Password

University of Maryland

The gEAR portal v2: a one-stop shop for ear related multi-omic data visualization and analysis

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Tool tip – hover over for

P0, mouse, RNA-seq. Hair cells vs epithelial non-hair cells

op Hair Cell Enriched genes

- lookup in zebrafish dataset

s this note private or public

Dataset Description

Pou4f3, Ptprq, Gfi1

Note-Taking Feature

◆Public ↓ Date ↓ Title

■ Title

■

E12.5-P30, mouse endolymphatic sac, single

No notes were found.

Create a new note below.

Drop-Down Menu

6 Info

The drop-down menu offers

additional features and tools

which may vary between

datasets

8a

E12.5-P30, mouse endolymp

E12.5-P30, mouse endolymp

E16_MRC_ave

P30_MRC_ave

Data filters / settings Log transformation

Fold change cutoff Show 3x or higher

Standard deviation

Representing bar graphs as 1 plot, 2

≛ Download

Compare

E16.5 Cochlea: 27.826





Introduction to the gEAR Portal

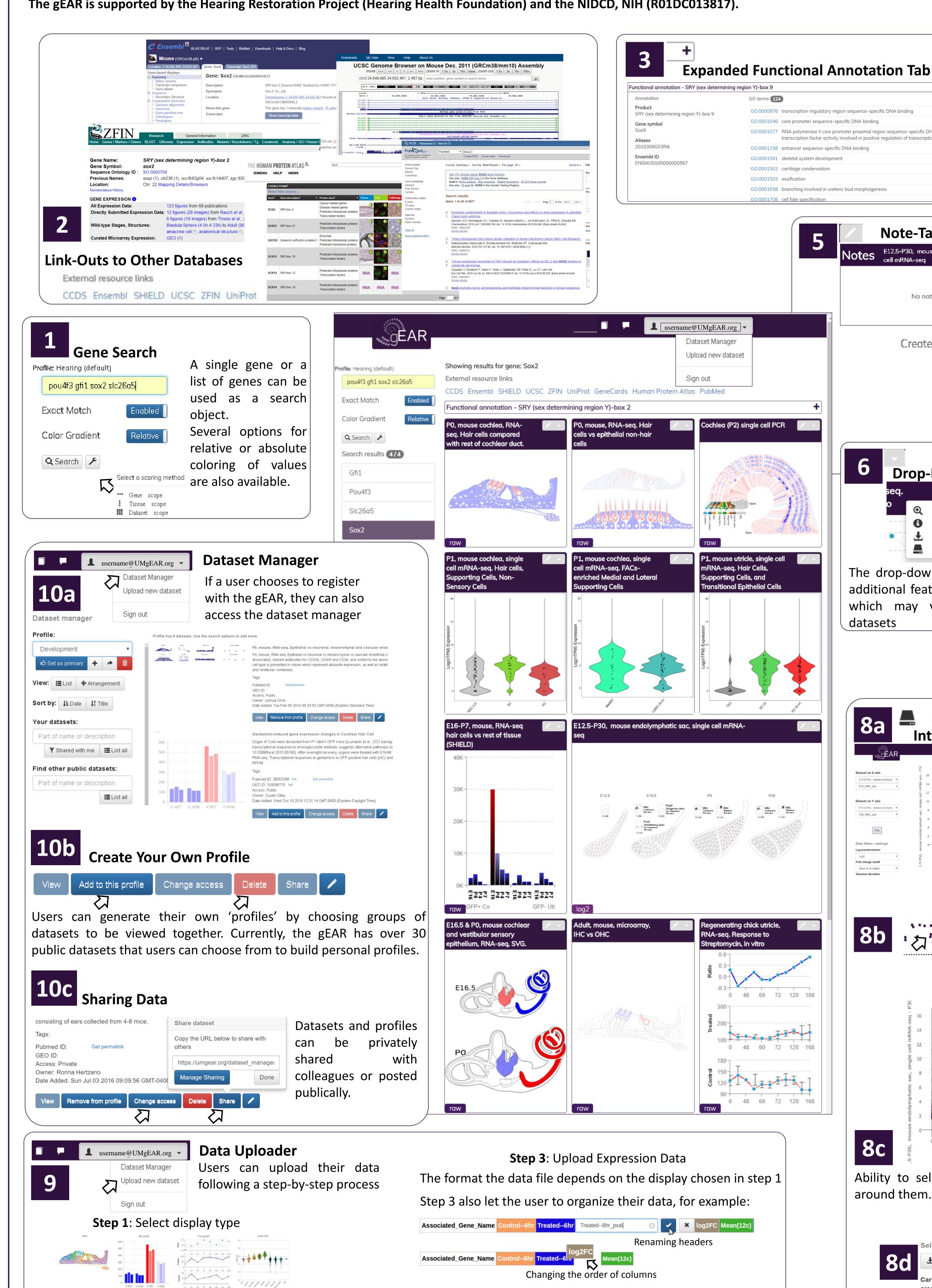
SCHOOL OF MEDICINE

Step 2: Describe Data

Title, description of sample, decide Private or Public

The gEAR portal (gene Expression Analysis Resource, umgear.org) is an online tool for multi-omic and multi-species data visualization, sharing, and analysis. Specifically, the 'Hearing' domain of the gEAR portal is designed and maintained for auditory and vestibular researchers. The gEAR is unique in its ability to allow users to upload, view and analyze their own data in the context of previously published datasets, as well as confidentially share their data with collaborators prior to publication. It is also unique in combining not only multiple species but multiple data types including