

Single cell RNASeq viewer (Shiny App)

Introduction

R Shiny based web application to view single cell data analyzed using Seurat

Project List

The app's dashboard lists all the datasets that are available. Select a project from the dropdown menu on the sidebar

The screenshot shows the 'Single Cell RNASeq data' Shiny App interface. On the left, a sidebar contains a 'Project List' section with a dropdown menu set to 'BGC3_Merge'. The main panel, titled 'scRNA Data Sets', displays a table of available datasets. The table has columns for Project Name, Project Description, Organism, and File type. The first row, 'BGC3_Merge', is highlighted in blue. Below the table, it shows 'Showing 1 to 6 of 6 entries' and navigation buttons for 'Previous', '1', and 'Next'.

Project Name	Project Description	Organism	File type
BGC3_Merge	Human Ctrl or IPF fibroblasts and IAT2s differentiated from SBC mutant or corrected patient ESCs are combined in a 3d organoid model and grown for days in different combinations before harvesting for scRNAseq	human	RDS
BGC3_update_hFib_plus_IAT2_organoid_scRNAseq	Human Ctrl or IPF fibroblasts and IAT2s differentiated from SBC mutant or corrected patient ESCs are combined in a 3d organoid model and grown for days in different combinations before harvesting for scRNAseq	human	RDS
FPR_I73T_Mesenchyme	To capture representative proportions of all major parenchymal and immune cell populations, we profiled IER-SftpcI73T/ Ptgfr+/+ and IER-SftpcI73T/ Ptgfr-/- animals with oral TAM and harvested the lungs at 14 and 28 days (n=2 per genotype per time point). Controls (n=4) consisted of one mouse each of uninduced IER-SftpcI73T/ Ptgfr+/+, IER-SftpcI73T/ Ptgfr-/-, SftpcWT/ Ptgfr+/+, and SftpcWT/ Ptgfr-/- genotypes. This is the Mesenchyme and Alveolar Epithelial object.	mouse	RDS
I73T_AlveolarEpithelial	To capture representative proportions of all major parenchymal and immune cell populations, we profiled IER-SftpcI73T/ Ptgfr+/+ and IER-SftpcI73T/ Ptgfr-/- animals with oral TAM and harvested the lungs at 14 and 28 days (n=2 per genotype per time point). Controls (n=4) consisted of one mouse each of uninduced IER-SftpcI73T/ Ptgfr+/+, IER-SftpcI73T/ Ptgfr-/-, SftpcWT/ Ptgfr+/+, and SftpcWT/ Ptgfr-/- genotypes. This is the Mesenchyme and Alveolar Epithelial object.	mouse	RDS
IAT2_ILD_Disease_modeling	UMAPs showing characterization of gene expression in SFTPCId73T/dT (clone 'C11') iPSC-derived alveolar epithelial type 2-like cells (AEC2s or IAT2s) compared to syngeneic, edited SFTPCIdT/dT AEC2s (clone 'B2'). Clustering of day 114 scRNA-seq transcriptomes is shown for each indicated AEC2 population using Uniform Manifold Approximation Projection (UMAP). All live AEC2s, irrespective of SFTPCIdTomato expression at this time point are included.	human	RDS
iPSCderived_humanLung_coCulture	Single cell transcriptomic profiling of iPSC-derived lung mesenchyme and primary adult lung fibroblasts co-cultured with SFTPC-I73T mutant and corrected iPSC-derived alveolar epithelial type 2 cells	human	RDS

Project Summary

Once the project is selected, the project summary tab will give details about the dataset such as project description, organism, number of cells before and after filtering, number of dimensions (principle components) used for clustering, number of cells in each cluster etc.

Note : Some of this information has to be available in the Seurat object for the site to display. If this information is not present in the 'misc' slot of the object, it will not show up

The screenshot shows the 'Single Cell RNASeq data' Shiny App interface with the 'Project Summary' tab selected. The sidebar dropdown is set to 'FPR_I73T_Mesenchyme'. The main panel displays the project details for 'FPR_I73T_Mesenchyme'.

