INTEGRATIVE WEB INTERFACE FOR THE VISUALIZATION OF COMPLEX PLANARIAN RNA-SEQ DATASETS
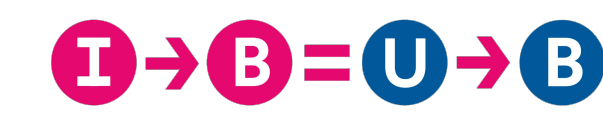
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ABSTRACT

Over the last decade, a huge amount of transcriptomic and genomic data for the planaria *Schmidtea mediterranea* has been generated, thanks to its new genome assembly and especially to the advent of single-cell RNA-seq technologies. Developing interfaces for dealing with such data is of crucial interest to the research community.

In order to bridge the gap between transcriptomic, genomic, and interactomic data we have developed PlanExp, a web-application to explore and visualize expression data from several experiments. PlanExp integrates tools for creating multiple interactive plots, tables, and visualizations; incorporating functional annotations performed both at the transcript and the genome level. Additionally, a prediction of gene regulatory networks has been performed in order to aid researchers to understand the complex planarian biology, and these predictions have been incorporated in the application, together with a full network editor and expression mapper powered by cytoscape.js.

PlanExp is available at: compgen.bio.ub.edu/PlanNET/planexp

Scan this QR code to download the **Full Article**
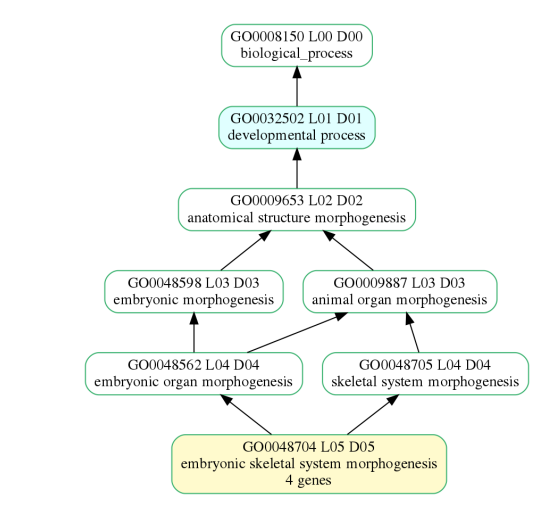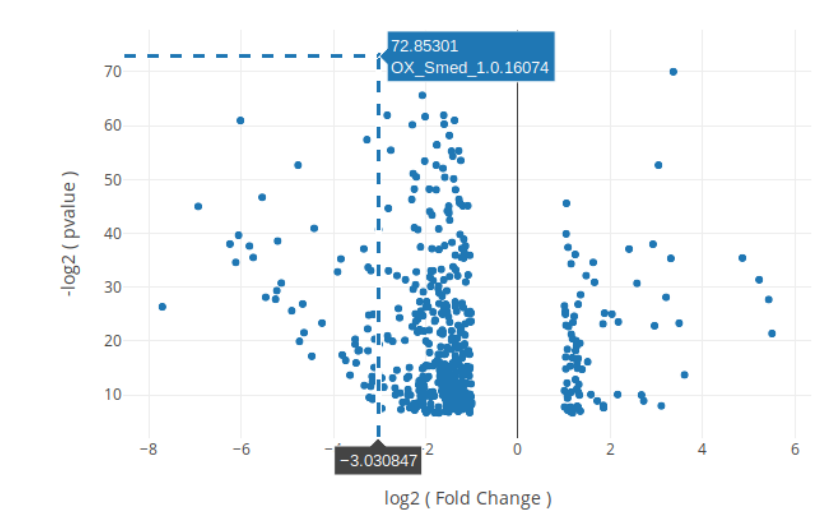
GENE EXPRESSION

