

The database mainly contains nine tabs (in grey panel) with interactive interface, with the opening page showing the **first tab (Spatial Plot)**. In this tab by typing part of the gene name, a list of genes will pop up for selection. Once one gene is selected from the list, it will be plot on the spatial plot, together with the gene expression comparison result. The spatial plot could be download as pdf with selected size.

HuMdb
A spatialtemporal gene expression database for human aging muscle regeneration

Introduction **Spatial Plot** SpotInfo vs GeneExpr SpotInfo vs SpotInfo GeneExpr vs GeneExpr Gene coexpression Violinplot / Boxplot Proportion plot
Bubbleplot / Heatmap Geneset Score User Guide

input gene symbol
COL1A1
search

Gene Summary

```

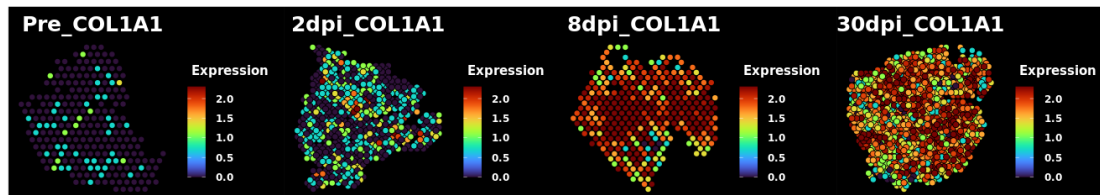
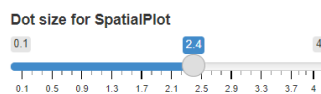
Symbol          COL1A1
ensembl_gene_id ENSG00000188821
chromosome      17
type_of_gene    "protein_coding"
description     "collagen type I alpha 1 chain [Source:HGNC Symbol;Acc:HGNC:2197]"
  
```

Differential expressed genes in different time points compared to sham

gene	pct_in_Pre	pct_in_2dpi	pct_in_8dpi	pct_in_30dpi	2dpi_to_Pre_avg_log2FC	2dpi_to_Pre_p_val	2dpi_to_Pre_p_val_adj	8dpi_to_2dpi_avg_log2FC	8dpi_to_2dpi_p_val	8dpi_to_2dpi_p_val_adj
COL1A1	2.17e-01	4.68e-01	9.93e-01	7.95e-01	5.389764e-01	5.602804e-54	9.304576e-50	3.049928e+00	0e+00	0e+00

* Wilcoxon Rank Sum test were used to identify differentially expressed genes between two groups of Spots
 * pct: The percentage of Spots where the gene detected in the group
 * avg_log2FC: log fold-change of the average expression between the two groups.
 * p_val_adj: Adjusted p-value, based on bonferroni correction using all genes in the dataset

Spatial gene expression: Spatial plot



PDF height: PDF width:

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Same as gene spatial plot, spatial geneset score section allow to type in part of the pathway of interested, so a list of geneset name will pop up for selection. Once one geneset is selected from the list, it will be plot on the spatial plot. The spatial plot could be also download as pdf with selected size.

Spatial geneset score: Spatial plot

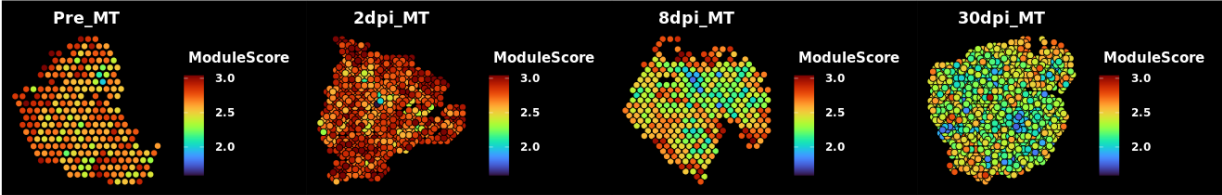
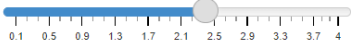
input geneset

