



InterMine is a powerful open source data warehouse system, created specifically for integrating and analyzing complex biological data. Benefiting from over a decade of data warehousing experience and input from a wide range of research collaborators, InterMine is still in active development. InterMine features include:

- Sophisticated data integration facilities
- Fast, flexible querying
- User-friendly web interface and analysis tools
- Extensive set of APIs and web tools
- Highly developed and extensible system

LegFed InterMines



JCVI and NCGR have been developing mines for LegFed:

MedicMine *Medicago truncatula* (developed along with ThaleMine)

BeanMine *Phaseolus vulgaris*, from LIS chado

SoyMine *Glycine max*, from SoyBase+

PeanutMine *Arachis duranensis* + *Arachis ipaensis*, from PeanutBase+

LegumeMine combines above

CowpeaMine soon: with genetics from UC-Riverside

These mines are all cross-linked via the “friendly mine” interface.

MedicMine enhancements 1



MedicMine *Medicago truncatula* genome database
Updated on Sep-16-2016 (v1.2.0, [Mt4.0v2](#) Release 08/2014)

help | about | software

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Search:

Gene : **Medtr2g036650** *M. truncatula*

DB Identifier	Medtr2g036650	Secondary Identifier	MTR_2g036650
Brief Description	plasma membrane H -ATPase	Probeset Identifier	Mtr.44243.1.S1_at

[SHARE](#)

MedicMine hosts the latest Mt4.0 genome and Mt4.0v2 annotation along with supporting datasets from NCBI, UniProt, GO Consortium, InterPro and KEGG.

Genome feature

Region:	gene	Length:	7998 FASTA...
Location:	chr2:15863690-15871687		

1 Organism

Genomics

Gene models - **Medtr2g036650** **Medtr2g036650**

Gene models

[Transcripts](#): 1 [Exons](#): 17 [Introns](#): 16 [CDSs](#): 1

Genome Browser

Center on **Medtr2g036650** [Full-screen view](#)

15,865,000 15,867,500 15,870,000 15,872,500

Gene

Lists

This Gene isn't in any lists. Upload a list.

Links to other Mines

BeanMine

P. vulgaris

- [Phvul.009G239000](#)
- [Phvul.001G058900](#)
- [Phvul.009G208000](#)
- [Phvul.005G180700](#)
- [Phvul.010G159400](#)
- [Phvul.003G159200](#)
- [Phvul.009G100900](#)
- [Phvul.003G143800](#)

SoyMine

G. max

- [Glyma.15G004300](#)
- [Glyma.06G076100](#)

MedicMine enhancements 2



LIS Gene Families

Data Source: [LegumeMine](#)

Manage Columns

Manage Filters

Manage Relationships

Generate Python code

Export

MedicMine uses LegumeMine web services to acquire gene family info and orthologs without hosting the data locally.

Showing rows 1 to 1 of 1

Gene Family Name	Gene Family Description	Genes DB identifier
phytozome_10_2.59279443	plasma membrane H ⁺ -ATPase IPR001757 (Cation-transporting P-type ATPase), IPR023214 (HAD-like domain), IPR023298 (P-type ATPase, transmembrane domain) GO:0000166 (nucleotide binding), GO:0006200 (ATP ...	74 Gene DB identifiers

NCGR mine enhancements



- Chado data importers (for LIS data)
- **Genetic** data extensions (markers, QTLs, genetic maps, etc.)
- Genetic data visualization (linkage group diagrams, genotyping)
- Shared motif search (e.g. upstream gene flanking regions)
- Expression heat maps

Note: core InterMine does not contain genetic data.

