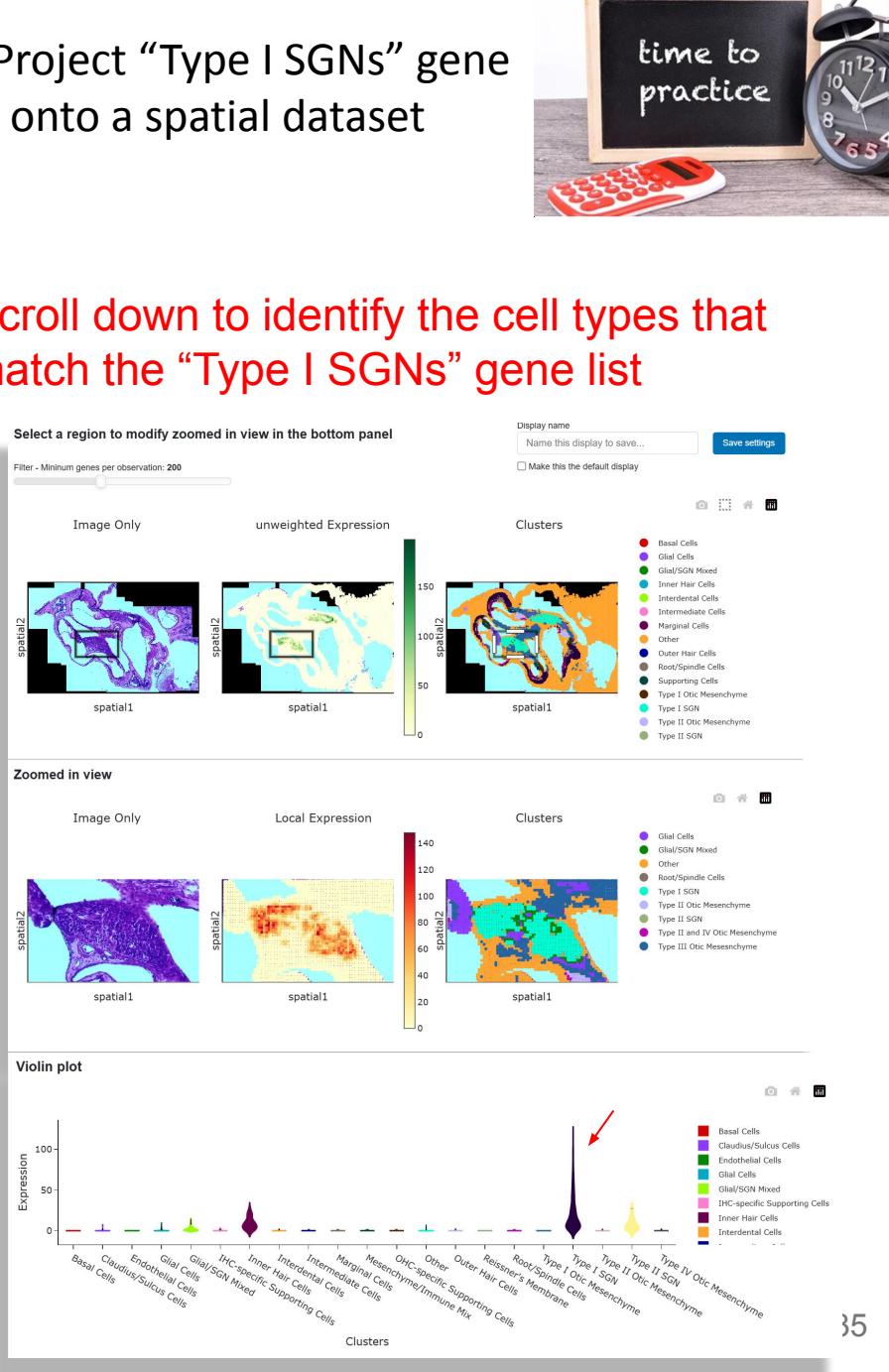


**Expand P7 CD-1 dataset**

## 2. Project “Type I SGNs” gene list onto a spatial dataset

time to practice

Scroll down to identify the cell types that match the “Type I SGNs” gene list



Violin plot

Expression

Clusters

Basal Cells, Claudius/Sulcus Cells, Endothelial Cells, Glial Cells, Glial/SGN Mixed, IHC-specific Supporting Cells, Inner Hair Cells, Interdental Cells, Intermediate Cells, Marginal Cells, Mesenchyme/Immune Mix, Other, Outer Hair Cells, Reissner's Membrane, Type I SGN, Type II SGN, Type II/Otic Mesenchyme, Type III/Otic Mesenchyme, Type IV/Otic Mesenchyme, Type I/Otic Mesenchyme, Type II/Otic Mesenchyme