MT-score1

search

Dot size for SpatialPlot

0.1 2.4 4



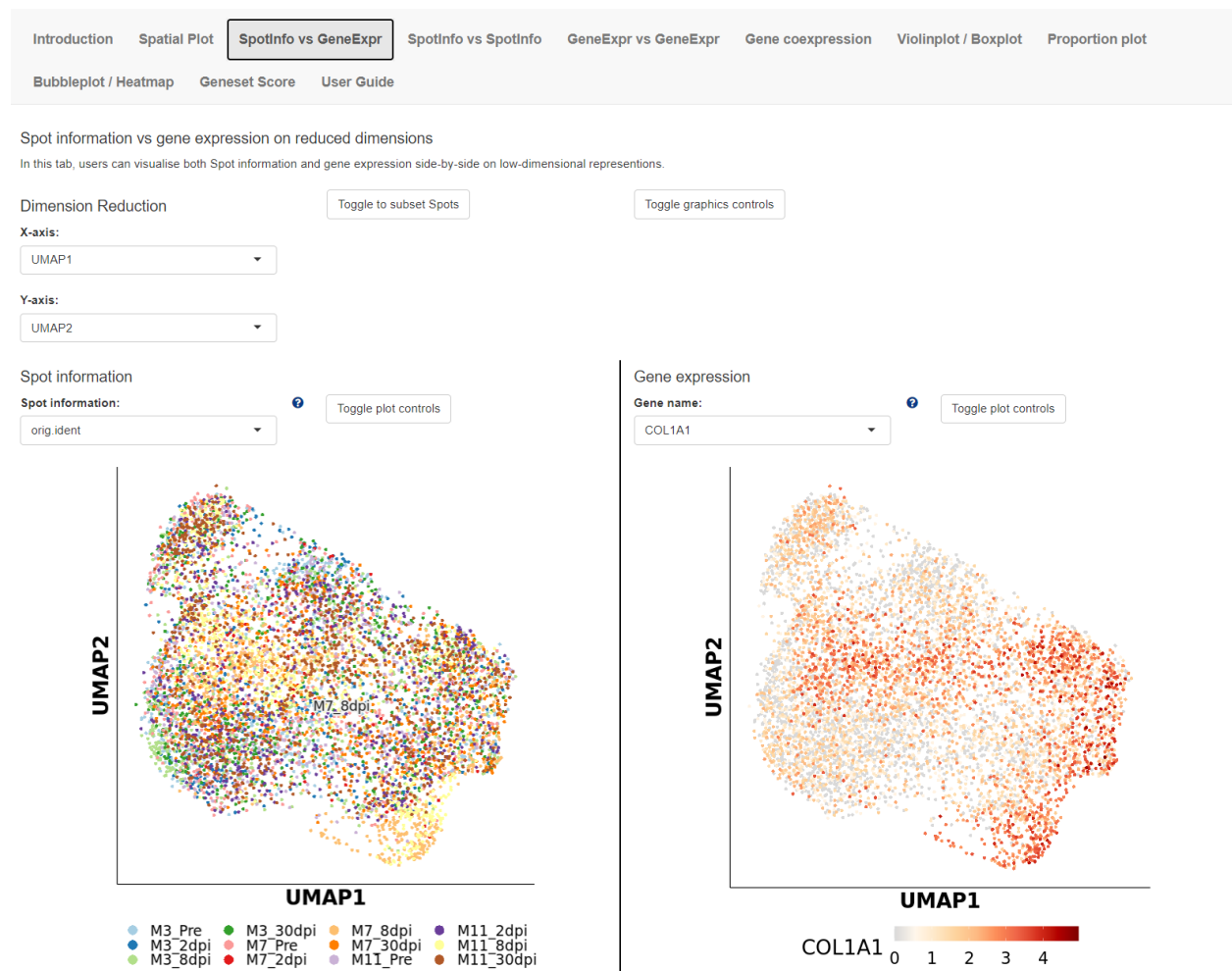
PDF height: 6 PDF width: 15

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In Spot Info vs GeneExpr tab (see below), plotting both Dot(Spot) information and gene expression side-by-side on reduced dimensions e.g. TSNE. Dimension reduction could be selected from PC, tSNE and UMAP by selecting from X-axis and Y-axis in “Dimension Reduction”. Samples color coding could be changed by selection of sample information.