Heat maps have K-means clustering



Date Created: 2016-10-24 13:37

PvGEA: *Phaseolus vulgaris* Gene Expression Atlas

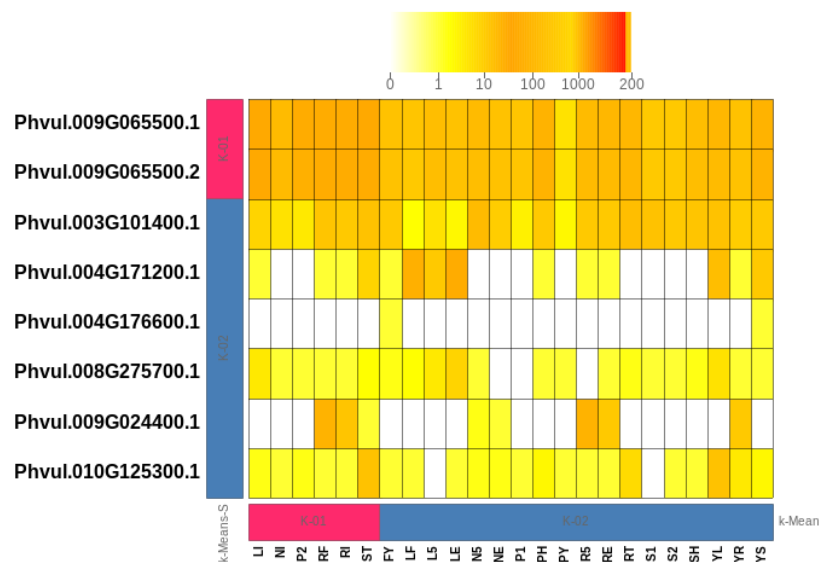
[View article on PubMed](#)

Heatmap visualization powered by [canvasXpress](#). Grab the edges with your mouse to resize the map. Zoom in/out on an area with your scroll wheel.

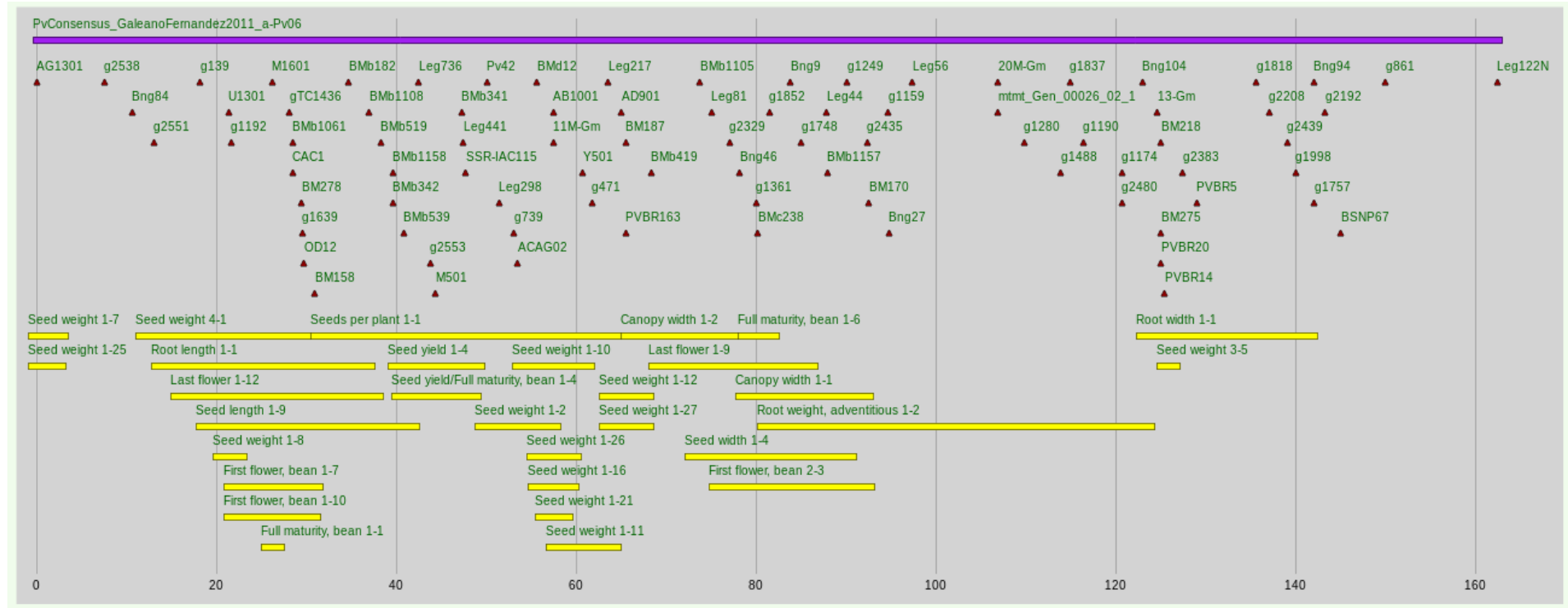
[Click to see/hide the expression map](#)

Expression K-means: 2 Tissue K-means: 2

mRNA RNA-seq expression (RPKM) : 8 transcripts



[More information](#)



Leaf morphology in Cowpea [*Vigna unguiculata* (L.) Walp]: QTL analysis, physical mapping and identifying a candidate gene using synteny with model legume species.