Project Summary

Project name: FPR_I73T_Mesenchyme
Project Description: To capture representative proportions of all major parenchymal and immune cell populations, we profiled IER-SftpcI73T/ Ptgfr+/+ and IER-SftpcI73T/ Ptgfr-/- animals with oral TAM and harvested the lungs at 14 and 28 days (n=2 per genotype per time point). Controls (n=4) consisted of one mouse each of uninduced IER-SftpcI73T/ Ptgfr+/+, IER-SftpcI73T/ Ptgfr-/-, SftpcWT/ Ptgfr+/+, and SftpcWT/ Ptgfr-/- genotypes. This is the Mesenchyme and Alveolar Epithelial object.

Organism: mouse
File type: RDS

Total number of cells before filtration: 114
Total number of cells after filtering: 114
Total number of genes: 114
Dimension: 114
Number of mitochondrial genes filtered: 114

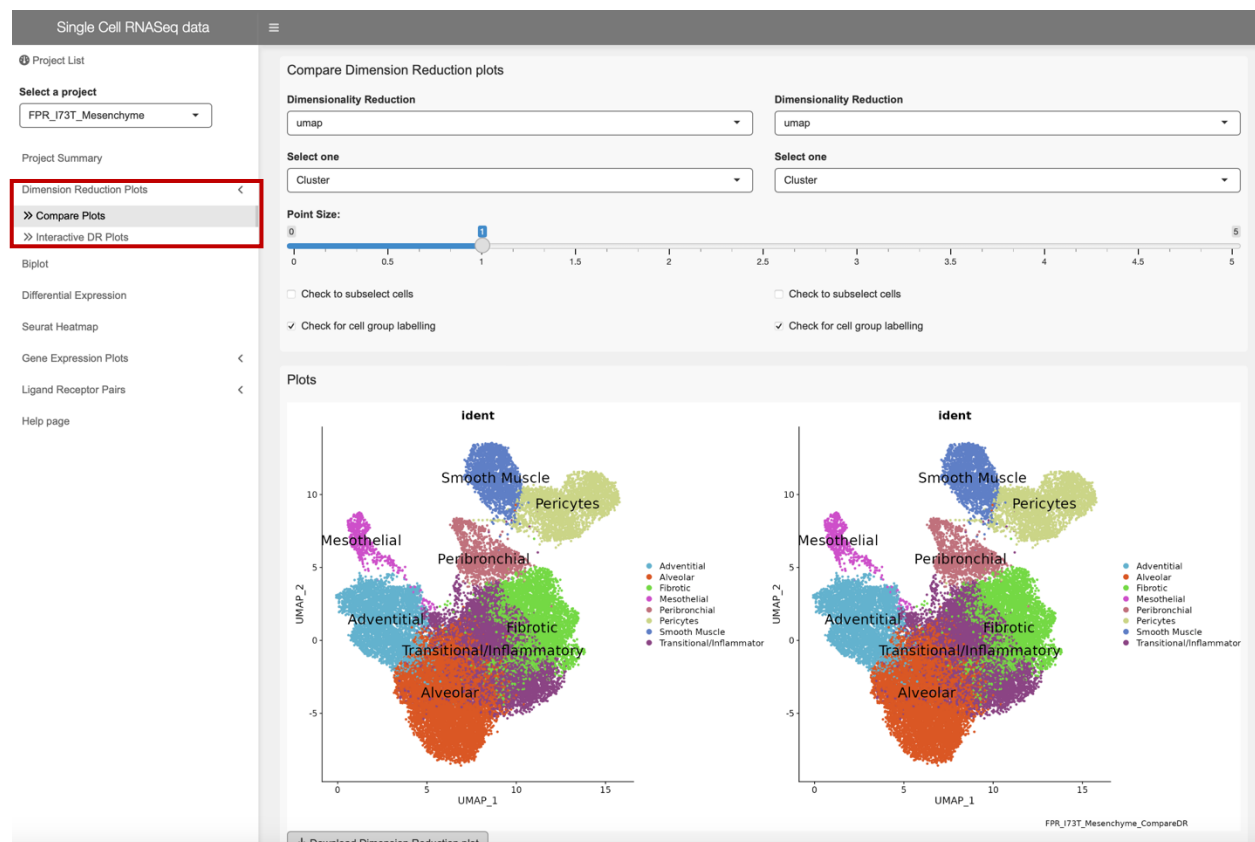
Cluster-wise number of cells:

