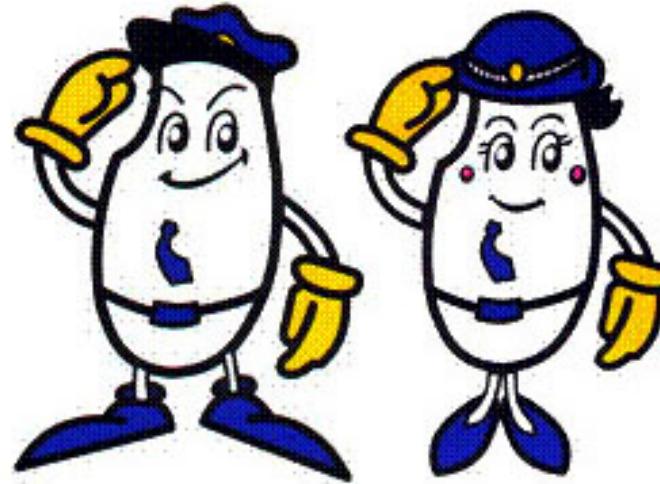
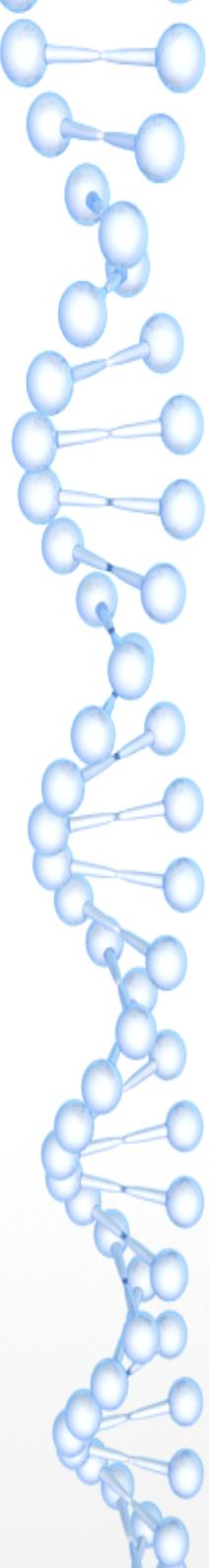


# RiceXPro: a platform for monitoring gene expression in japonica rice grown under natural field conditions



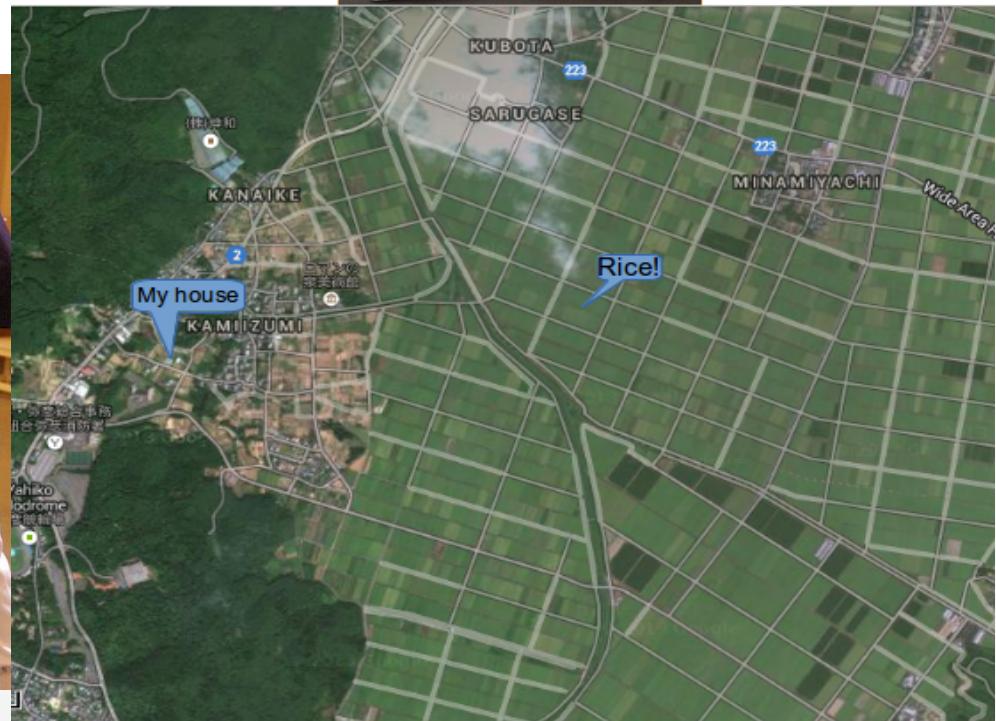


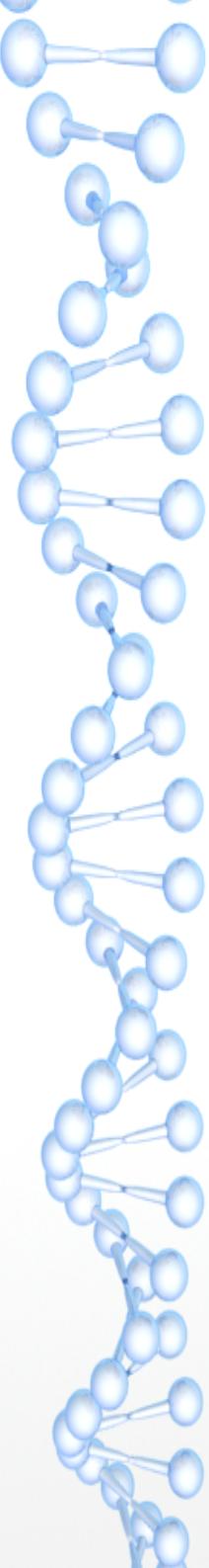
# Why study rice?

- Major cereal crop that provides food for roughly half of the world's population.
- Genetically interesting species to study
- *Oryza sativa* is the cereal with the smallest genome.
  - 430Mb across 12 chromosomes
  - Easy to genetically modify
  - Model organism for cereal biology
- Lots of interesting problems to solve!
  - Better crop yields through selective cross-breeding of hardy strains
  - Bio-fortification (Golden rice project)
  - Evolutionary modeling (The rice diversity project)

# 僕は新潟県に住んでいます。

- I live in the heart of rice growing country in Niigata Prefecture.
- Rice **is** our life!