PlanExp allows users to investigate gene expression changes across conditions thanks to the inclusion of several visualization options, such as differential gene expression tables, heatmaps, violin plots, and line-charts.
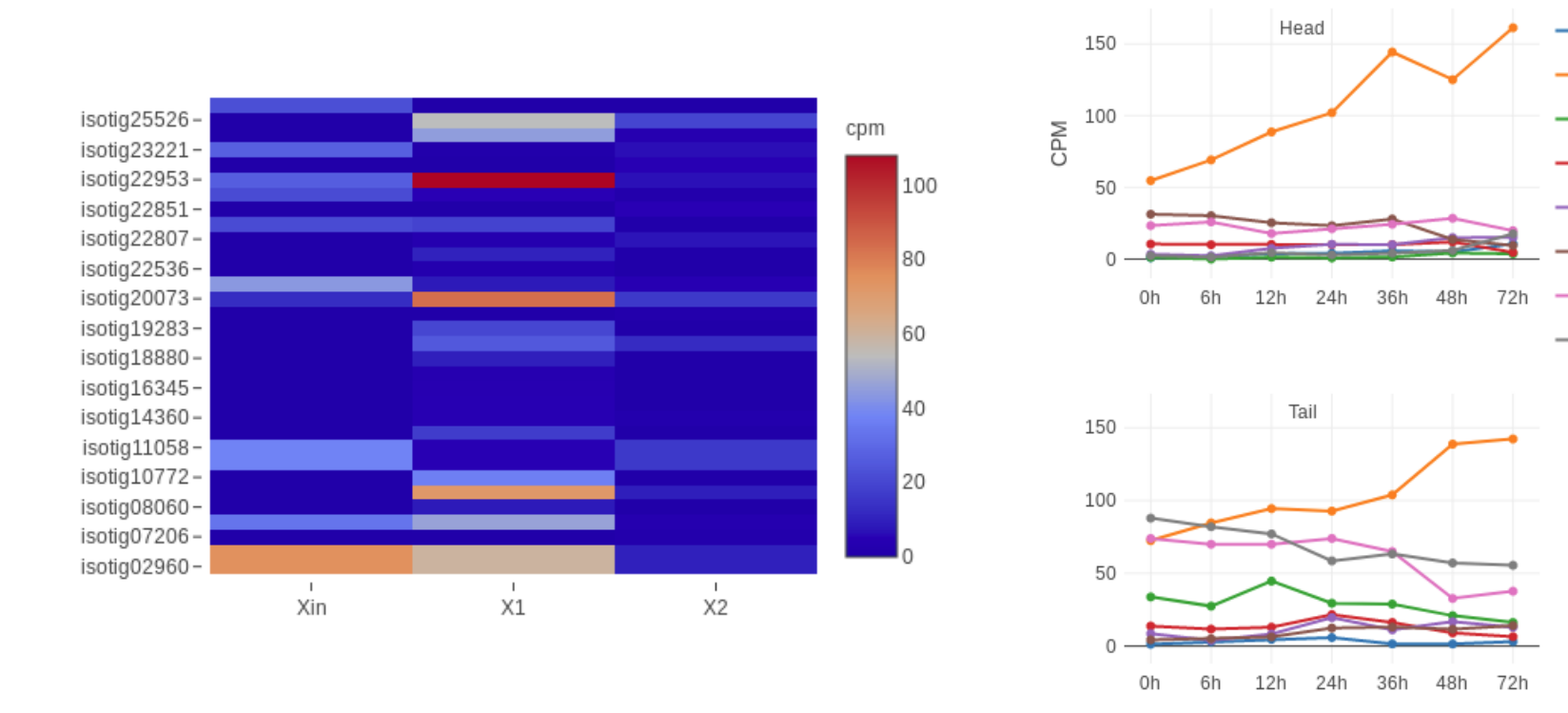
All plots are interactive, and users can display additional information on hover and show/hide genes and conditions thanks to Plotly.js.

- Diferential Gene Expression
- GO Enrichment analysis
- Interactive Plots

SINGLE CELL RNA-SEQ

Two single-cell RNA-seq experiments have been included in PlanExp, and the application has a variety of plot types and tools made specifically for the exploration of such data.

Cell type expression patterns can be plotted and studied in detail thanks to the interactive nature of all the visualizations in PlanExp.

Additionally, PlanExp provides tools to uncover genes that are co-expressed in multiple cells.

