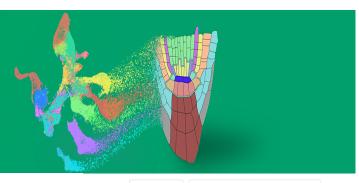


Integrated Plant Single- Cell Database

iPscDB is a single-cell transcriptomics data resource that provides a comprehensive and relatively accurate atlas of cell integration for different tissues of different plants.



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Overview

Welcome to iPscDB

iPscDB is a single cell transcriptomic data resource that includes cell markers, single cell maps, and a wealth of data analysis tools. At present, data from 23 species of model plants, including Arabidopsis thaliana, rice, corn, tomato, and tobacco, including more than 270,480 marker genes and more than 3 million single cell data, have been collected, providing comprehensive and relatively accurate cell markers and cell maps for cell integration and single cell research in different plants and tissues

Datasets and usage

iPscDB mainly provides five modules:

Browser - Including meta information, sample QC, sample intergration, and download options for both .rds file formats for our datasets.

Atlas - Including 23 species atlases and 33 tissue atlases, each of which can be viewed and downloaded, and contains a variety of displays.

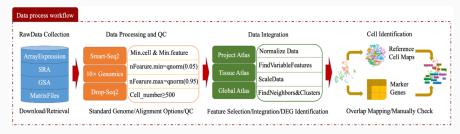
Marker - Including general and classic two types of markers, and the data can be found in the summary and details marker tables

Search - Three search methods, include marker gene search, cell type search and sequence search using Blast.

Tools - Including seven tools: Cross-species cell annotation, Cell-Cell interactions, Developmental trajectory, eSCP, Plant CelliD, Plant Cell-Blast, and Plant CtAmr.

A.Datasets

PscDB downloaded SRA data from databases such as NCBI, ENI and GSA for 691 experiments in 41 projects, covering 23 plant species (including model plants such as Arabidopsis, rice, maize, soybean, tomato and tobacco), and we aligned the original data with reference genomes. At the same time, two different types of cell markers were collected: experimentally validated marker genes, and differentially expressed genes of specific cells identified by scRNA-seq. In order to ensure the unity of tissue and cell types, we normalized tissue and cell type names into standard bibliographies based on the Plant Ontology database.



B.Usage

The home page provides a global view of 23 plant tissue maps, and by clicking on hyperlinks embedded in web images, you can quickly explore the cell maps of entire plants and tissues. The tissue chart of different plants can be switched by clicking on the picture in the upper right corner. The Tissue chart makes it easy to quickly browse the map of listed cell types, and a detailed interface for painting the map can be accessed by clicking the tissue icon.

4534

4405

36

26

16

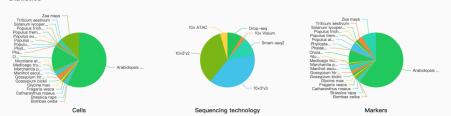


Browser

In this module, iPscDB provides all data statistics, details of each data set, and data integration operations. The data statistics show the number of species, data sets, cell maps, number of genes, number of cell markers and so on.



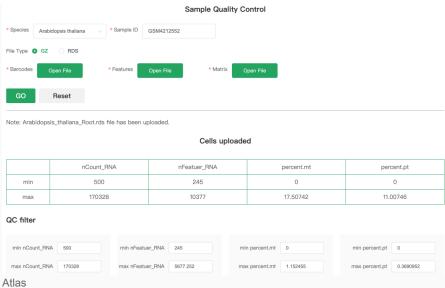
Statistics



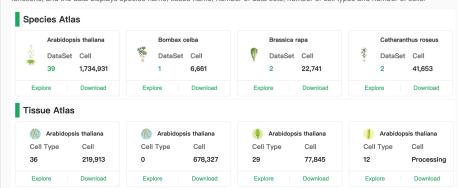
In addition, meta information is provided for each data set, Information includes dataset, BioProject, Species, Tissue, Treatment, Genotype, Libraries, AGE, Samples, Cells and Publication, Users can use browser buttons or download datasets.

=	Species	Tissue	BioProject	Dataset \$	Condition	Genotype	Libraries		Explore
	Arabidopsis thaliana	Root tip	PRJNA640389	SRP267870	•	•	10x Genomics	5 days	Download
	Arabidopsis thaliana	Root tip	PRJNA594539	SRP235541	•	•	10x Genomics	6 days	Download
	Arabidopsis thaliana	Root tip	PRJNA507252	SRP171040	•	•	10x Genomics	5 d ger	Download
	Arabidopsis thaliana	Root tip	PRJNA517021	SRP182008	•	•	10x Genomics	10 days	Download
	Arabidopsis thaliana	Whole root	PRJNA497883	SRP166333	•	•	10x Genomics	7 days	Download

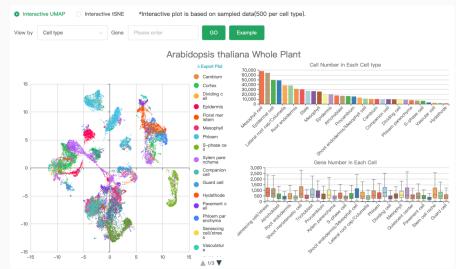
Finally, we provide online Sample quality control and data integration analysis. After selecting the above data set, click the Sample QC button, you can enter the cell quality control interface, submit relevant parameters for operation, and download the rds file after quality control.



In this module, we provide two types of Atlas: Species atlas and Tissue atlas. The interface provides browsing and downloading functions, and the data displays species name, tissue name, number of data sets, number of cell types and number of cells.