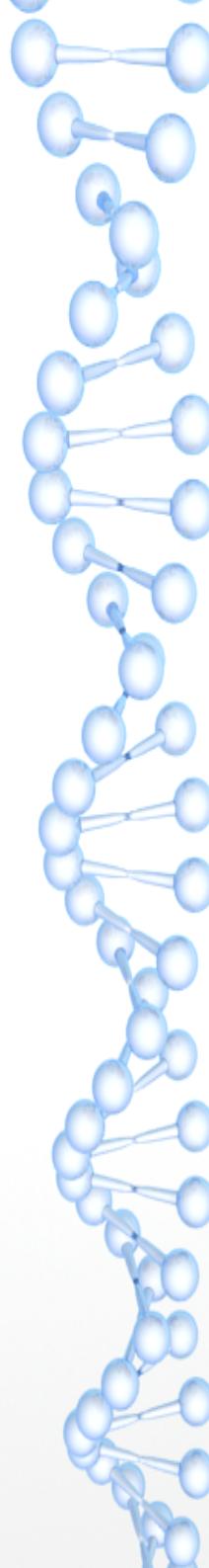
# What is RiceXPro?

- Global gene expression database
- Provides an overview of the transcriptional changes throughout the growth of rice plants in the field under natural conditions.
- A repository of expression data encompassing growth in the field, providing a baseline for genes that underlie various agronomically important traits in rice.

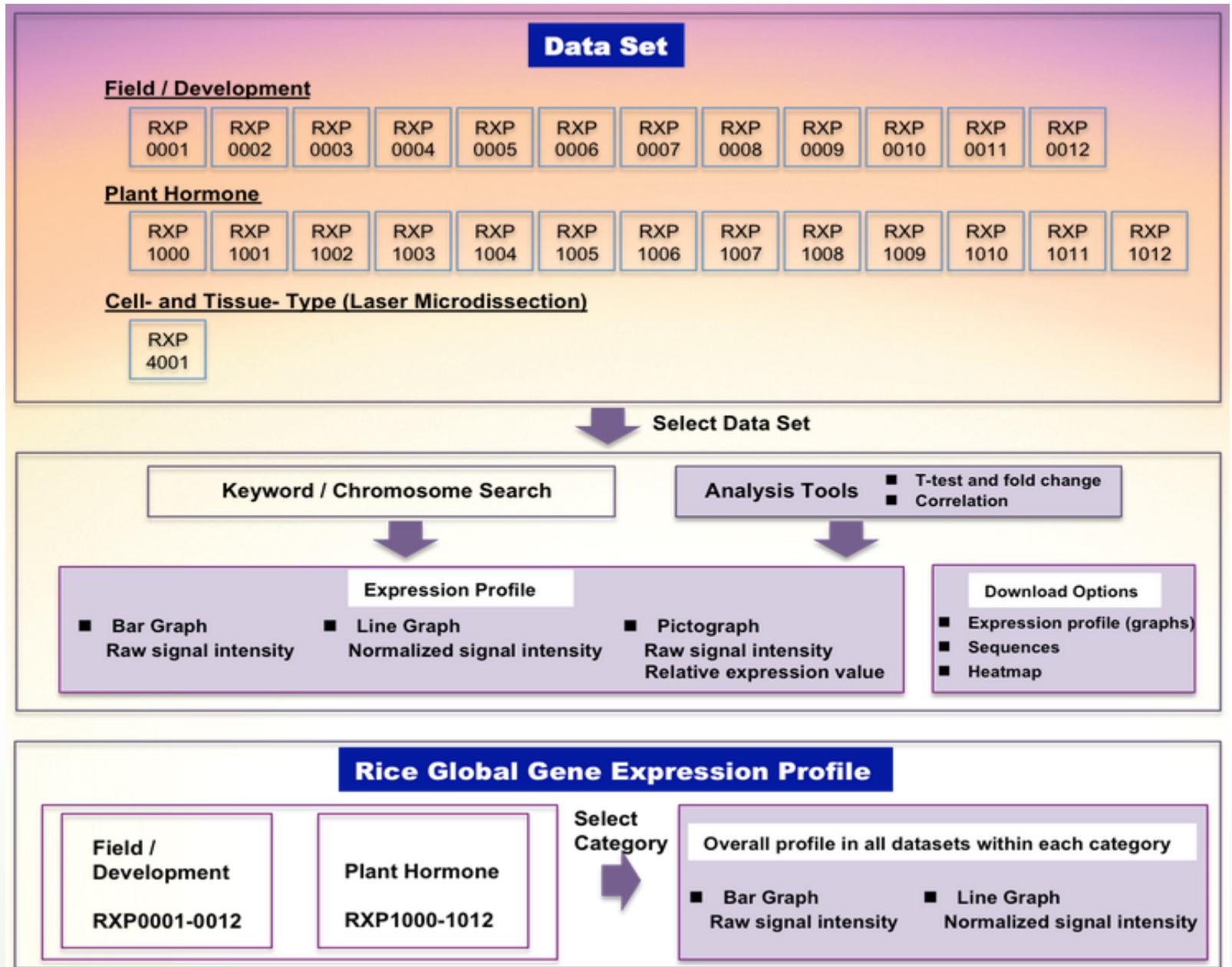
# Let's have a look at RiceXPro!