- Adventitial
- Alveolar
- Fibrotic
- Mesothelial
- Peribronchial
- Pericytes
- Smooth Muscle
- Transitional/Inflammatory

Dimension Reduction Plots

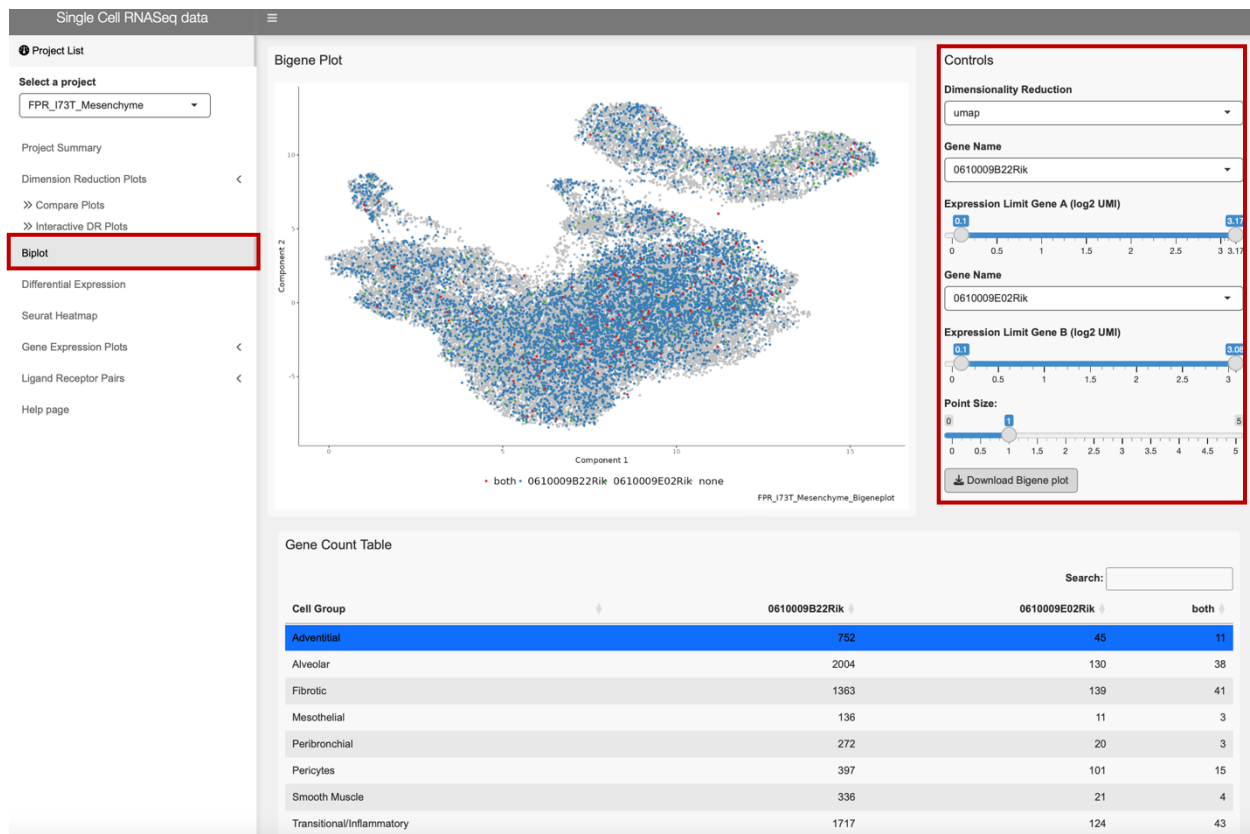
The *Compare plots* subtab under Dimension Reduction plots tab in the sidebar, displays two plots with same options. Users can choose the Dimensionality reduction method (usually either Umap or tsne) as well as pick between categories (all columns in the metadata slot of Seurat object), clusters and gene expression. Selecting gene expression will auto populate a dropdown menu with all genes in the dataset. There are additional options to turn off/on labelling in the plot as well as subselect cells based on clusters or a range of numeric values. The plot can also be downloaded as a pdf.