35

**3. Determine what cell type the “Unknown Spatial Example” is.**

time to practice

Projection Search

Unknown Spatial Example AND Spatial Transcriptomics

Search and select a Pattern

Saved Items

- Favorites >
- Recent >
- Saved patterns >

Type II Hair Cell P7 (3 genes)  
Type II SGNs (2 genes)  
Unknown Spatial Example (5 genes)  
Vestibular Pan HC (6 genes)

Weights  
unweighted

P30 CD-1 Cochlea: Visium HD

Select a region to modify zoomed in view in the bottom panel

Filter - Minimum genes per observation: 100

Image Only      unweighted Expression      Clusters

Zoomed in view

Violin plot

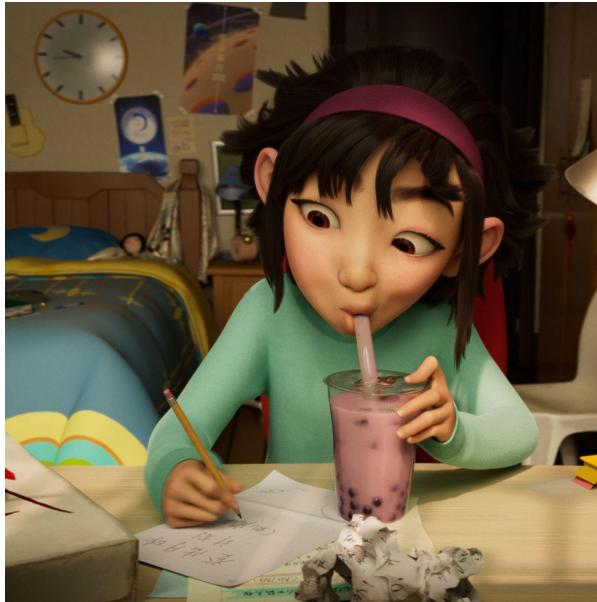
Expression

Clusters

136

Additional slides for *de novo* analysis of a  
scRNA-seq datasets

## 9. Explore scRNA-seq datasets – *de novo* analysis



Single cell RNA-seq has revolutionized our ability to understand the molecular identity of cells. Every cell in the tissue has its entire transcriptome recorded allowing a wealth of information to be captured.

However, for people with no informatics background, scRNA-seq datasets can be intimidating.



Kcnj10 OR Quick search using Gene Lists IN Lateral wall (Hoa)

Exact match  Single-gene Display  Multi-gene Display

Search results (1) **kcnj10**

Showing results for: **kcnj10 - potassium inwardly-rectifying channel, subfamily J, member 10**

External Resource Links  Deafness Gene Annotation   
CCDS UCSC UniParc Uniprot/SWISSPROT ENSEMBL PubMed HomoloGene SHIELD DVD PhosphoSite

Functional annotation

P30, mouse, scRNA-seq, Stria Vascularis (Hoa)

**Kcnj10**

tSNE\_2

tSNE\_1

**cell\_type**

tSNE\_2

tSNE\_1

Choose Display  
 Dataset Information  
 Dataset publication  
 GEO Information  
 Take Notes  
 Single Cell Workbench  
 Comparison Tool  
 Single-gene Curator  
 Multi-gene Displays  
 Download Bundle  
 Download H5AD  
 Download Image



## 1 Select a dataset ✓

Current dataset: P30, mouse, scRNA-seq, Stria Vascularis (Hoa)

[Expand dataset selection tool](#)

## 2 Select new or saved analysis ✓

Current analysis: New

New

Select an analysis

New

Imported analysis

Primary analysis

Public saved analyses

EARssentials ex 3

Unlabeled 2022-1-7 14:1:38

Your saved analyses

None found

Your recent unsaved analyses

None found



### ③ Primary dataset filtering ✓

The initial dataset contains many observations (cells), some of which may hold no significant value to the downstream analysis. Here you can perform multiple filtering steps to remove empty captures, doublets and genes not expressed in this dataset.