Select a specific QTL or search on trait text

Trait text search

Reset

Show 25 lines

2 18633 on iSelect-consensus-2016 1 at 1.41 cM

IG Marker	1 0.00 2.30247	1 0.00 2.52445	1 1.41 2.18633	1 2.02 2.27318	1 2.19 1.1275	1 2.19 2.07033	1 2.19 2.17899	1 2.19 2.17900	1 2.19 2.27319	1 2.19 2.27320	1 2.19 2.29068	1 2.19 2.46616	1 2.38 2.06641	1 2.55 2.01622	1 2.55 2.07086	1 2.55 2.21129	1 2.76 2.01008	1 2.76 2.03191	1 2.76 2.03192	1 2.76 2.06555	1 2.76 2.06536	1 2.76 2.12640	1 2.76 2.12641	1 2.76 2.17163	1 2.76 2.17164	IG Position Marker
THA-1	B	b	b	b	b	B	B	B	B	B	b	b	b	B	B	B	b	b	b	b	B	B	b	B	B	THA-1
THA-2	A	a	a	a	a	A	A	A	A	A	A	a	a	A	A	A	a	a	a	a	A	A	a	A	A	THA-2
THA-3	B	b	b	a	a	A	A	A	A	A	A	a	a	A	A	A	a	a	a	a	A	A	a	A	A	THA-3
THA-4	A	a	a	a	a	A	A	A	A	A	A	a	a	A	A	A	a	a	a	a	A	A	a	A	A	THA-4
THA-6	B	b	b	b	b	B	B	B	B	B	B	b	b	B	B	B	b	b	b	b	B	B	b	B	B	THA-6
THA-8	A	a	a	a	a	A	A	A	A	A	A	a	a	A	A	A	a	a	a	a	A	A	a	A	A	THA-8
THA-10	A	a	a	a	a	A	A	A	A	A	A	a	a	A	A	A	a	a	a	a	A	A	a	A	A	THA-10
THA-11	A	a	a	a	a	A	A	A	A	A	A	a	a	A	A	A	a	a	a	a	A	A	a	A	A	THA-11
THA-12	B	b	b	b	b	B	B	B	B	B	B	b	b	B	B	B	b	b	b	b	B	B	b	B	B	THA-12
THA-13	B	b	b	b	b	B	B	B	B	B	B	b	a	A	A	A	a	a	a	a	A	A	a	A	A	THA-13
THA-15	A	a	a	a	a	A	A	A	A	A	A	a	a	A	A	A	a	a	a	a	A	A	a	A	A	THA-15
THA-17	A	a	a	a	a	A	A	A	A	A	A	a	a	A	A	A	a	a	a	a	A	A	a	A	A	THA-17
THA-18	A	a	a	a	a	A	A	A	A	A	A	a	a	A	A	A	a	a	a	a	A	A	a	A	A	THA-18
THA-19	A	a	a	a	a	A	A	A	A	A	A	a	a	A	A	A	a	a	a	a	A	A	a	A	A	THA-19
THA-20	B	b	b	b	b	B	B	B	B	B	B	b	b	B	B	B	b	b	b	b	B	B	b	B	B	THA-20
THA-21	B	b	b	b	b	B	B	B	B	B	B	b	b	B	B	B	b	b	b	b	B	B	b	B	B	THA-21
THA-22	A	a	a	a	a	A	A	A	A	A	A	a	a	A	A	A	a	a	a	a	A	A	a	A	A	THA-22
THA-23	B	b	b	b	b	B	B	B	B	B	B	b	b	B	B	B	b	b	b	b	B	B	b	B	B	THA-23
THA-24	A	a	a	a	a	A	A	A	A	A	A	a	a	A	A	A	a	a	a	a	A	A	a	A	A	THA-24
THA-25	B	b	b	b	b	B	B	B	B	B	B	b	b	B	B	B	b	b	b	b	B	B	b	B	B	THA-25
THA-26	A	a	a	a	a	A	A	A	A	A	A	a	a	A	A	A	a	a	a	a	A	A	a	A	A	THA-26
THA-27	A	a	a	a	a	A	A	A	A	A	A	a	a	A	A	A	a	a	a	a	A	A	a	A	A	THA-27
THA-28	B	b	b	b	b	B	B	B	B	B	B	b	b	B	B	B	b	b	b	b	B	B	b	B	B	THA-28
THA-30	A	a	a	a	a	A	A	A	A	A	A	a	a	A	A	A	a	a	a	a	A	A	a	A	A	THA-30
THA-31	A	a	a	a	a	A	A	A	A	A	A	a	a	A	A	A	a	a	a	a	A	A	a	A	A	THA-31