bulk RNA-seq, sorted cell RNA-seq, single cell RNA-seq (scRNA-seq) and epigenomics in a one page, user-friendly, browseable format. Most recently, scRNA-seq has matured to a commonly used technique for measuring gene expression across tissues. To provide researchers access to scRNAseq data regardless of their programming knowledge, we have integrated a scRNA-seq workbench into the gEAR. The gEAR scRNA-seq workbench provides access to both the raw data of scRNA-seq datasets, as well as to saved expert analyses where cell types have already been assigned – giving researchers rapid insight into gene expression of their cell type of interest. This poster presentation functions as a step-by-step introduction to the gEAR portal, now a mainstream multi-omic data source for the ear research community.

The gEAR is supported by the Hearing Restoration Project (Hearing Health Foundation) and the NIDCD, NIH (R01DC013817).



The Single Cell Analysis Workbench

QC - filter by

mitochondrial content

Principal Component

Principal Compone Analysis (PCA)

Analysis (PCA)

Identify high-variable

The Single Cell Analysis Workbench is a tool under active development. This tool currently implements much of the Seurat pipeline in a graphical user-interface and in an implementation that allows faster data processing and visualization than standard R-based pipelines.

The analysis workbench is accessible from the dropdown menu

After choosing the dataset (1) and obtaining the 'dataset structure' (2) work through the steps of the analysis using the 'toggle buttons'

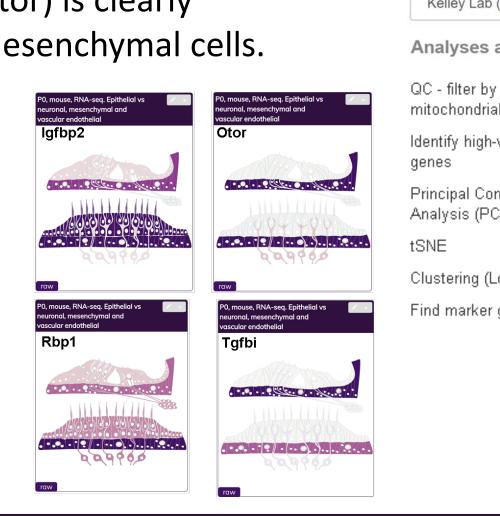
A quality control step follows (3). This filters cells based on their mitochondrial content.