The *Interactive DR Plot subtab* displays the same as in the *Compare tSNE plots* tab except these plots are interactive. Users can zoom in, subselect and hover over for point information



Bigene plots

The Bigene plot is similar to Seurat's plot with the 'overlap' option. Users specify dimensionality reduction method (tSNE or UMAP), 2 genes and the expression limit of each gene in terms of log₂UMI to view a Bigene plot based on the expression of the two genes. The tab also shows a table with the number of cells in each cell group expressing the first gene, the second gene and both genes.



Differential Expression

The differential expression tab generates a table of marker genes specific to a cell group as well as plots showing the expression of each of those marker genes in each cell group as a feature plot, violin plot and a ridge plot. By default, the results displayed are each cell group against every other cell group. User can, however, find marker genes by checking the *Check to choose a different category to compare* option and selecting one cell group that can be compared against one or multiple other groups.

Below the plot is a table, that is the result of FindMarkers function in Seurat. It gives a list of all marker genes, the percentage of that particular gene's expression in the first cell group of comparison and the second group of comparison. For example, if you were finding markers specifically between Adventitial fibroblast and Alveolar fibroblasts, percentage 1 would be the percentage of Adventitial fibroblasts expressing that gene and percentage 2

would be percentage of Alveolar fibroblasts expressing that gene. The table also gives adjusted p.value and fold change associated with the comparison as well as each gene’s link to gene cards.



Marker genes

Search:

	p_val	avg_log2FC	Percentage expressed in Cell Group 1	Percentage expressed in Cell Group 2	p_val_adj	cluster	gene	Link
Dcn	0	1.387482754655812	0.948	0.405	0	Adventitial	Dcn	Dcn
Pi16	0	1.221699984432227	0.595	0.018	0	Adventitial	Pi16	Pi16
Ly6a	0	1.049767610784274	0.727	0.203	0	Adventitial	Ly6a	Ly6a
Serpinf1	0	1.044267289487636	0.791	0.234	0	Adventitial	Serpinf1	Serpinf1
Col14a1	0	0.9765999776937959	0.824	0.305	0	Adventitial	Col14a1	Col14a1
Clec3b	0	0.9620122501569571	0.891	0.434	0	Adventitial	Clec3b	Clec3b
Igfbp6	0	0.8795957857260938	0.871	0.459	0	Adventitial	Igfbp6	Igfbp6
Cygb	0	0.833851789748545	0.903	0.524	0	Adventitial	Cygb	Cygb
Rbp4	0	0.832074091802043	0.581	0.145	0	Adventitial	Rbp4	Rbp4
Fbln2	0	0.8201334811927368	0.624	0.169	0	Adventitial	Fbln2	Fbln2

Showing 1 to 10 of 159 entries

Previous 1 2 3 4 5 ... 16 Next

Seurat Heatmap

The Heatmap tab in the sidepanel generates heatmaps. Users can choose different options for the genelist that goes into generating the heatmap. These options can be selected from dropdown menu between