**Filtered shape:**

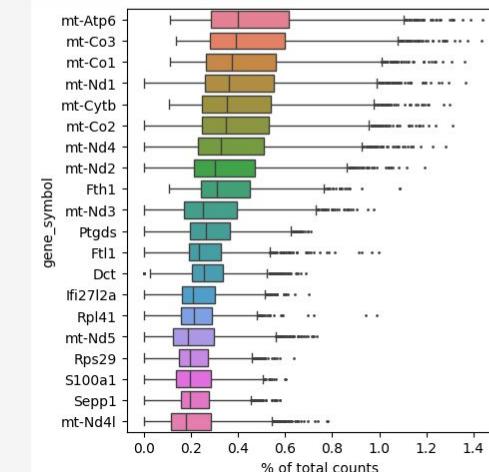
13886 genes x 2407 obs

Apply filters as desired.

- Exclude cells with <  genes
- Exclude cells with >  genes
- Exclude genes in <  cells
- Exclude genes in >  cells

Apply filters

### Genes with highest fraction of counts per cell



Toggle icon guide

### ④ QC - filter out mitochondrial content ✓

### ⑤ Identify highly-variable genes

### ⑥ Perform Principal Component Analysis (PCA)

### ⑦ Perform t-SNE or UMAP analysis

### ⑧ Perform clustering

### ⑨ Find marker genes

### ⑩ Rename, merge, or delete clusters

### ④ QC - filter out mitochondrial content ✓

Mitochondrial gene prefix (case-insensitive)

Filter by percent

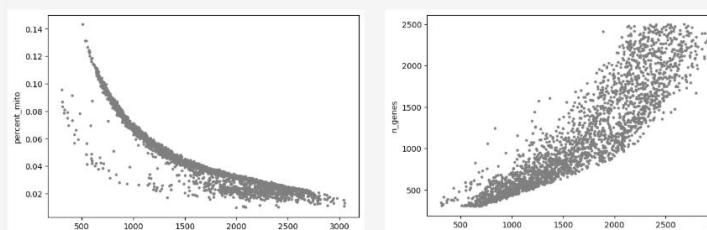
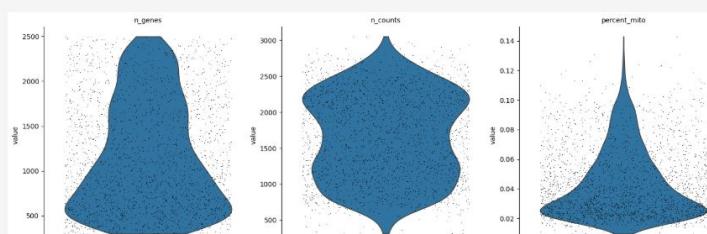
Filter by read counts

Saved

Saving genes will filter the dataset in an irreversible way.

Post-QC shape:

13886 genes x 1643 obs



[Toggle icon guide](#)**3 Primary dataset filtering****4 QC - filter out mitochondrial content****5 Identify highly-variable genes****6 Perform Principal Component Analysis (PCA)****7 Perform t-SNE or UMAP analysis****8 Perform clustering****9 Find marker genes****10 Rename, merge, or delete clusters****5 Identify highly-variable genes**

## Convention

[Seurat](#)

## Normalized counts per cell

1e4

## N top genes

2000

Fields below are ignored if this is set

## Min mean

0.0125

## Max mean

3

## Min dispersion

0.5

[Saved](#)

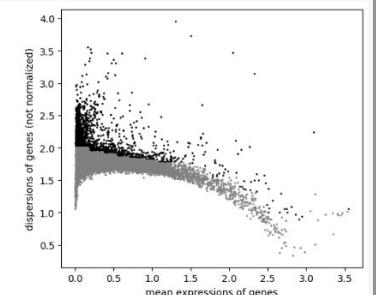
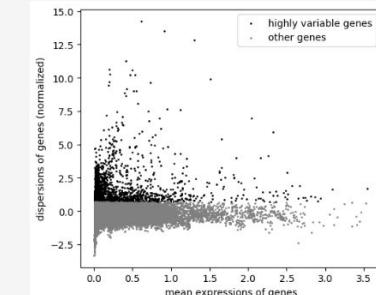
Saving genes will filter the dataset in an irreversible way.