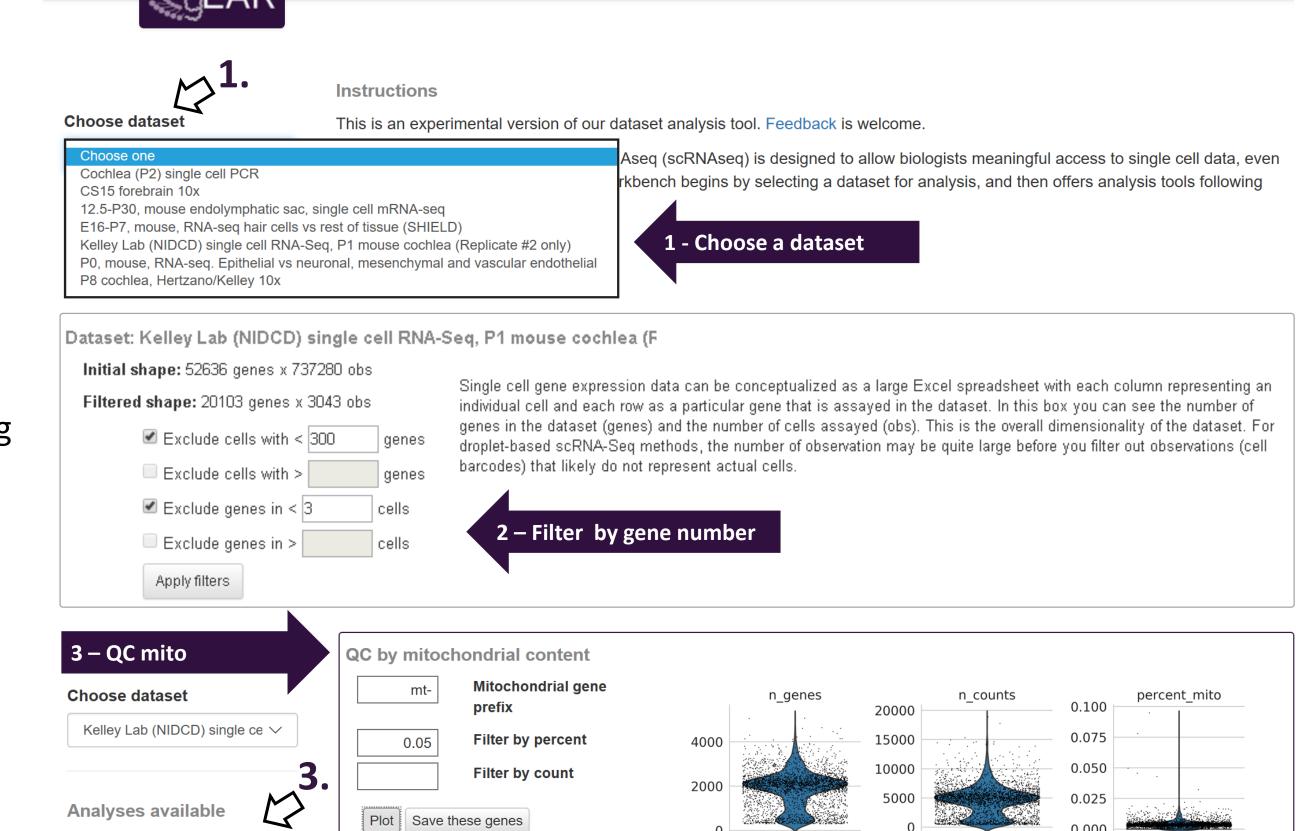
To perform the downstream principal component and tSNE analysis first identify a group of **highly variable** genes (4). For efficiency, the workbench limits users to a maximum of 2,000 genes.