Cell type expression

Gene co-expression
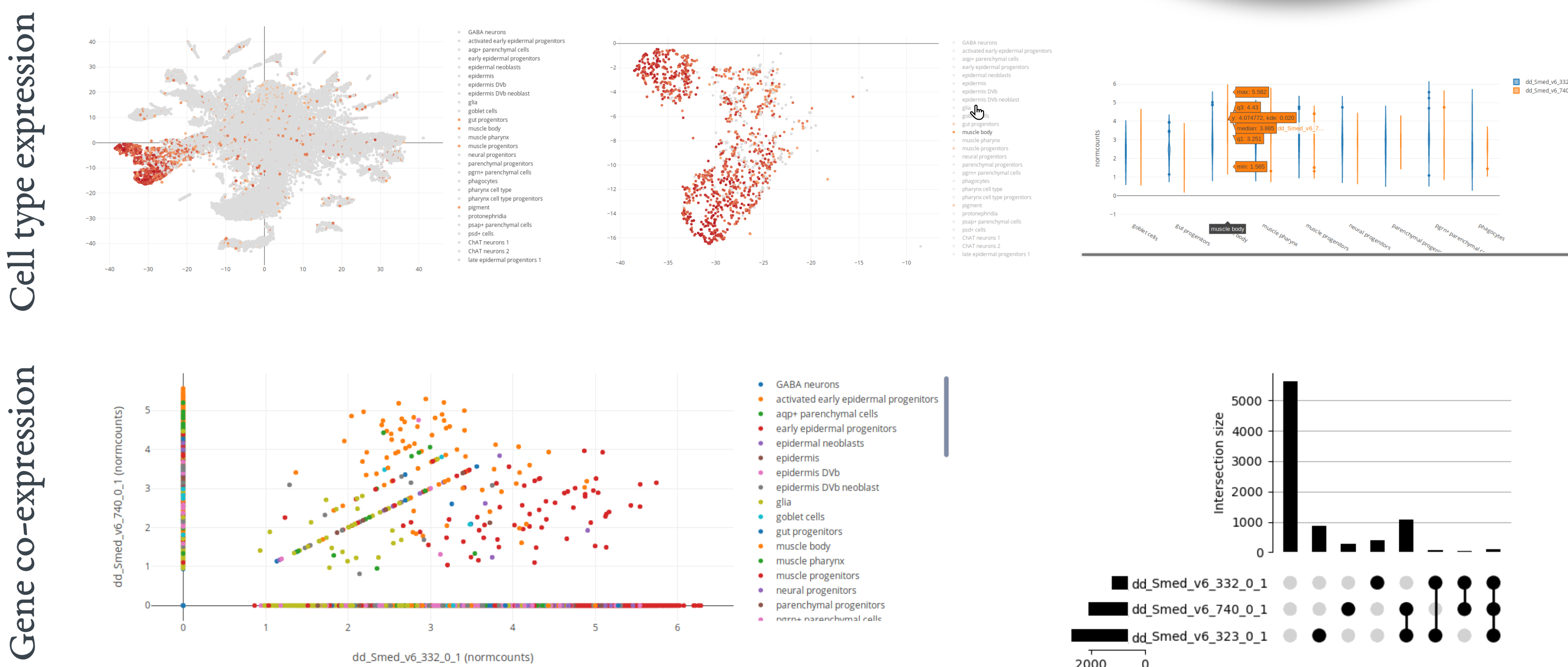
OMICS INTEGRATION

The integration with the database PlanNET facilitates the search of genes using a variety of identifiers, such as gene symbols, PFAM domain names, transcript IDs, human homologs, etc. independently of the selected experiment.

Clicking on any gene name or transcript ID in the plots or tables of PlanExp will show an information card summarizing the data available for that gene, such as homology information, genomic context, predicted protein-protein interactions, and inferred *cis* regulatory elements from ATAC-seq and ChIP-seq data.