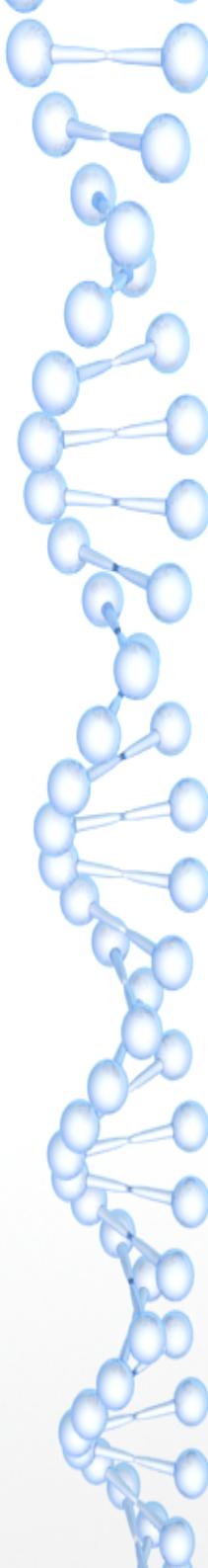
- Website: <http://ricexpro.dna.affrc.go.jp/>





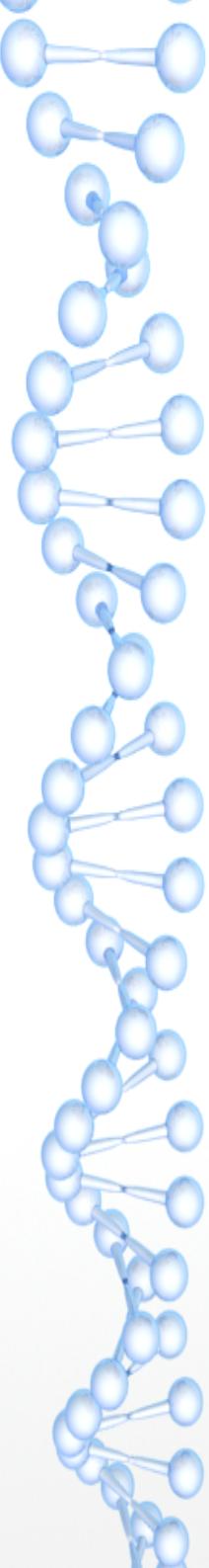
# The Data Sets





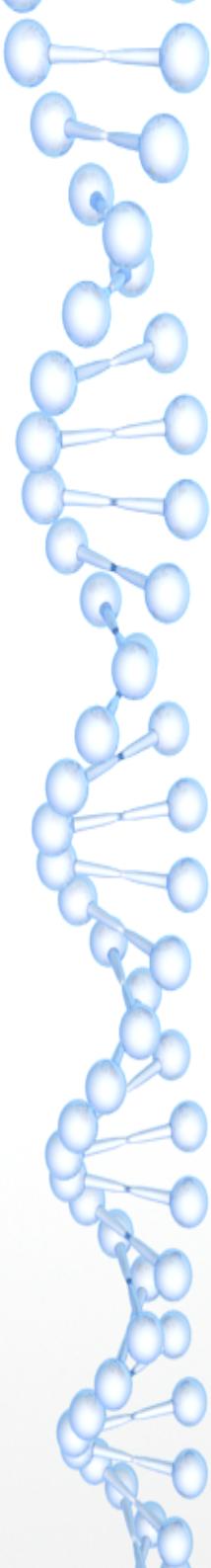
# Where the data comes from

- The RiceXPro database is part of a project on rice transcriptome analysis using microarray technology.
- Aimed at characterizing the expression profile of all **predicted genes** in rice and providing reference information that can be used in functional genomics.
- All expression profiles were generated using a **single microarray platform** (Agilent 44k Rice ChiP microarray)
- Based on manually curated gene models in RAP-DB and rice full-length cDNA sequence information in the KOME database.



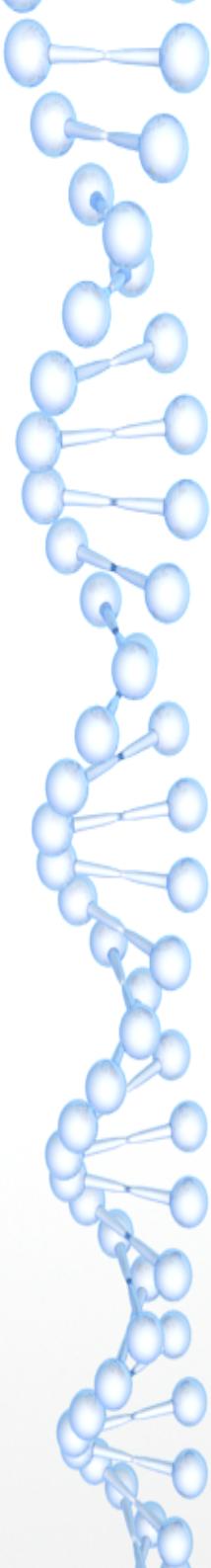
# More on the data

- RiceXPro currently contains gene expression data sets corresponding to spatio-temporal gene expression profiling
- Based on 48 different tissue and organ types at various developmental stages using continuous profiling of leaves from transplanting until harvesting
- Grown under natural field conditions
- All expression data were generated by one-color cyanine fluorescent dye (Cy3) micro array hybridization protocol.
- Background correction of the Cy3 raw signals was performed with the Agilent Feature Extraction software (version 9.5.3.1).
- Each expression data was subjected to 75 percentile normalization and log2 transformation using R



# Micro array construction

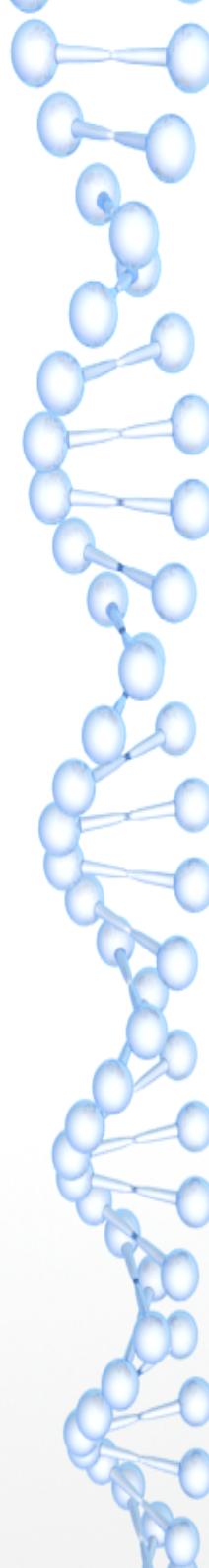
- Design based on the manually curated rice genome detailed by the Rice Annotation Project Database (RAPD)
  - 60-mer oligo sequence probes, corresponding to 27,800 RAP loci
  - Transcripts based on full length cDNA
  - Transcripts based on expressed sequence tag (EST) support
  - And predicted loci
- For RAP locus with several mapped full length cDNAs, multiple 60-mer probes were used
  - These redundant probes provide evidence of replicability and reliability of genome expression