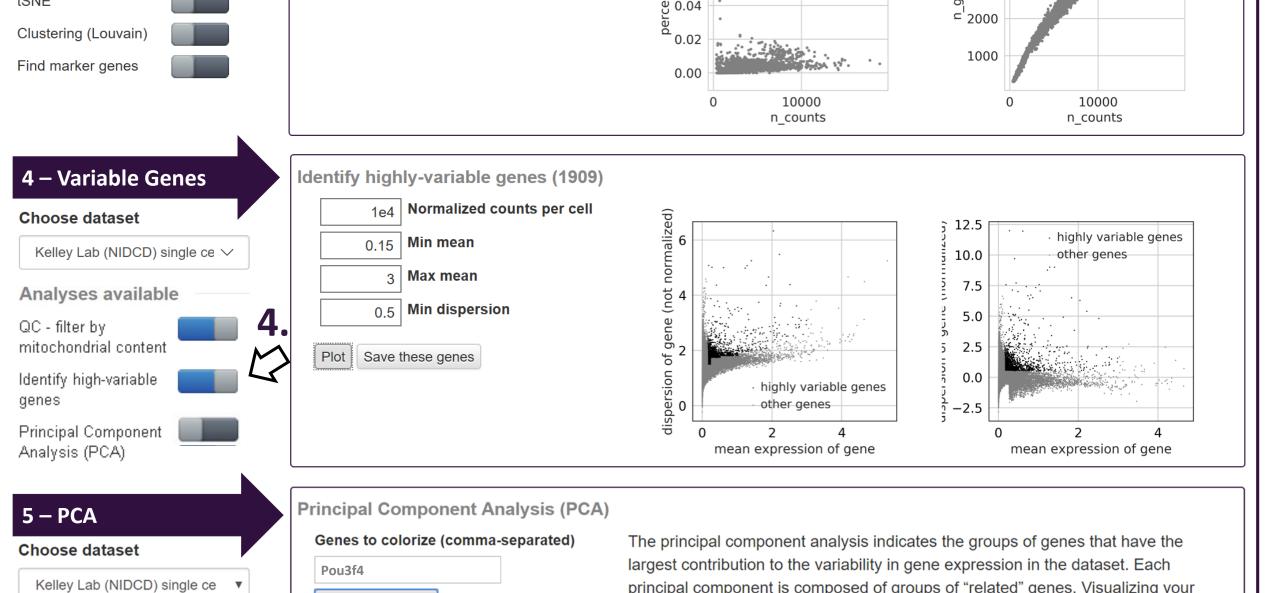
The **PCA** (5) outlines the number of principle components identified and allows users to examine the expression of genes in the first and second PCs. Coming soon – Heat Maps for the genes contributing to each PC.

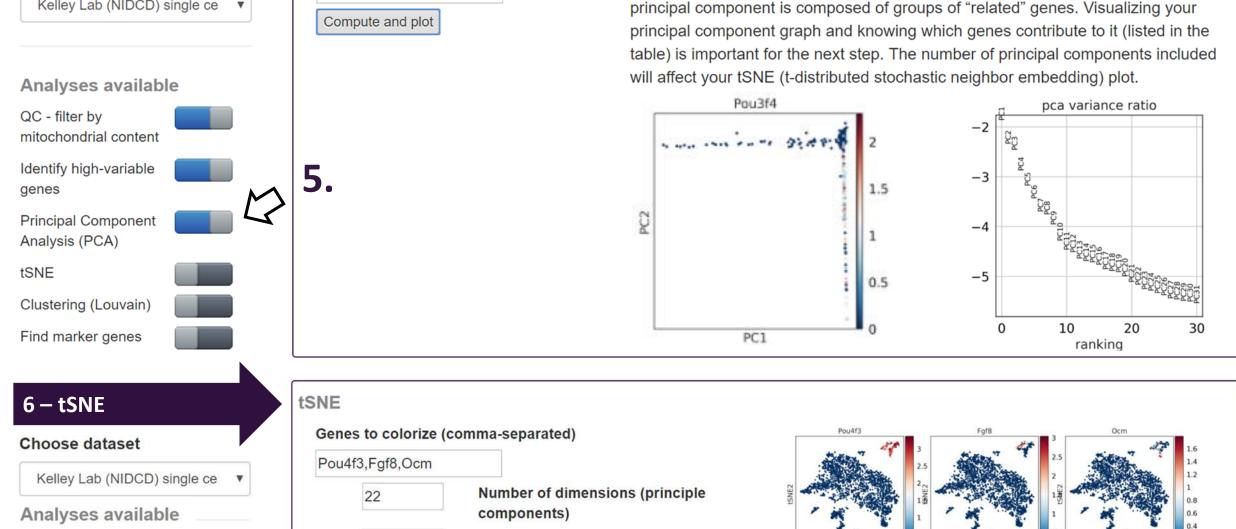
Generate a tSNE plot (6) by selecting the number of PCs to incorporate. You may check expression of genes of interest by typing their symbols in the search box.