Dot(Spots) could be subsetted with “Toggle to subset Spots” bottom to select the groups of samples you would like to show. Plot could be adjusted with “Toggle plot control” bottom, including color, plot order etc. Point and font size could be changed with “Toggle graphic controls” bottom.

To select the gene of interest, simply type the first few letters in “Gene name” box and select from the list.



In Violinplot-Boxplot tab you could plots the distribution of continuous Spot information e.g. nUMI or module scores or gene expression across each cluster / group using violin plots or box plots.

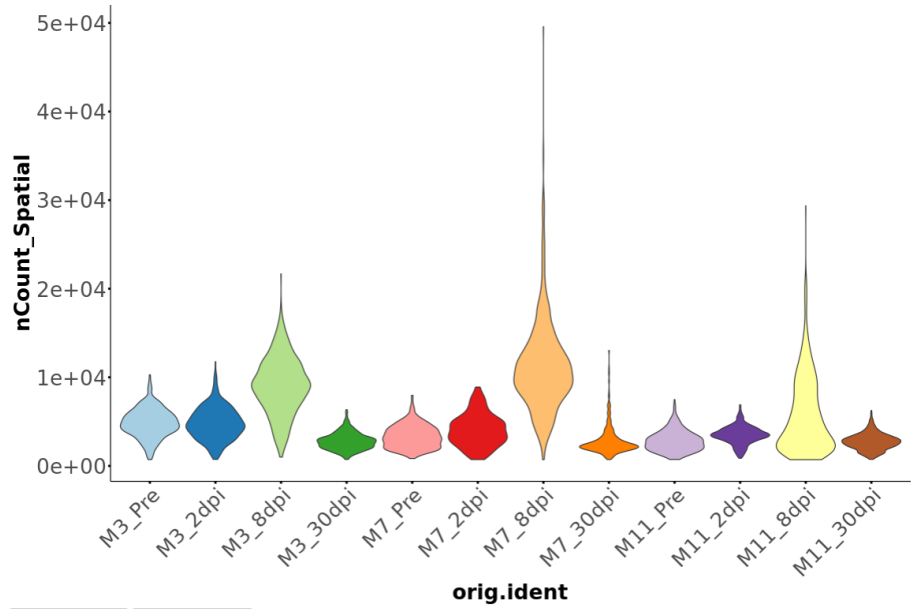
Spot information / gene expression violin plot / box plot

In this tab, users can visualise the gene expression or continuous Spot information (e.g. Number of UMIs / module score) across groups of Spots (e.g. library / clusters).

Spot information (X-axis):
orig.ident

Spot Info / Gene name (Y-axis):
nCount_Spatial

Plot type:
 violin boxplot
 Show data points
Toggle to subset Spots
Toggle graphics controls



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In Proportion plot tab you could plots the composition of different clusters/groups of Spots using proportion plots. Users can also plot the Spot numbers instead of proportions.

Proportion / Spot numbers across different Spot information

In this tab, users can visualise the composition of single Spots based on one discrete Spot information across another discrete Spot information. Usage examples include the library or Spotcycle composition across clusters.

Spot information to plot (X-axis):

Time

Spot information to group / colour by:

Subject

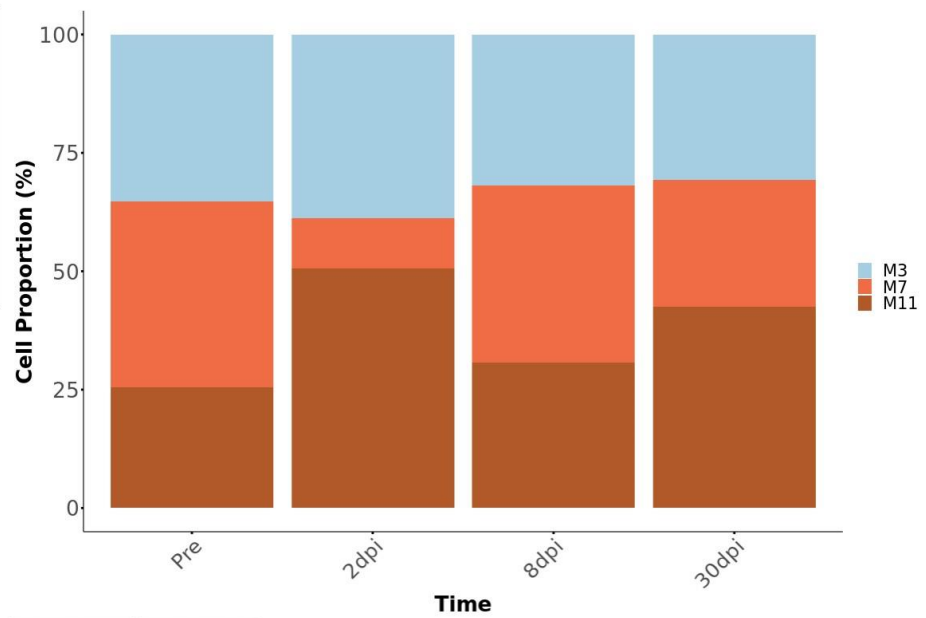
Plot value:

Proportion SpotNumbers

Flip X/Y

Toggle to subset Spots

Toggle graphics controls



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8 10

In Bubbleplot / Heatmap tab you could visualise the expression of multiple genes across each cluster / group using bubbleplots / heatmap. The genes (rows) and groups (columns) can be furthered clustered using hierarchical clustering.

Gene expression bubbleplot / heatmap

In this tab, users can visualise the gene expression patterns of multiple genes grouped by categorical Spot information (e.g. library / cluster). The normalised expression are averaged, log-transformed and then plotted.

List of gene names
(Max 50 genes, separated by , or ; or newline):

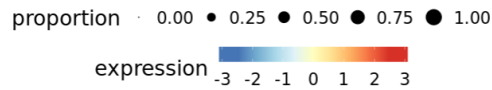
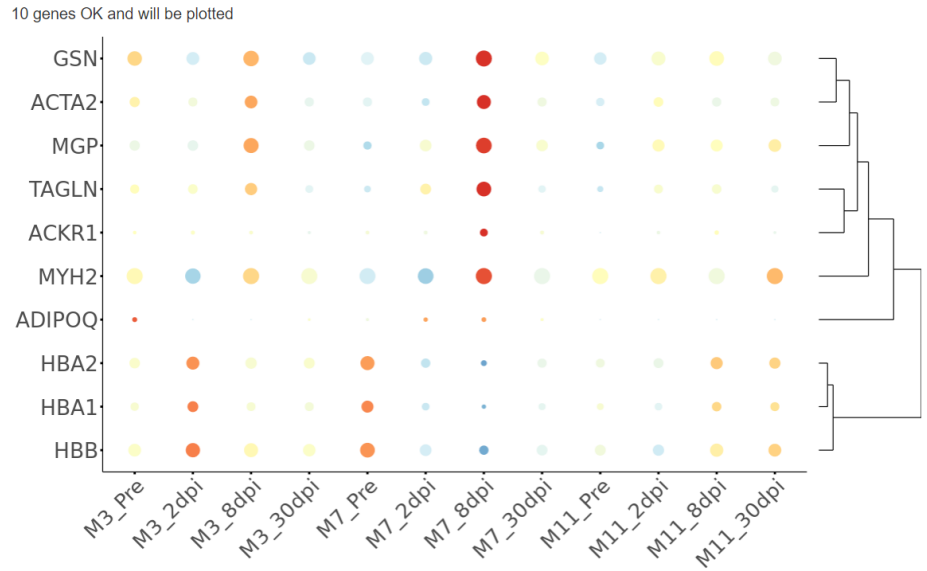
HBA2, HBB, HBA1, MYH2, ACTA2, TAGLN, ADIPOQ, GSN, MGP, ACKR1

Group by:
orig.ident

Plot type:
 Bubbleplot Heatmap
 Scale gene expression
 Cluster rows (genes)
 Cluster columns (samples)

Toggle to subset Spots

Toggle graphics controls



In Geneset Score tab, by typing part of the pathway of interest, a list of pathway will pop up. Once one pathway is selected, the score will be plot as violin plot. The dot could be grouped by selecting from Spot information.