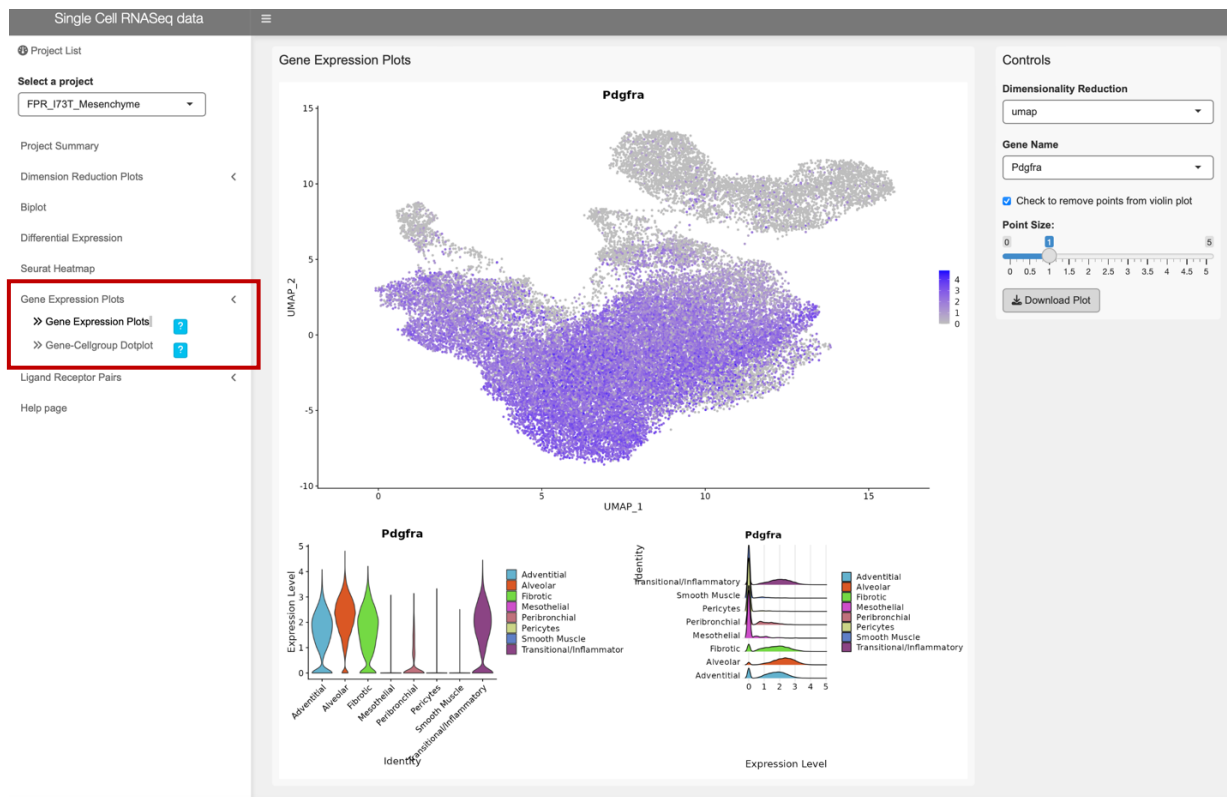
- Differentially expressed genes – users can also choose specific clusters
- Top genes across all clusters – users can also pick number of top genes per cluster
- Transcription factors
- Ligands
- Receptors

The control panel also provides other options like selecting the grouping variable and a download option.