# An example of using RiceXPro

- Let's walk through an example of using RiceXPro to examine the difference in gene expression at various stages of a rice plant's development.
- First, we will select “Global Profile”
- Clicking the “Example” button will auto-populate the search field with sample search values.
  - Os01g0102700 [a RAP Locus ID for **Oryza Sativa**]
  - LOC\_Os01g01070 [MSU ID]
  - AK067670 [an accession number]

# Global Profile



**RiceXPro**

HOME GLOBAL PROFILE DATA SETS EXP\_BLAST ExProFlip

## Global Gene Expression Profile

A global expression profile of each gene can be viewed from two major dataset categories, namely, 'field / development' and 'plant hormone'. The field/development datasets correspond to microarray data derived from tissues/organs at various stages of development under natural field conditions. The plant hormone datasets correspond to microarray data from roots and shoots of seedlings treated with various plant hormones. Search options provide an overview of the overall transcriptome of the rice plant under each category.

### Data category

Select a data category to get the overall expression profile of a gene / genes.

Field / Development

### Search options

Keyword search [Help](#)  
Enter RAP locus ID, MSU ID, Accession number, or gene name.

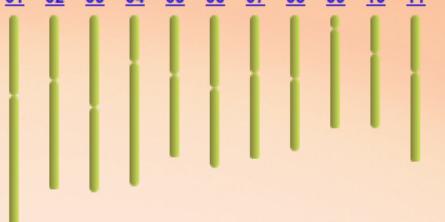
Example

0s01g0102700  
LOC\_0s01g01070  
AK067670

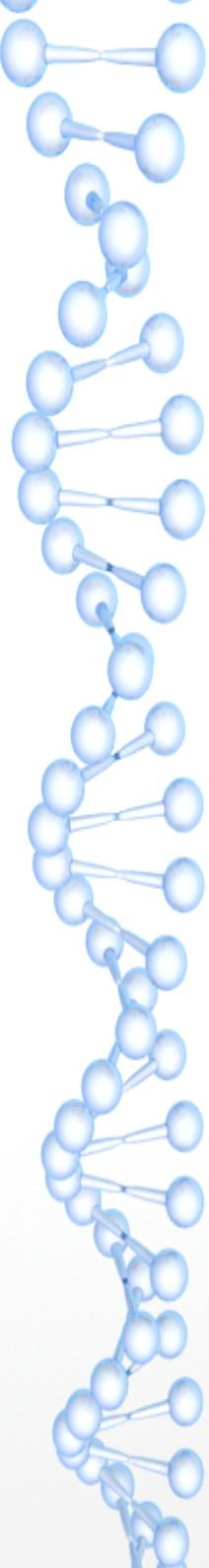
Search Reset

Chromosome / Region search  
Click a chromosome to get a tabular list of all genes in sequential order.

01 02 03 04 05 06 07 08 09 10 11 12



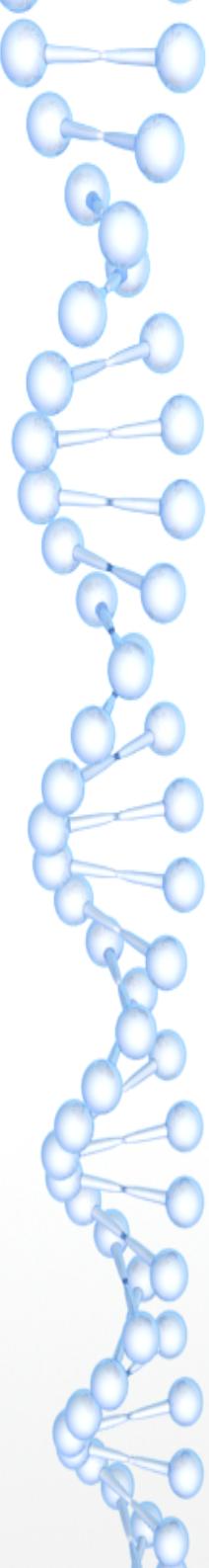
Search genes located in between two loci Example  
Locus 1  Locus 2   
Search



# Searching the database

- Keywords placed alone on separate lines in the search box are logically joined together by the OR operator.
- Terms placed on the same line are logically joined by AND.
- In our example search, clicking “Search” will take us to the next screen and show us the results.

# Search Results



**RiceXPro** 

HOME GLOBAL PROFILE DATA SETS EXP\_BLAST ExProFlip

---

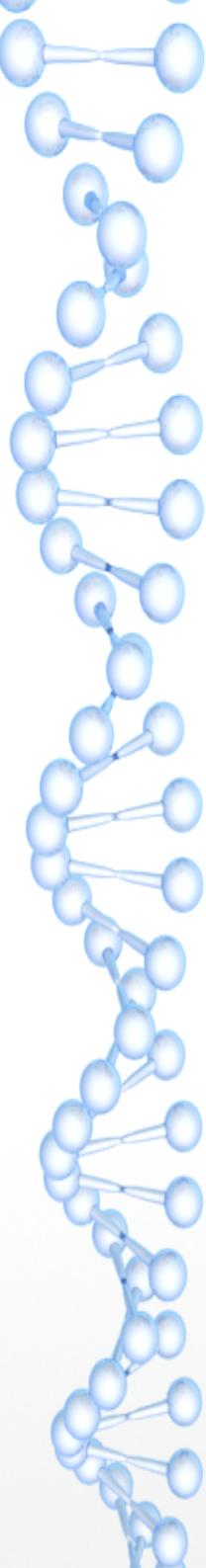
## Field / Development

[\[Back to search page\]](#)

Search keyword:[os01g0102700" OR "loc\_os01g01070" OR "ak067670"]