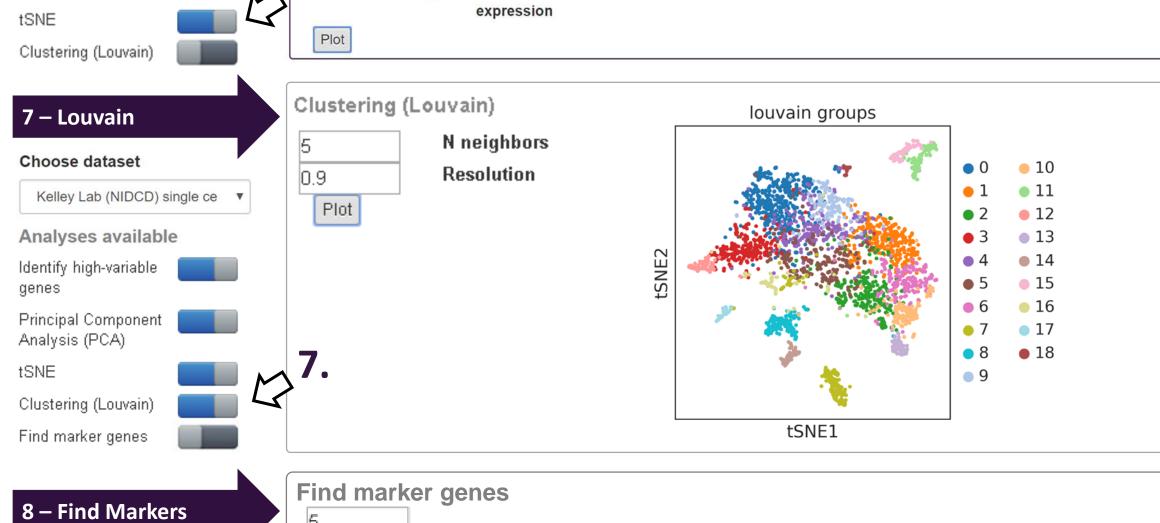
Following the **Louvain** clustering (7) marker genes can be identified (8) and downloaded as a table to then use as input to search other datasets for validation. For example – population '6' (top gene Otor) is clearly mesenchymal cells.