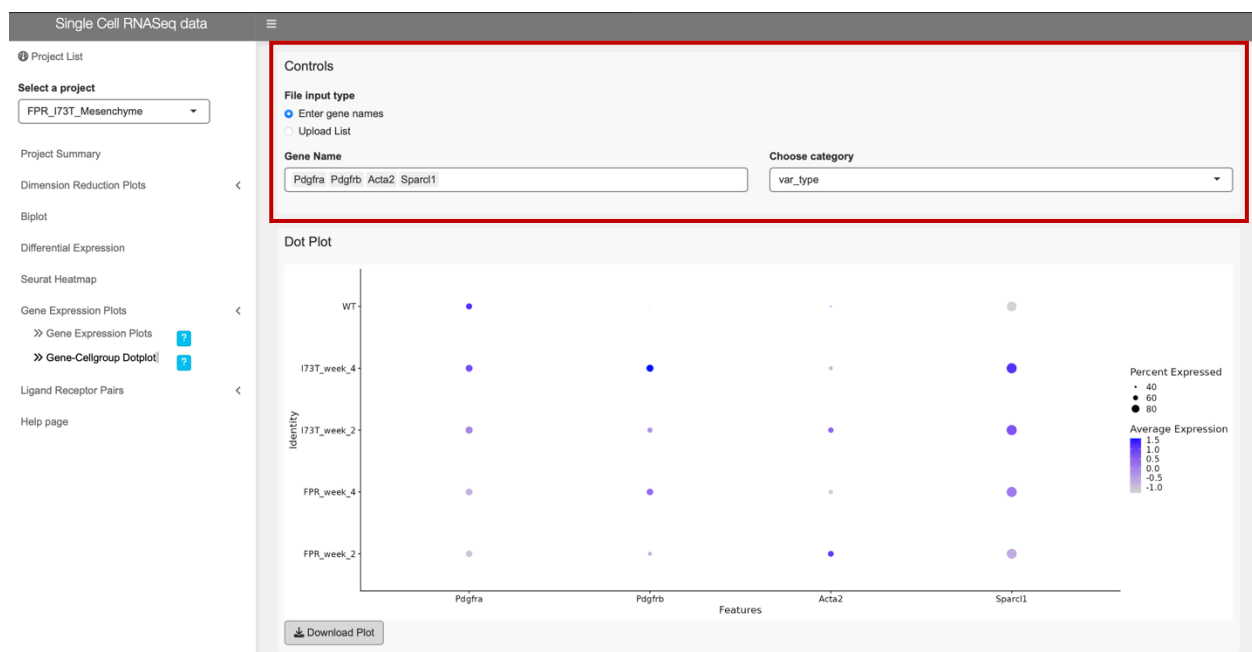


Gene Expression plots

The Gene Expression plots tab displays the same expression, violin and ridge plots as in the Differential Expression tab. However, instead of having to select from a table, in this tab, users can manually specify the gene name they are interested in.