3 loci found 1-3 listed of 3

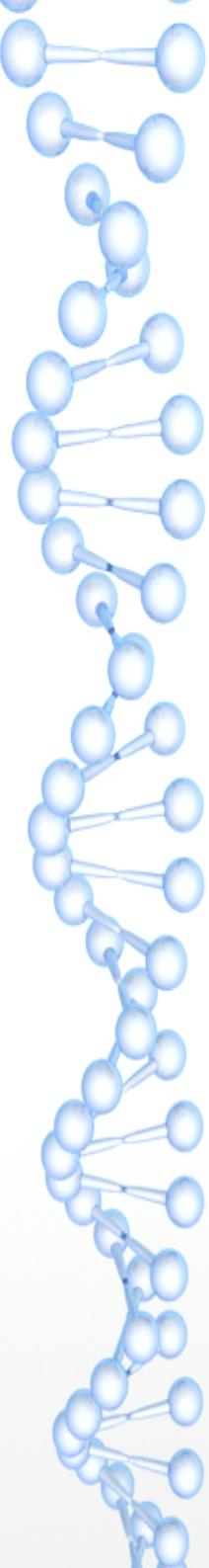
Locus ID / Links	FeatureNum (Link to graph)	Accession	Probe Sequence ID (Link to SeqInfo)	Description	MSU ID
<a href="#">Os01g0100800</a>	<a href="#">22150</a>	AK122012	<a href="#">S-18431</a> (unique)	Protein of unknown function DUF1664 family protein.	<a href="#">LOC_Os01g01070</a>
<a href="#">Os01g0102700</a>	<a href="#">17684</a>	AK063774	<a href="#">S-14818</a> (unique)	Translocon-associated beta family protein.	<a href="#">LOC_Os01g01307</a>
	<a href="#">19792</a>	AK099081	<a href="#">S-16540</a> (unique)	Translocon-associated beta family protein.	<a href="#">LOC_Os01g01307</a>
	<a href="#">35628</a>	AK099360	<a href="#">S-29011</a> (unique)	Translocon-associated beta family protein.	<a href="#">LOC_Os01g01307</a>
<a href="#">Os01g0102900</a>	<a href="#">21342</a>	AK067670	<a href="#">S-17781</a> (unique)	Light regulated Lir1 family protein.	<a href="#">LOC_Os01g01340</a>



# Chromosomes and Loci-based searching

- If we return to the search screen, we notice there are chromosomes on the right hand side. Clicking on a chromosome will give us a table with all the known genes in sequential order.
- We can also search between two known loci by populating the locus1 and locus2 fields with known RAP Locus IDs.
- Let's select Example here and run a search!

# Loci Search



**RiceXPro**

HOME GLOBAL PROFILE DATA SETS EXP\_BLAST ExProFlip

## Global Gene Expression Profile

A global expression profile of each gene can be viewed from two major dataset categories, namely, 'field / development' and 'plant hormone'. The field/development datasets correspond to microarray data derived from tissues/organs at various stages of development under natural field conditions. The plant hormone datasets correspond to microarray data from roots and shoots of seedlings treated with various plant hormones. Search options provide an overview of the overall transcriptome of the rice plant under each category.

### Data category

Select a data category to get the overall expression profile of a gene / genes.

Field / Development ▾

### Search options

Keyword search [Help](#)  
Enter RAP locus ID, MSU ID, Accession number, or gene name.

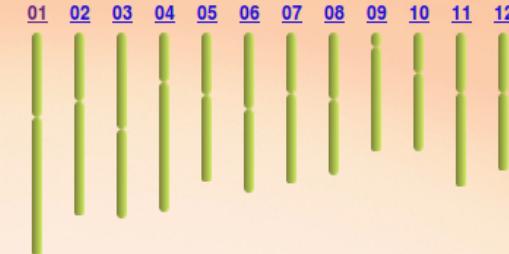
Example

Search Reset

### Chromosome / Region search

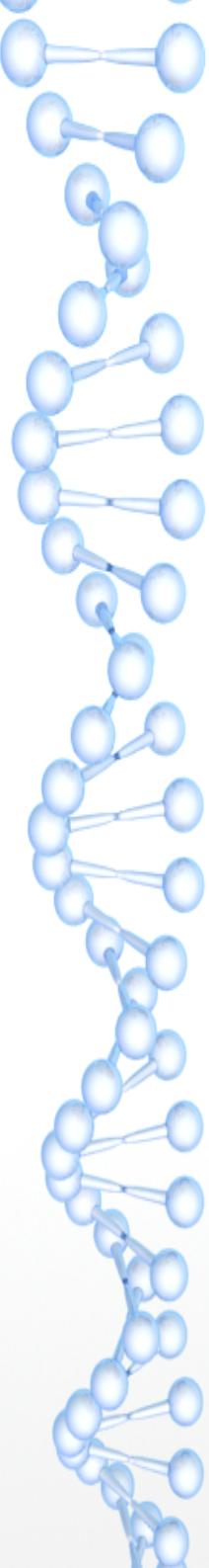
Click a chromosome to get a tabular list of all genes in sequential order.

01 02 03 04 05 06 07 08 09 10 11 12



Search genes located in between two loci Example  
Locus 1 Os01g0101200 Locus 2 Os01g0102700  
Search

# Loci Search Results



**RiceXPro**

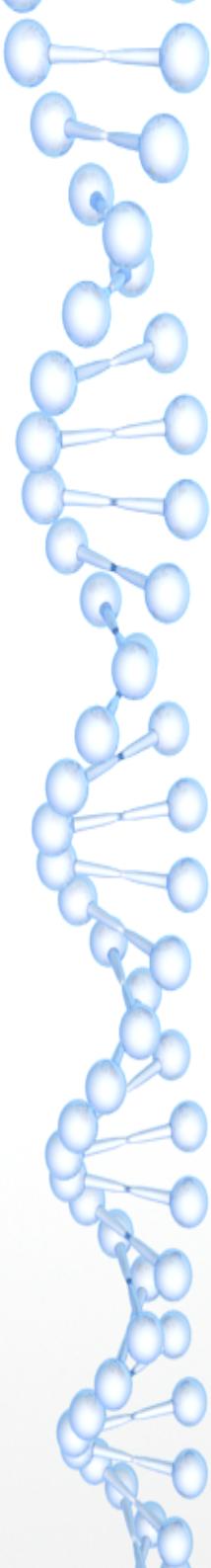
HOME GLOBAL PROFILE DATA SETS EXP\_BLAST ExProFlip