PlanNET · SCHMIDTEA MEDITERRANEA NETWORK DATABASE
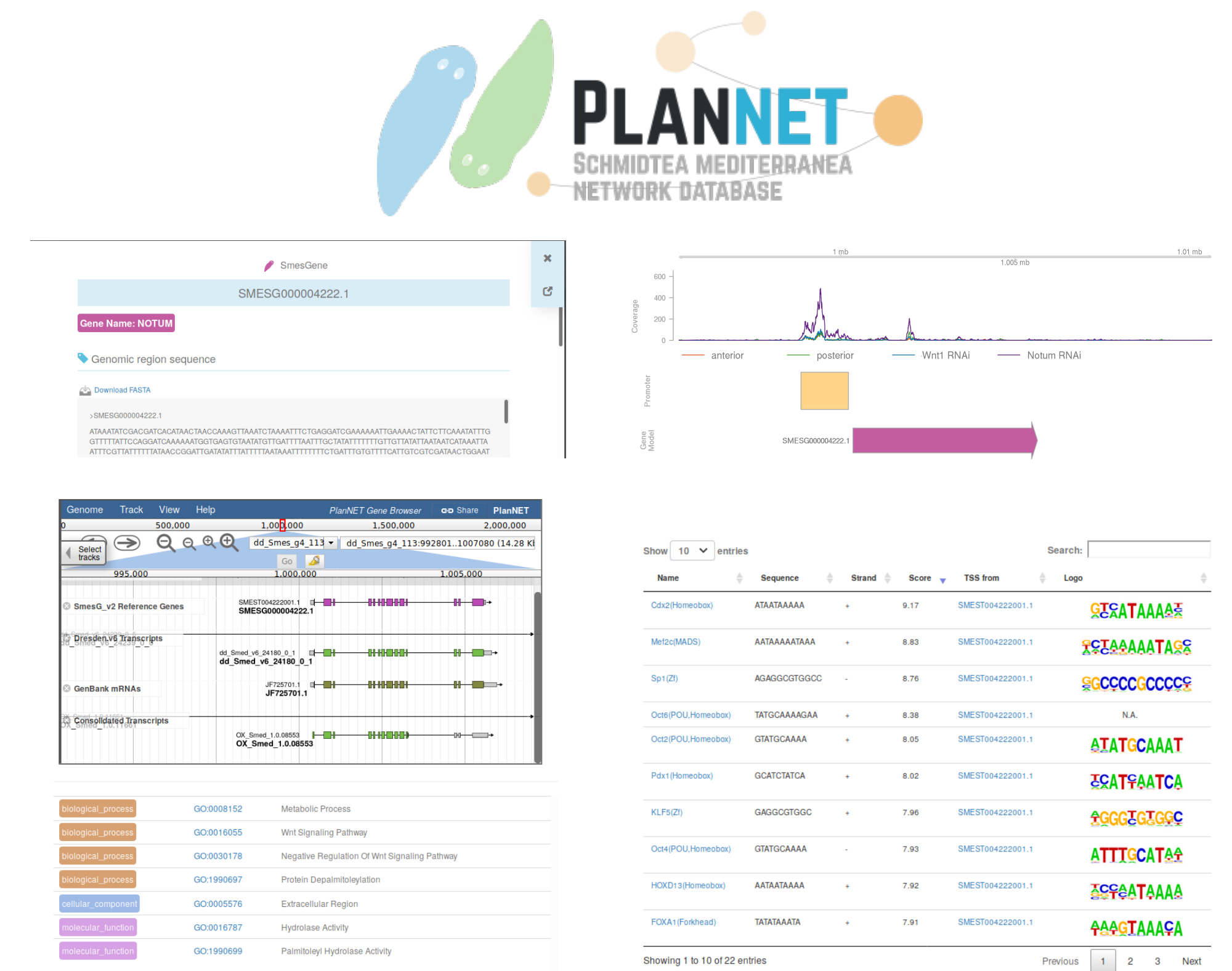
GENE REGULATORY NETWORK PREDICTION

A prediction of gene regulatory interactions has been performed by using GRNBoost from the SCENIC pipeline. These predictions were made over the two available single-cell RNA-seq experiments in PlanExp. They have been annotated with human REACTOME pathway identifiers, and compared to annotate those interactions common in both predictions.

Several known regulatory links have been retrieved, such as 23 interactions that may play a role in the regeneration of the planarian nervous system, as well as interactions involved in the protonephridia regeneration.

PlanExp offers multiple ways to explore the interactions, including a tool to map expression data onto the networks, as well as editing them to incorporate known regulatory links or external predictions.

- Searchable Tables
- Network editor
- Network Expression Mapper

Export Options:

Powered by: django · MySQL · neo4j · plotly · Cytoscape.js · JBrowse