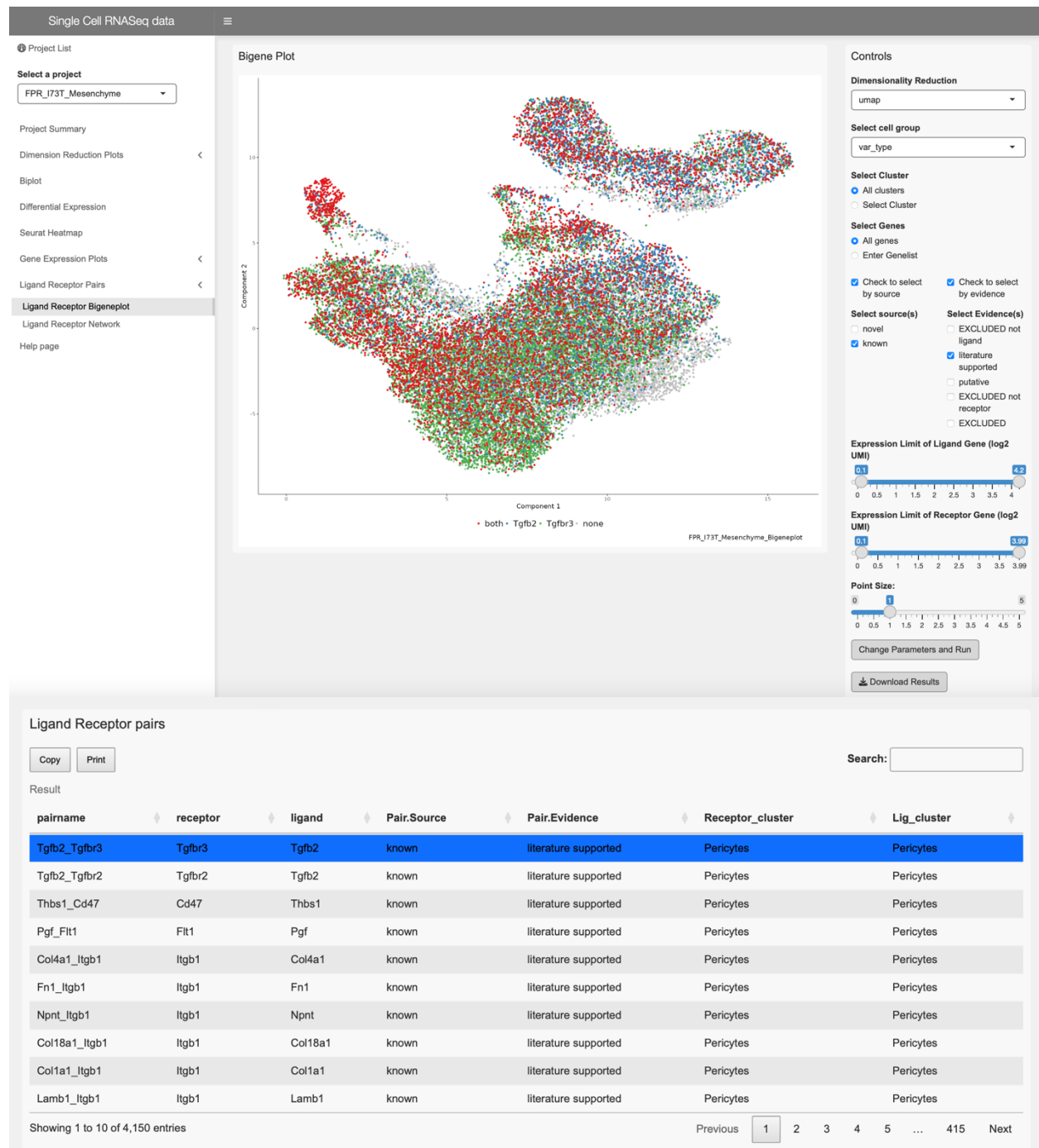
The Gene-Cellgroup Dotplot tab displays a dotplot like the one shown below where the genes are rows, cell-groups are the columns and the size of the dots show percentage of cells expressing that gene. Users can either enter select gene names from the dropdown options or upload text files with one gene per line