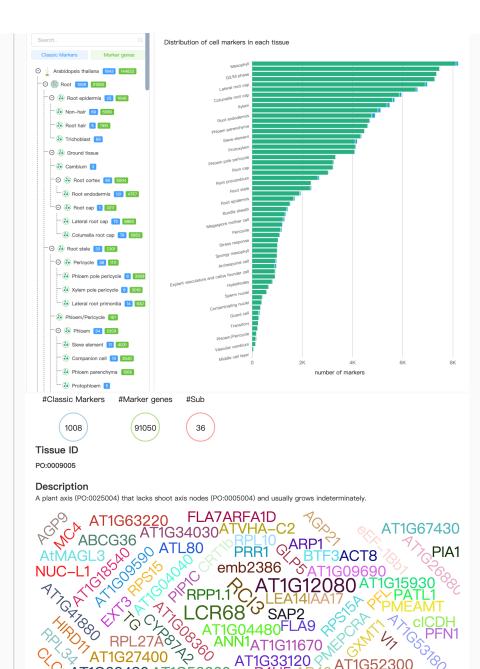


In the explore interface, the gene retrieval function could be found in the upper part, the Umap infographic of Atlas, a variety of information was displayed diagrams, and the cell markers and sample tables were displayed below.



Marker

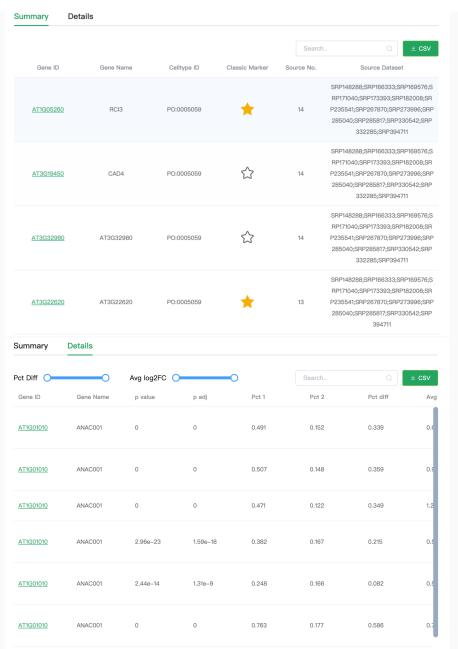
Here, iPscDB offers an informative module that provides marker gene information for each cell type across various species. Users can easily select a cell type using either the Bar chart or the Tree list. In the specific cell type panel, scPlantDB offers informative visualizations in the form of word clouds that display the number of source datasets for each marker gene. Additionally, users can access meta-information about the cell type, including the number of plant species and tissues that share this cell type.



In the tables of marker genes, the times of the gene are displayed, which has been reported in a certain cell type, and whether the gene has been validated experimentally. If it is a classic gene, its pentagram will light up. At the same time, in the details table, the P-value and fold-change value of each marker gene are displayed.

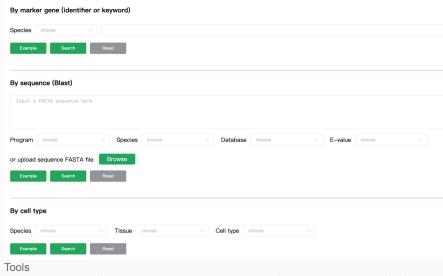
C> AT1G27400 72 0 AT1G33120 AT1G52300 PAH5 APAN AT1G52300

AT1G27400 72

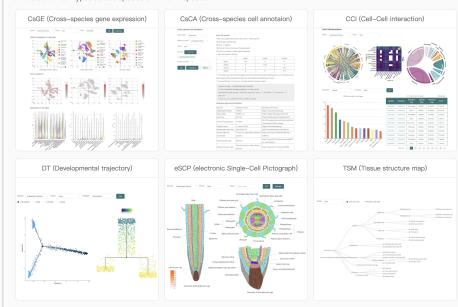


Search

Users can easily access the search panel in iPscDB by simply clicking on the search icon in the navigation bar. The search panel offers two efficient methods to help users quickly find the desired information: marker/cell type name searching and sequence searching. The marker/cell type name search allows users to enter keywords related to the cell type or marker they are looking for, including both exact matches and partial matches of markers description. On the other hand, the sequence search mainly relies on BLAST algorithm, allowing users to input a nucleotide or amino acid sequence and compare it against sequences of species in the database. Both searching methods offer convenient and precise results to meet users' various research needs.



iPscDB provides a wealth of online single-cell data analysis capabilities, includes Cross-species gene expression, Cell-Cell interaction, Developmental trajectory analysis, electronic Single-Cell Pictograph, Plant Cell iDentification, Plant Cell Blast and Plant cell type annotation with multiple references tools, users can choose the appropriate tools according to the needs of data analysis for analysis. Among these 7 tools, we provide 3 cell type annotation and classification analysis tools, enabling accurate and rapid annotation of cell types across species and within species.



Contact us

Comments and suggestions are welcomed

If you meet any troubles or find any bugs when you visit iPscDB, please email to penglu2004@hotmail.com, peijiancao@163.com Address: No.2 Fengyang Street, High-Tech Zone, Zhengzhou, P. R, 450001

Submit data

Welcome to submit single-cell data to the iPscDB

If you have a group of single-cell data in plants and would like to submit them to iPscDB.Please email your expression matrix data to penglu2004@hotmail.com, peijiancao@163.com with the following format:

- 1.RDS file
- 2. Barcodes, Features, and Matrix files
- 3.H5 file
- 4.Reference genome version

Sinale-cell data will be uploaded after manuscript acceptance. All submissions will be really appreciated!