Shape after filtering for highly variable genes:

2000 genes x 1643 obs

Suggested highly-variable genes:

Gypa, Cd24a, Hba-a2, S100a9, Ngp

**6 Perform Principal Component Analysis (PCA)**

## Genes to colorize

Gypa, Cd24a, Hba-a2, S100a9, Ngp

Compute and plot

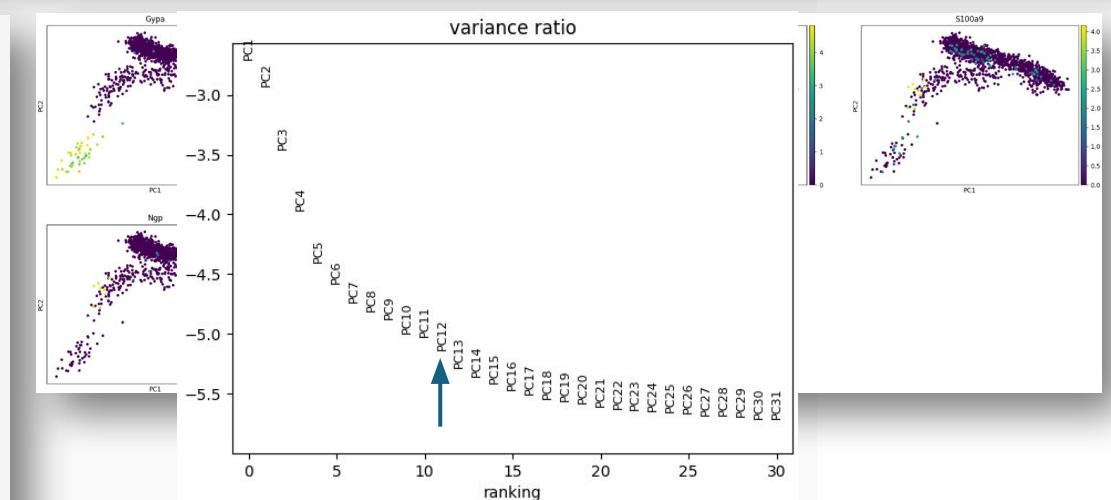
## Principal Components to view top genes

Comma-separated list of principal components, ideally between 2 and 5 PCs, just the number only (omit the "PC").

[View top genes per PC](#)

## Save New Weighted Gene List

Enter name of gene list

[Save PCs as a pattern signature](#)



Current dataset: P30, mouse, scRNA-seq, Stria Vascularis (Hoa)  
Current analysis: New

Analysis  
options:

Download analysis H5AD

Rename

Save

Delete

1 - Dataset selection

2 - Analysis selection

3 - Primary filter

4 - QC: filter out  
mitochondrial content

5 - Identify highly-variable  
genes

6 - Perform Principal  
Component Analysis (PCA)