## Field / Development

[Back to search page]

Search keyword:[Os01g0101200 - Os01g0102700]  
11 loci found 1-11 listed of 11

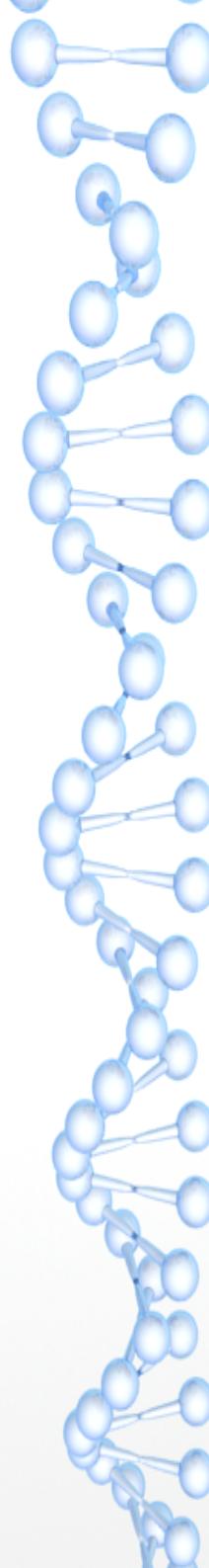
Locus ID / Links	FeatureNum (Link to graph)	Accession	Probe Sequence ID (Link to SeqInfo)	Description	MSU ID
Os01g0101200	<a href="#">4386</a>	AK119457	<a href="#">S-3634</a> (unique)	2,3-diketo-5-methylthio-1-phosphopentane phosphatase domain containing protein.	<a href="#">LOC_Os01g01120</a>
	<a href="#">12559</a>	AK104517	<a href="#">S-10615</a> (unique)	2,3-diketo-5-methylthio-1-phosphopentane phosphatase domain containing protein.	<a href="#">LOC_Os01g01120</a>
	<a href="#">21297</a>	AK104625	<a href="#">S-17746</a> (non-unique)	2,3-diketo-5-methylthio-1-phosphopentane phosphatase domain containing protein.	<a href="#">LOC_Os01g01120</a>
	<a href="#">29991</a>	AK104752	<a href="#">S-17746</a> (non-unique)	2,3-diketo-5-methylthio-1-phosphopentane phosphatase domain containing protein.	<a href="#">LOC_Os01g01120</a>
	<a href="#">34331</a>	AK067866	<a href="#">S-28012</a> (unique)	2,3-diketo-5-methylthio-1-phosphopentane phosphatase domain containing protein.	<a href="#">LOC_Os01g01120</a>
Os01g0101300	<a href="#">8176</a>	CI016681	<a href="#">S-6925</a> (unique)	Conserved hypothetical protein.	<a href="#">LOC_Os01g01130</a>
Os01g0101600	<a href="#">5385</a>	AK122118	<a href="#">S-4505</a> (non-unique)	RNA-binding region RNP-1 (RNA recognition motif) domain containing protein.	<a href="#">LOC_Os01g01150</a>
	<a href="#">40093</a>	AK103820	<a href="#">S-4505</a> (non-unique)	RNA-binding region RNP-1 (RNA recognition motif) domain containing protein.	<a href="#">LOC_Os01g01150</a>
	<a href="#">44280</a>	AK099952	<a href="#">S-35368</a> (unique)	RNA-binding region RNP-1 (RNA recognition motif) domain containing protein.	<a href="#">LOC_Os01g01150</a>
Os01g0101700	<a href="#">13215</a>	CI525185	<a href="#">S-11171</a> (unique)	Heat shock protein DnaJ, N-terminal domain containing protein.	<a href="#">LOC_Os01g01160</a>
Os01g0101800	<a href="#">11072</a>	AK103498	<a href="#">S-9371</a> (unique)	Conserved hypothetical protein.	<a href="#">LOC_Os01g01170</a>
Os01g0102000	<a href="#">33502</a>	AK101065	<a href="#">S-27361</a> (unique)	Phosphoesterase family protein.	<a href="#">LOC_Os01g01190</a>
Os01g0102300	<a href="#">28978</a>	AK067320	<a href="#">S-23855</a> (unique)	Conserved hypothetical protein.	<a href="#">LOC_Os01g01280</a>
Os01g0102400	<a href="#">43275</a>	CI453282	<a href="#">S-34702</a> (unique)	Histone-fold domain containing protein.	<a href="#">LOC_Os01g01290</a>
Os01g0102500	<a href="#">6380</a>	AK100002	<a href="#">S-5381</a> (unique)	Conserved hypothetical protein.	<a href="#">LOC_Os01g01295</a>
Os01g0102600	<a href="#">7978</a>	AK062086	<a href="#">S-6760</a> (non-unique)	Shikimate kinase domain containing protein.	<a href="#">LOC_Os01g01302</a>
	<a href="#">40338</a>	AK064812	<a href="#">S-6760</a> (non-unique)	Shikimate kinase domain containing protein.	<a href="#">LOC_Os01g01302</a>
Os01g0102700	<a href="#">17684</a>	AK063774	<a href="#">S-14818</a> (unique)	Translocon-associated beta family protein.	<a href="#">LOC_Os01g01307</a>
	<a href="#">19792</a>	AK099081	<a href="#">S-16540</a> (unique)	Translocon-associated beta family protein.	<a href="#">LOC_Os01g01307</a>
	<a href="#">35628</a>	AK099360	<a href="#">S-29011</a> (unique)	Translocon-associated beta family protein.	<a href="#">LOC_Os01g01307</a>



# Great, now what?!?!

- If you mouse over the links, you will be presented with sub-menus In our example search we have a RAP Locus ID Os01g0101200.
- Mousing over this, we get a menu, from here we can select a Database to draw results from. I have selected Field/Development, which will present us with the next screen to select further options to get at the data we are searching for.

