# Mouse Olfactory Mucosa Atlas

## User Manual

In this website you can visualize gene expression in the Mouse Olfactory Mucosa in 3D (data from our article) and per cell type (single cell data from Fletcher, R.F. et. Al., 2017) as well as information related to the different zones of this tissue defined in (our article. The website is divided in 4 tabs: **"Main"** (where you are), **"3D Zones"**, **"Gene search",** and **"Correlation between 2 genes".**

### 3D Zones

In this section, you can see the area belonging to each zone in a 3D map of the Olfactory Mucosa when clicking the button **"see 3D zones"**. The 3D tissue can be virtually sliced and slices along each axis can be visualized depending on the option selected in "Slices Projection":

When the option **"LML x DV"** is selected (default), slices with the Lateral – Middle – Lateral (LML) axis as the x axis and the Dorsal – Ventral (DV) axis as the y axis will be displayed. If you select the option **"AP x DV"**, slices with the Anterior – Posterior (AP) axis as the x axis and the Dorsal – Ventral (DV) axis as the y axis will appear. Finally, when you select the option **"AP x LML"**, the Anterior – Posterior (AP) axis will be the x axis and the Lateral – Middle – Lateral (LML) axis the y axis in the slices.

### Gene search

Here you can select any of the 17628 genes that were detected along all of the 3 axes in the TOMO-seq data from (our article) and visualize its 1D expression (RPM normalised). You can download our RPM normalized gene expression data along each axis using the options **"Download axis 1D data (all genes)".**

Gene 3D expression in the Olfactory Mucosa is also available, you must click the button **"Calculate 3D pattern"** and it will be displayed after a few seconds. The virtual slicing of the tissue is done as above. Log10 RPM expression values per voxel are shown. It is possible to download 3D gene expression data for one gene at a time by clicking the button **"Download 3D data"**. You will get a table where the first 3 columns indicate the coordinates of each voxel and the column named "value" contains the expression value of the gene in the corresponding voxel. **PD: Make sure you press the button "Calculate 3D pattern" before trying to download the 3D data!! (Otherwise, you might get expression values for the previously searched gene)**

Below the 3D pattern section we can find a bar plot related to the probability of finding the selected gene in each of the zones defined in (our article), this probabilities are referred to as **"Degrees of belonging"**. This information is also available for download clicking on **"Download degrees of belonging (all non random genes)"**.

The last displayed figure are box plots showing the log10 TPM normalized expression of the selected gene in single cells of different kinds (data from Fletcher, R.F. et. Al., 2017). There's an option to download this data **("Download Single cell data").** This will give you a table where rows are genes and cells are columns. Columns are named the following way: x-y where: x = cell type number; y = cell number. Cell type numbers as listed below:

**Cell types:**

1. HBC = Horizontal Basal Cells
2. INP1 = Immediate Neuronal Precursors group 1
3. GBC = Globose Basal Cells
4. mSC = mature Sustentacular Cells
5. tHBC2 = transitional Horizontal Basal Cells group 2
6. Small cluster 1 (unclassified cells)
7. iSC = immature Sustentacullar Cells
8. tHBC1 = transitional Horizontal Basal Cells group 1
9. iOSN = immature Olfactory Sensory Neurons
10. INP3 = Immediate Neuronal Precursors group 3
11. MVC1 = Microvillous Cells group 1
12. mOSN = mature Olfactory Sensory Neurons
13. Small cluster 2 (unclassified cells)
14. INP2 = Immediate Neuronal Precursors group 2
15. MVC2 = Microvillous Cells group 2

**Correlation between 2 genes**

If you are curious about how the spatial patterns of 2 different genes correlate, here you can visualize it: You need to introduce the names of the two genes of your choice in the boxes **"Gene 1"** and **"Gene 2".** Three scatter plots (one per axis) will be displayed. The x axis of the scatter plot will represent the expression of Gene 1 along the indicated axis; and the y axis of the scatter plot will indicate the expression of Gene 2 along the corresponding axis. The Spearman correlation coefficient and p-value from correlation test will be at the top of the plot.