Showing 1 to 25 of 122 entries

Markers

Previous lines

1

1

3

4

5

Next lines

Select linkage group and advance through markers

A = Parent A, B = Parent B. Lower case: genotype calls reversed based on parental alleles.

Shared motif search = realtime analysis



Date Created: 2016-10-24 13:39
Click to toggle Shared Motif Search ▼

Shared Motif Search

11 motifs close to top scorer:

A TTTACATAAATGGAAA A

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18

Show 10 entries

Motifs can be filtered: Search: CATAAATGGAAA

Motif	Length	Num	Score	Regions
TTACATAAATGGAAA*	15	5	3970	Phvul.004G171200 5.0kb upstream:1266-1280 Phvul.004G176600 5.0kb upstream:783-797 Phvul.009G024400 5.0kb upstream:1692-1706 Phvul.009G065500 5.0kb upstream:2044-2058 Phvul.010G125300 5.0kb upstream:3957-3971 List
TACATAAATGGAAAA*	15	4	3176	Phvul.004G176600 5.0kb upstream:784-798 Phvul.008G275700 5.0kb upstream:3610-3624 Phvul.009G065500 5.0kb upstream:2045-2059 Phvul.010G125300 5.0kb upstream:3958-3972 List
TTACATAAATGGAAAA*	16	3	2520	Phvul.004G176600 5.0kb upstream:783-798 Phvul.009G065500 5.0kb upstream:2044-2059 Phvul.010G125300 5.0kb upstream:3957-3972 List
TACATAAATGGAAA*	14	3	2247	Phvul.004G171200 5.0kb upstream:1267-1280 Phvul.008G275700 5.0kb upstream:3610-3623 Phvul.009G024400 5.0kb upstream:1693-1706 List
CATAAATGGAAAA	13	3	2109	Phvul.004G171200 5.0kb upstream:1315-1327 Phvul.008G275700 5.0kb upstream:3612-3624 Phvul.009G065500 5.0kb upstream:2047-2059 List
ATTACATAAATGGAAAA*	18	2	1862	Phvul.009G065500 5.0kb upstream:2042-2059 Phvul.010G125300 5.0kb upstream:3955-3972 List
ATTACATAAATGGAAAT*	17	2	1770	Phvul.004G171200 5.0kb upstream:1265-1281 Phvul.009G024400 5.0kb upstream:1691-1707 List

Showing 1 to 7 of 7 entries (filtered from 101 total entries)

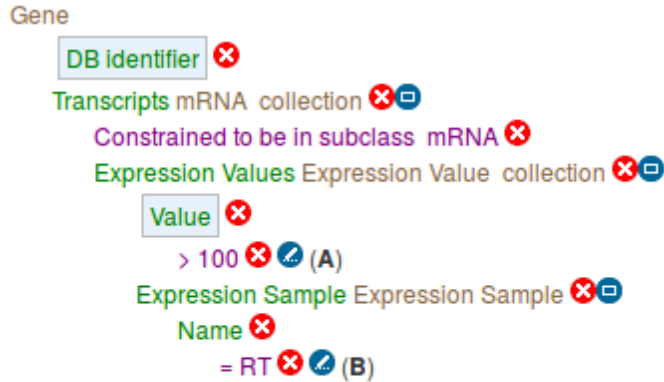
Previous 1 Next

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Example: intersect lists from queries