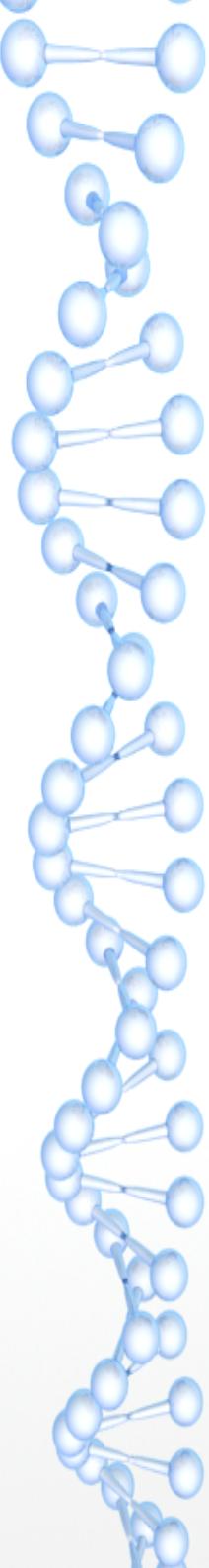
# Mousing over a result



A screenshot of a web browser displaying the RiceXPro gene search results. The page title is "Field / Development". A search keyword was entered: [Os01g0101200 - Os01g0102700]. 11 loci were found, listed 1-11.

Locus ID / Links	FeatureNum (Link to graph)	Accession	Probe Sequence ID (Link to SeqInfo)	Description	MSU ID
Os01g0101200		AK119457	<a href="#">S-3634</a> (unique)	2,3-diketo-5-methylthio-1-phosphopentane phosphatase domain containing protein.	<a href="#">LOC_Os01g01120</a>
	Link: Field / Development				
	Link: Plant Hormone	AK104517	<a href="#">S-10615</a> (unique)	2,3-diketo-5-methylthio-1-phosphopentane phosphatase domain containing protein.	<a href="#">LOC_Os01g01120</a>
	Link: RiceFRENDS				
	Link: Rice TOGO Browser	AK104625	<a href="#">S-17746</a> (non-unique)	2,3-diketo-5-methylthio-1-phosphopentane phosphatase domain containing protein.	<a href="#">LOC_Os01g01120</a>
	Link: RAP-DB				
	Link: SAL AD ver3.0				
	Link: FT-DB	AK104752	<a href="#">S-17746</a> (non-unique)	2,3-diketo-5-methylthio-1-phosphopentane phosphatase domain containing protein.	<a href="#">LOC_Os01g01120</a>
	34331	AK067866	<a href="#">S-28012</a> (unique)	2,3-diketo-5-methylthio-1-phosphopentane phosphatase domain containing protein.	<a href="#">LOC_Os01g01120</a>
Os01g0101300	<a href="#">8176</a>	CI016681	<a href="#">S-6925</a> (unique)	Conserved hypothetical protein.	<a href="#">LOC_Os01g01130</a>
Os01g0101600	<a href="#">5385</a>	AK122118	<a href="#">S-4505</a> (non-unique)	RNA-binding region RNP-1 (RNA recognition motif) domain containing protein.	<a href="#">LOC_Os01g01150</a>
	<a href="#">40093</a>	AK103820	<a href="#">S-4505</a> (non-unique)	RNA-binding region RNP-1 (RNA recognition motif) domain containing protein.	<a href="#">LOC_Os01g01150</a>
	<a href="#">44280</a>	AK099952	<a href="#">S-35368</a> (unique)	RNA-binding region RNP-1 (RNA recognition motif) domain containing protein.	<a href="#">LOC_Os01g01150</a>
Os01g0101700	<a href="#">13215</a>	CI525185	<a href="#">S-11171</a> (unique)	Heat shock protein DnaJ, N-terminal domain containing protein.	<a href="#">LOC_Os01g01160</a>
Os01g0101800	<a href="#">11072</a>	AK103498	<a href="#">S-9371</a> (unique)	Conserved hypothetical protein.	<a href="#">LOC_Os01g01170</a>
Os01g0102000	<a href="#">33502</a>	AK101065	<a href="#">S-27361</a> (unique)	Phosphoesterase family protein.	<a href="#">LOC_Os01g01190</a>
Os01g0102300	<a href="#">28978</a>	AK067320	<a href="#">S-23855</a> (unique)	Conserved hypothetical protein.	<a href="#">LOC_Os01g01280</a>
Os01g0102400	<a href="#">43275</a>	CI453282	<a href="#">S-34702</a> (unique)	Histone-fold domain containing protein.	<a href="#">LOC_Os01g01290</a>
Os01g0102500	<a href="#">6380</a>	AK100002	<a href="#">S-5381</a> (unique)	Conserved hypothetical protein.	<a href="#">LOC_Os01g01295</a>
Os01g0102600	<a href="#">7978</a>	AK062086	<a href="#">S-6760</a> (non-unique)	Shikimate kinase domain containing protein.	<a href="#">LOC_Os01g01302</a>
	<a href="#">40338</a>	AK064812	<a href="#">S-6760</a> (non-unique)	Shikimate kinase domain containing protein.	<a href="#">LOC_Os01g01302</a>
Os01g0102700	<a href="#">17684</a>	AK063774	<a href="#">S-14818</a> (unique)	Translocon-associated beta family protein.	<a href="#">LOC_Os01g01307</a>
	<a href="#">19792</a>	AK099081	<a href="#">S-16540</a> (unique)	Translocon-associated beta family protein.	<a href="#">LOC_Os01g01307</a>
	<a href="#">35628</a>	AK099360	<a href="#">S-29011</a> (unique)	Translocon-associated beta family protein.	<a href="#">LOC_Os01g01307</a>

# Field/Development DB Results



The RiceXPro logo is displayed at the top left, featuring the text "RiceXPro" in a bold, black, sans-serif font, with a colorful dot pattern to its right. To the right of the logo is a horizontal navigation bar with five items: "HOME", "GLOBAL PROFILE", "DATA SETS", "EXP\_BLAST", and "ExProFlip".

