



PULSE CROP DATABASE

Genomic, Genetic, and Breeding Resources
for Pulse Crop Improvement

Issue 9 | October 2023

What's new in PCD?

Outreach

- [How to go from a trait to a GWAS to a gene and to an ortholog](#) (2:52 mins)
- [How to use the Expression Heatmap Tool](#) (2:23 mins)

Upcoming Workshops

- BIC & NAPIA Breeding Tools Workshop featuring [Breeding Information Management System](#), Nov. 5, 2-5 PM
- [NRSP10 Database Workshop at PAG](#) featuring Pulse Crop Database, Jan. 14, 1:30-3:40 PM

Tool Improvements

- Expression Heatmap Tool added to view RNA-seq expression datasets, data also displayed on gene/mRNA pages

New Data

- 12,457 genetic markers, 7 genetic maps, 82 QTL, and 187 GWAS added in last quarter
- 5 expression datasets (chickpea, pea, lentil, bean)
- Differentially methylated region track in mung bean genome JBrowse

Viewing Expression Data

You can now explore gene or mRNA expression levels on PCD using the Expression Heatmap Tool. This tool displays expression levels of genes or mRNA from published manuscripts. Access the tool via the "Expression Heatmap" link in the Tools menu. You then are taken to an overview page with a few different sections. First note the table

of Expression Datasets that are available with links to more information about the study and the genome the data is aligned to. You can create the heatmap by adding gene/mRNA names to the text box or by selecting the organism and then selecting features from the box or searching for a gene/mRNA name. Then click "Display Expression Heatmap" (also see video linked above).

The screenshot shows the 'Expression Feature Explorer' tool. Annotations include:

- Choose organism and select from list that populates below:** Points to the 'Organism' dropdown menu.
- Enter gene or mRNA names here:** Points to the 'Enter feature unique names' text box.
- Links to dataset and genome details:** Points to the 'Expression Datasets' table.

The 'Expression Datasets' table is as follows:

Expression Analysis	Aligned to
Expression: Chickpea drought stress response	Cicer arietinum CDC Frontier genome v1.0
Expression: Chickpea heat stress response	Cicer arietinum CDC Frontier genome v1.0
Expression: Lentil seed development	Lens culinaris CDC Redberry genome v2.0

Heatmap and Gene/mRNA and Biosample Pages

There are links to details about the gene/mRNA and the sequenced samples along the axes of the heatmap. You can also adjust what is displayed on the heatmap and download the data.

Feature Expression Heatmap

Select an analysis to display

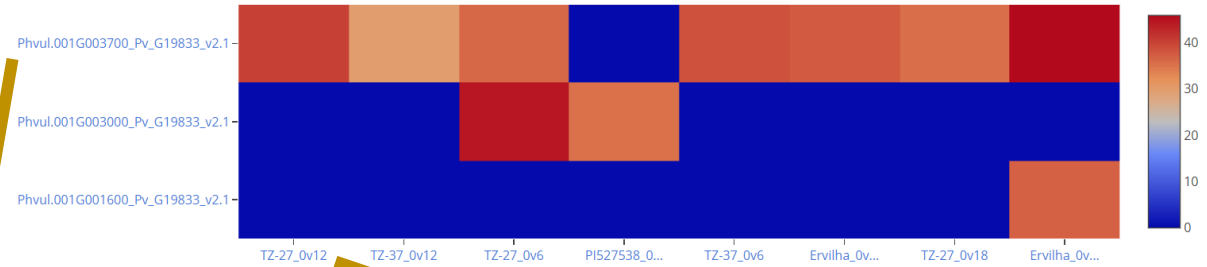
Expression: Soaked dry beans gene expression profiling

Select a property to sort

biomaterial_accession

Adjust how the data is displayed

Expression: Soaked dry beans gene expression profiling Expression



Biosample Overview

Name	TZ-27_0v12
Organism	Phaseolus vulgaris (Common bean)
Analysis	Expression: Soaked dry beans gene expression profiling
Collection Date	2018-09
Location	USA
Tissue	mature seed
Description	This biomaterial: TZ-27_0v12, was created for the analysis: profiling
Biomaterial accession	SAMN30135913
Sample name	TZ-27_0v12
Cultivar	TZ-27
Isolation source	MSU Montcalm Research Center
Treatment	12 hours of soaking in distilled water
Biosample accession	SAMN30135913
Sra accession	SRS14447941
Biomaterial provider	Dr. Karen Cichy (USDA-ARS)
Phenotype	Slow cooking brown bean
Population	Andean
Sample type	Whole seed
Specimen voucher	ADP0027

Expression

Available Analyses

- Expression: Soaked dry beans gene expression profiling

Select an Expression Analysis

Expression: Soaked dry beans gene expression profiling

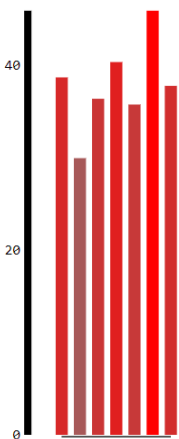
Select a property to group and sort biological samples | biomaterial_accession

Select a property to color biological samples | Expression value

Hover the mouse over a column in the graph to view more information about that biological samples along the x-axis. You can also click and drag to move the legend.

Only Non-Zero Values | Reset

Expression by



Expression Details pane on gene or mRNA details page

Details about samples that were sequenced

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