7 - Perform t-SNE or UMAP  
analysis

8 - Perform clustering

9 - Find marker genes

10 - Rename, merge, or  
delete clusters

11 - Compare genes

Toggle icon guide

3 Primary dataset filtering ✓

4 QC - filter out mitochondrial content ✓

5 Identify highly-variable genes ✓

6 Perform Principal Component Analysis (PCA) ✓

7 Perform t-SNE or UMAP analysis

8 Perform clustering

9 Find marker genes

10 Rename, merge, or delete clusters

7 Perform t-SNE or UMAP analysis ✓

Genes to colorize

Gypa, Cd24a, Hba-a2, S100a9, Ngp

Comma-separated list of gene symbols

Number of neighbors

7

Number of nearest neighbors to consider for each cell

Number of dimensions

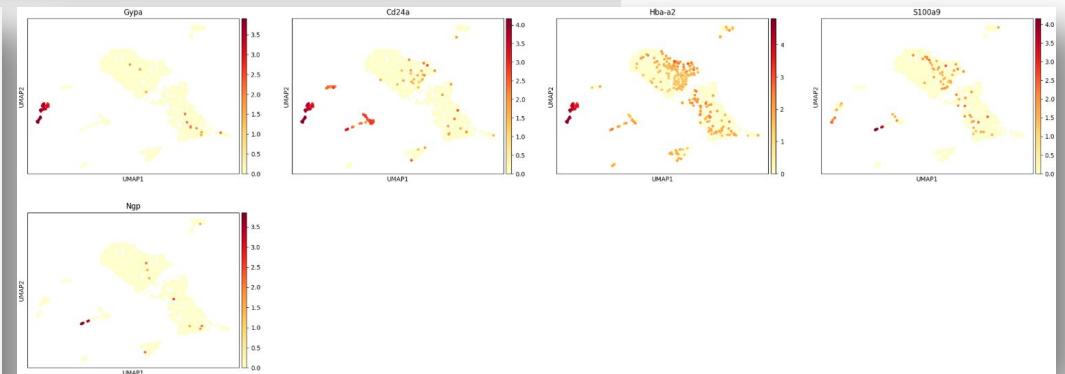
12

Number of principal components to be embedded into the plot

Dimensionality reduction method

t-SNE  
 UMAP

Compute and plot

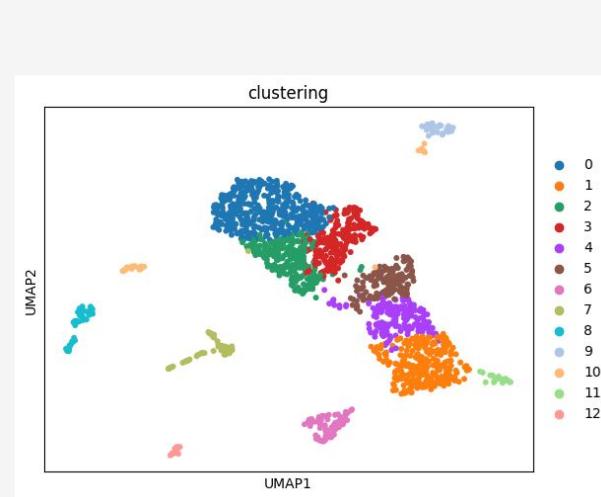


8 Perform clustering ✓

Resolution

0.5

Compute and plot



[Toggle icon guide](#)**3 Primary dataset filtering** ✓**9 Find marker genes** ✓

This analysis step will show you the marker genes within each group of cells as defined by the clustering method used. You can adjust the number of genes you would like to see for each cluster by adjusting the 'N genes' value.

**N genes**

5

**Compute**

	0	1	2	3	4	5	6	7	8	9	10	11	12
0	Rsrp1	Gas2	Met	Malat1	Gas2	Fth1	Cldn11	Rplp0	Cd24a	Pipp3	Tma7	Atp1b2	C1qa
1	Taf1d	Mt3	Tyr	Tyr	mt-Co2	Cox8b	Actn1	Rps16	Gypa	Apod	Rpl7	Lrp2	Tyrobp
2	Phlda1	Igf1	Nrp2	Hpse	mt-Co1	Ifi27l2a	Apod	H3f3a	Hba-a2	Tmsb10	Rpl6	Alcam	C1qb
3	Malat1	Kcne1	Gpnmb	Hba-a1	mt-Nd4	Gsta4	Clu	Fau	Hbb-bt	Mdk	Skp1a	Igf1	Ctss
4	Son	Gpx3	Ednrb	Atp1b1	mt-Nd2	Cox8a	Gsn	Tmsb4x	Hba-a1	Rbp1	Fbxo2	Kcne1	Fcer1g