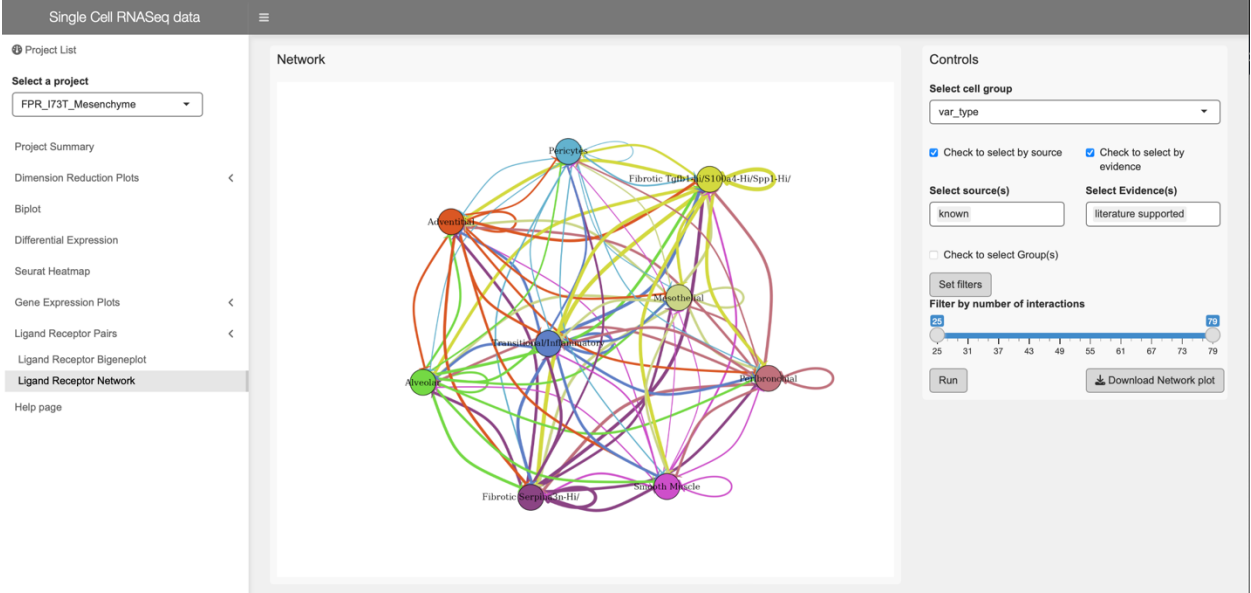
T

Ligand Receptor interactions

The Ligand Receptor Pairs tab in the side panel generates a table of all possible ligand receptor pairs (from FANTOM5) between each of the cell groups. Expression of each receptor/ligand gene per cell group is counted if it is expressed in at least 20% of the cells (by default. Users can change this and go up to 100%). This tab also displays a bigene plot for each of the ligand-receptor pair in the table



The Ligand Receptor Network tab displays a network where each cell group is a node and the edges denote the frequency of ligand-receptor pairs between the nodes. This tab also performs GO analysis on the selected pairs and displays the results in a table.



GO Analysis

Select Receptor Group for GO Analysis

Adventitial

Select Ligand Group for GO Analysis

Mesothelial

GO Terms

Copy

Print

Search:

go_id	name_1006	definition_1006
GO:0005576	extracellular region	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
GO:0008083	growth factor activity	The function that stimulates a cell to grow or proliferate. Most growth factors have other actions besides the induction of cell growth or proliferation.
GO:0005615	extracellular space	That part of a multicellular organism outside the cells proper, usually taken to be outside the plasma membranes, and occupied by fluid.
GO:0005160	transforming growth factor beta receptor binding	Binding to a transforming growth factor beta receptor.
GO:0048731	system development	The process whose specific outcome is the progression of an organismal system over time, from its formation to the mature structure. A system is a regularly interacting or interdependent group of organs or tissues that work together to carry out a given biological process.
GO:0009887	animal organ morphogenesis	Morphogenesis of an animal organ. An organ is defined as a tissue or set of tissues that work together to perform a specific function or functions. Morphogenesis is the process in which anatomical structures are generated and organized. Organs are commonly observed as visibly distinct structures, but may also exist as loosely associated clusters of cells that work together to perform a specific function or functions.
GO:0035295	tube development	The process whose specific outcome is the progression of a tube over time, from its initial formation to a mature structure. Epithelial and endothelial tubes transport gases, liquids and cells from one site to another and form the basic structure of many organs and tissues including lung and trachea, kidney, the mammary gland, the vascular system and the gastrointestinal and urinary-genital tracts.
GO:0051781	positive regulation of cell division	Any process that activates or increases the frequency, rate or extent of cell division.
GO:0045893	positive regulation of DNA-templated transcription	Any process that activates or increases the frequency, rate or extent of cellular DNA-templated transcription.
GO:0010718	positive regulation of epithelial to mesenchymal transition	Any process that increases the rate, frequency, or extent of epithelial to mesenchymal transition. Epithelial to mesenchymal transition is where an epithelial cell loses apical/basolateral polarity, severs intercellular adhesive junctions, degrades basement membrane components and becomes a migratory mesenchymal cell.

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