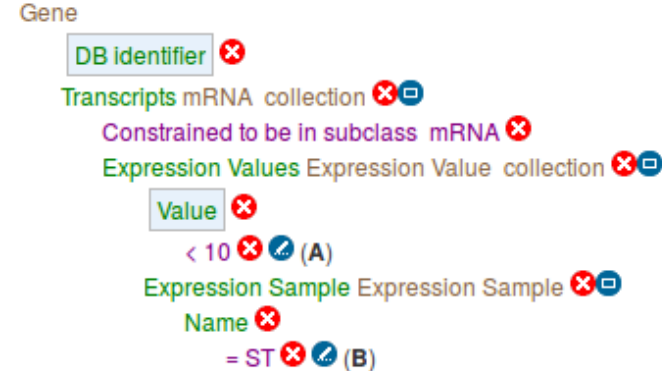
Question: which Pv genes express highly in root tips (RT) but poorly in shoot tips (ST) in the 2nd trifoliate stage?



Constraint logic: A and B

A and B

RT > 100 RPKM query



Constraint logic: A and B

A and B

ST < 10 RPKM query


Intersect resulting lists



Intersection of query lists results in 39 genes

✓ Created list "RT gt 100 AND ST It 10" as INTERSECT of ST It 10 and RT gt 100.

Hide



Lists

View your own and public lists, search by keyword and compare or combine the contents of lists. Click on a list to view graphs and summaries in an analysis page, select lists using checkboxes to perform set operations. Click 'Upload' above to import a new list.

Filter: Reset

Actions: ☒ Union | ☒ **Intersect** | ☐ Subtract | ☐ Asymmetric Difference | Copy Delete **Options:** ☒ Show descriptions

You are not logged in. [Log in](#) to save lists permanently and to mark items as favourites ★.

<input type="checkbox"/>	RT gt 100 AND ST It 10 39 Genes
MY	
<input checked="" type="radio"/>	ST It 10 14983 Genes
MY	
<input checked="" type="radio"/>	RT gt 100 1784 Genes
MY	

View resulting list → “list analysis page”



PvGEA: *Phaseolus vulgaris* Gene Expression Atlas

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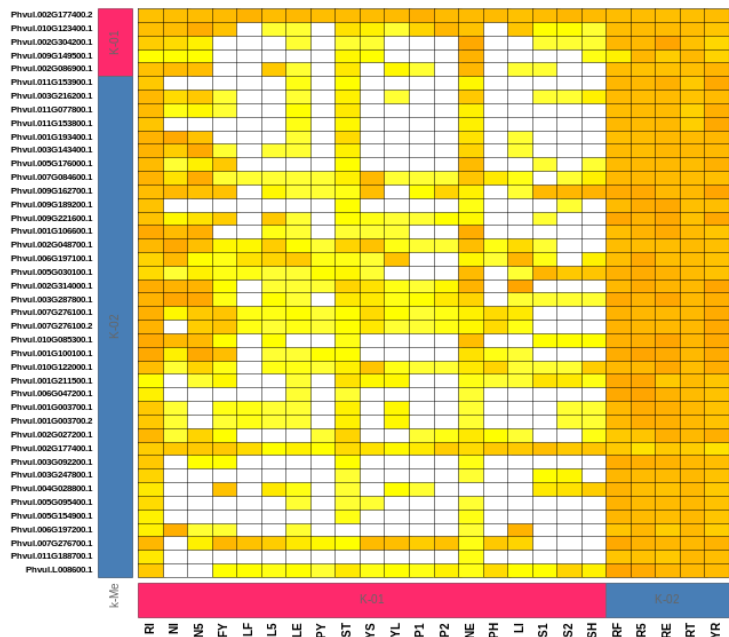
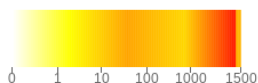
Heatmap visualization powered by [canvasXpress](#). Grab the edges with your mouse to resize the map. Zoom in/out on an

Click to see/hide the expression map ▼

Expression K-means: 2

Tissue K-means: 2

mRNA RNA-seq expression (RPKM) : 42 transcripts



The list analysis page includes a heatmap, plus standard IM “widget” analyses like GO term enrichment and chromosome distribution.

It's not hard to write new widgets.