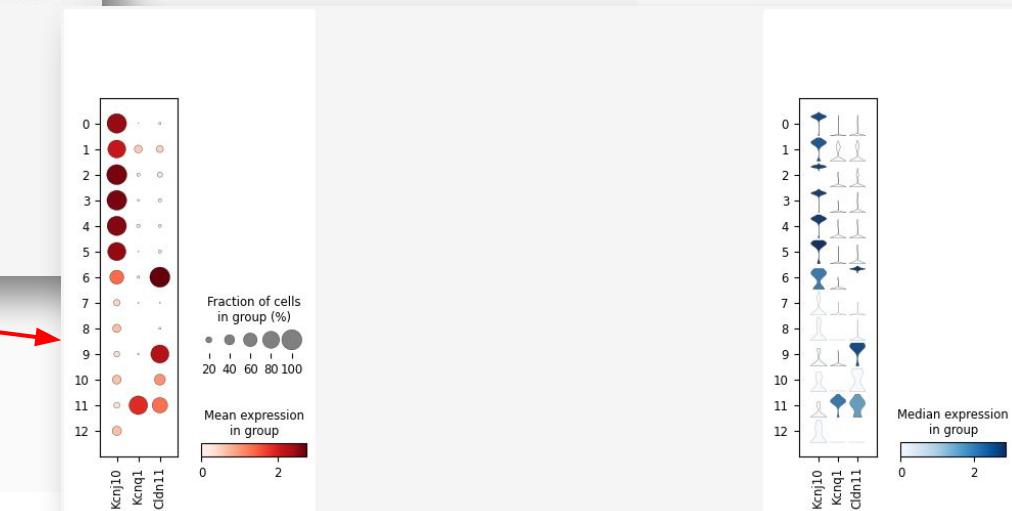
**Marker gene visualization**

Select desired marker genes in the table above and/or type gene symbols in the field below to visualize

Enter gene symbols (comma-separated)

Kcnj10,Kcnq1,Cldn11

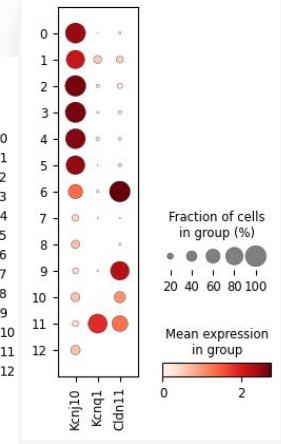
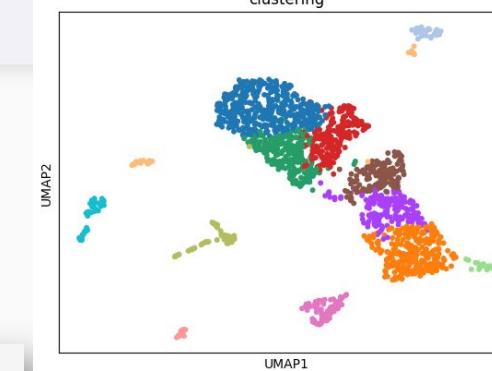
- Unique marker genes selected in table: 0
- Unique marker genes manually entered: 3
- Total unique genes selected: 3

**Visualize****10 Rename, merge, or delete clusters** ✓

[Toggle icon guide](#)**3 Primary dataset filtering****4 QC - filter out mitochondrial content****5 Identify highly-variable genes****10 Rename, merge, or delete clusters****6 Perform Principal Component Analysis (PCA)****7 Perform t-SNE or UMAP analysis****8 Perform clustering****9 Find marker genes****10 Rename, merge, or delete clusters**

Merging and/or deleting clusters is irreversible.

clustering

 Check to merge clusters with duplicate labels

Group	Num Cells	Markers	New label	Keep
0	404	Rsrp1	Intermediate	<input checked="" type="checkbox"/>
1	274	Gas2	Gas2	<input checked="" type="checkbox"/>
2	217	Met	Intermediate	<input checked="" type="checkbox"/>
3	192	Malat1	Intermediate	<input checked="" type="checkbox"/>
4	163	Gas2	Intermediate	<input checked="" type="checkbox"/>
5	139	Fth1	Intermediate	<input checked="" type="checkbox"/>
6	65	Cldn11	Basal	<input checked="" type="checkbox"/>
7	50	Rplp0	Rplp0	<input checked="" type="checkbox"/>
8	43	Cd24a	Erythrocytes	<input checked="" type="checkbox"/>
9	32	Plpp3	Plpp3	<input checked="" type="checkbox"/>
10	27	Tma7	Tma7	<input checked="" type="checkbox"/>
11	20	Atp1b2	Marginal	<input checked="" type="checkbox"/>
12	17	C1qa	C1qa	<input checked="" type="checkbox"/>

[Rerun with labels](#)