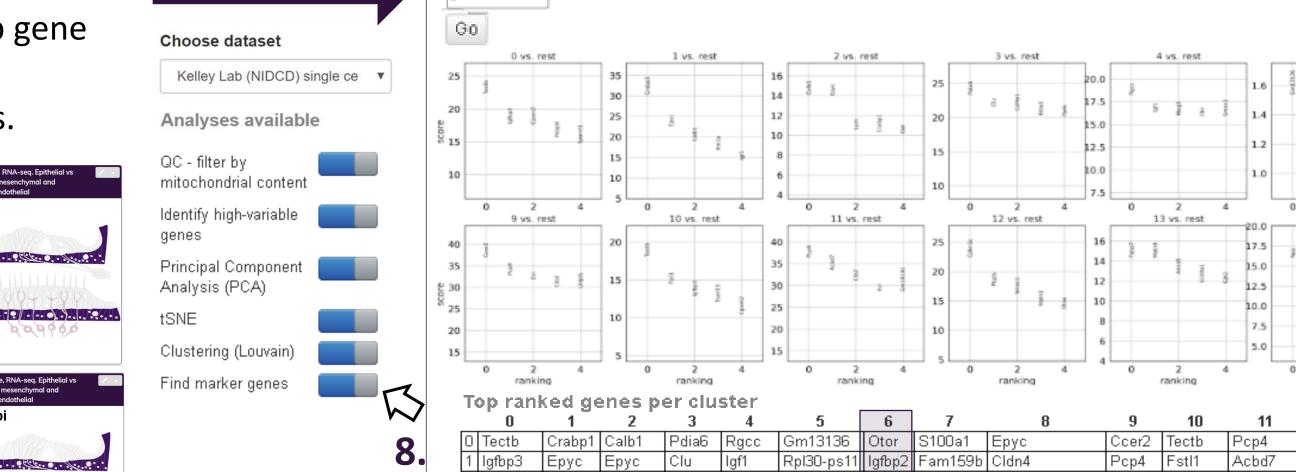


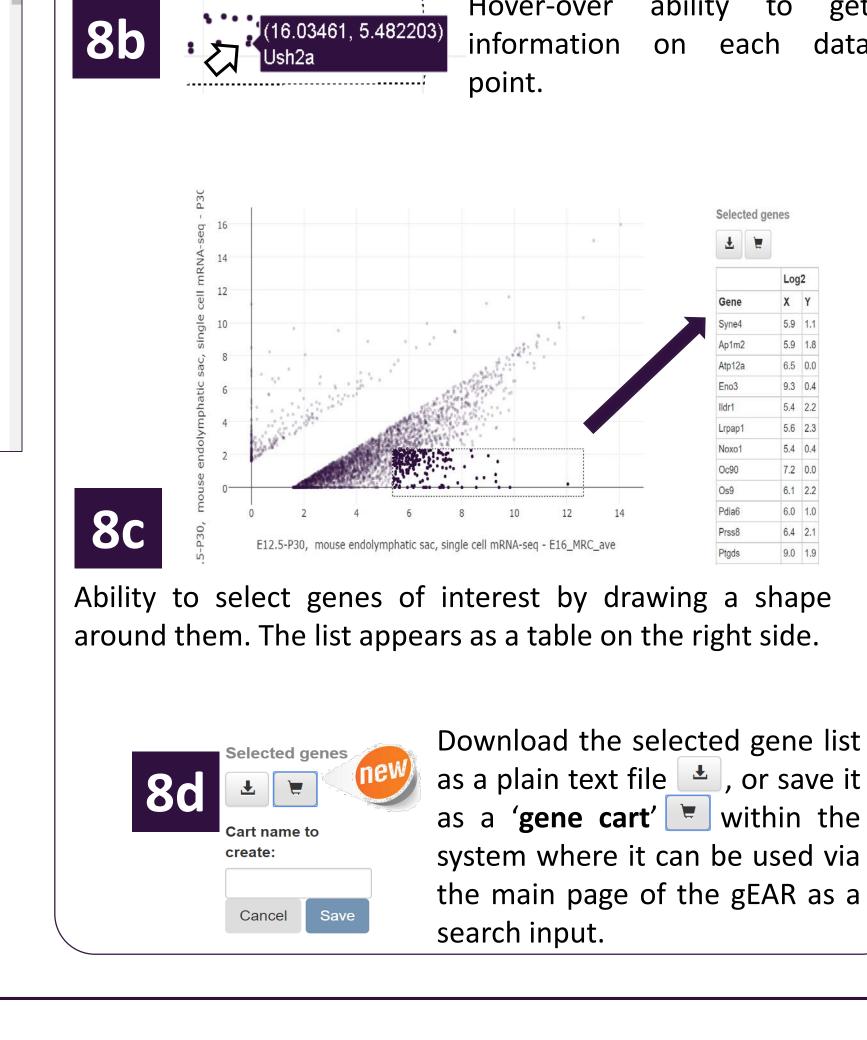




Random state

Use scaled and corrected





Interactive Compare Tool