## Field / Development

[[Back to search page](#)]

Search keyword: "os01g0101200"  
1 locus found 1-1 listed of 1

Locus ID / Links	FeatureNum (Link to graph)	Accession	Probe Sequence ID (Link to SeqInfo)	Description	MSU ID
<a href="#">Os01g0101200</a>	<a href="#">4386</a>	AK119457	<a href="#">S-3634</a> (unique)	2,3-diketo-5-methylthio-1-phosphopentane phosphatase domain containing protein.	<a href="#">LOC_Os01g01120</a>
	<a href="#">12559</a>	AK104517	<a href="#">S-10615</a> (unique)	2,3-diketo-5-methylthio-1-phosphopentane phosphatase domain containing protein.	<a href="#">LOC_Os01g01120</a>
	<a href="#">21297</a>	AK104625	<a href="#">S-17746</a> (non-unique)	2,3-diketo-5-methylthio-1-phosphopentane phosphatase domain containing protein.	<a href="#">LOC_Os01g01120</a>
	<a href="#">29991</a>	AK104752	<a href="#">S-17746</a> (non-unique)	2,3-diketo-5-methylthio-1-phosphopentane phosphatase domain containing protein.	<a href="#">LOC_Os01g01120</a>
	<a href="#">34331</a>	AK067866	<a href="#">S-28012</a> (unique)	2,3-diketo-5-methylthio-1-phosphopentane phosphatase domain containing protein.	<a href="#">LOC_Os01g01120</a>

# Field/Development Results for Feature 4386

**RiceXPro** RICE GENE TOOL

HOME GLOBAL PROFILE DATA SETS EXP\_BLAST ExProFlip

Data Category: Field / Development

## Field / Development

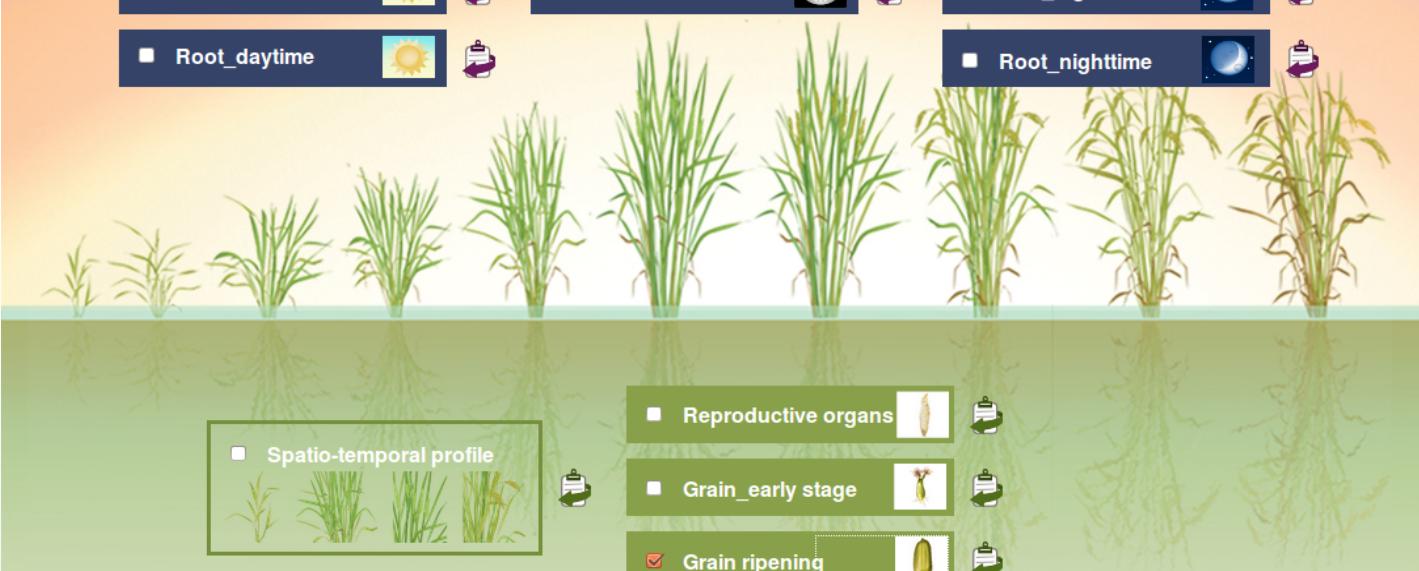
Growth condition

Locus ID	FeatureNum	Accession	Description
Os01g0101200	4386	AK119457	2,3-diketo-5-methylthio-1-phosphopentane phosphatase domain containing protein.

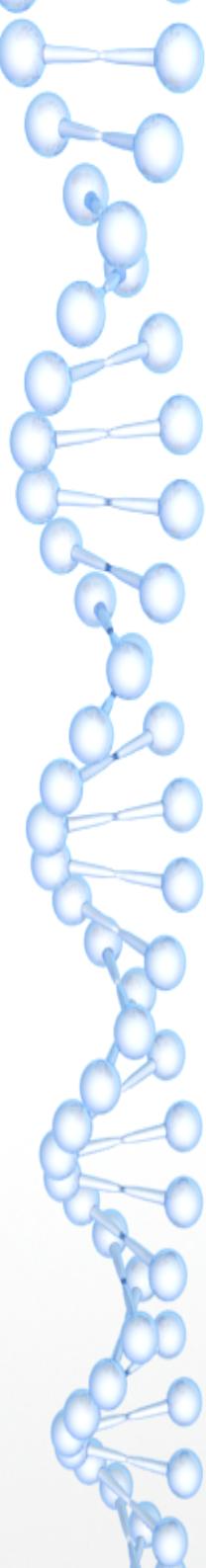
Select All  Download selected graph

Leaf\_sunrise Leaf\_diurnal Leaf\_sunset  
Leaf\_daytime Root\_diurnal Leaf\_nighttime  
Root\_daytime Root\_nighttime

Reproductive organs Spatio-temporal profile  
Grain\_early stage Grain ripening



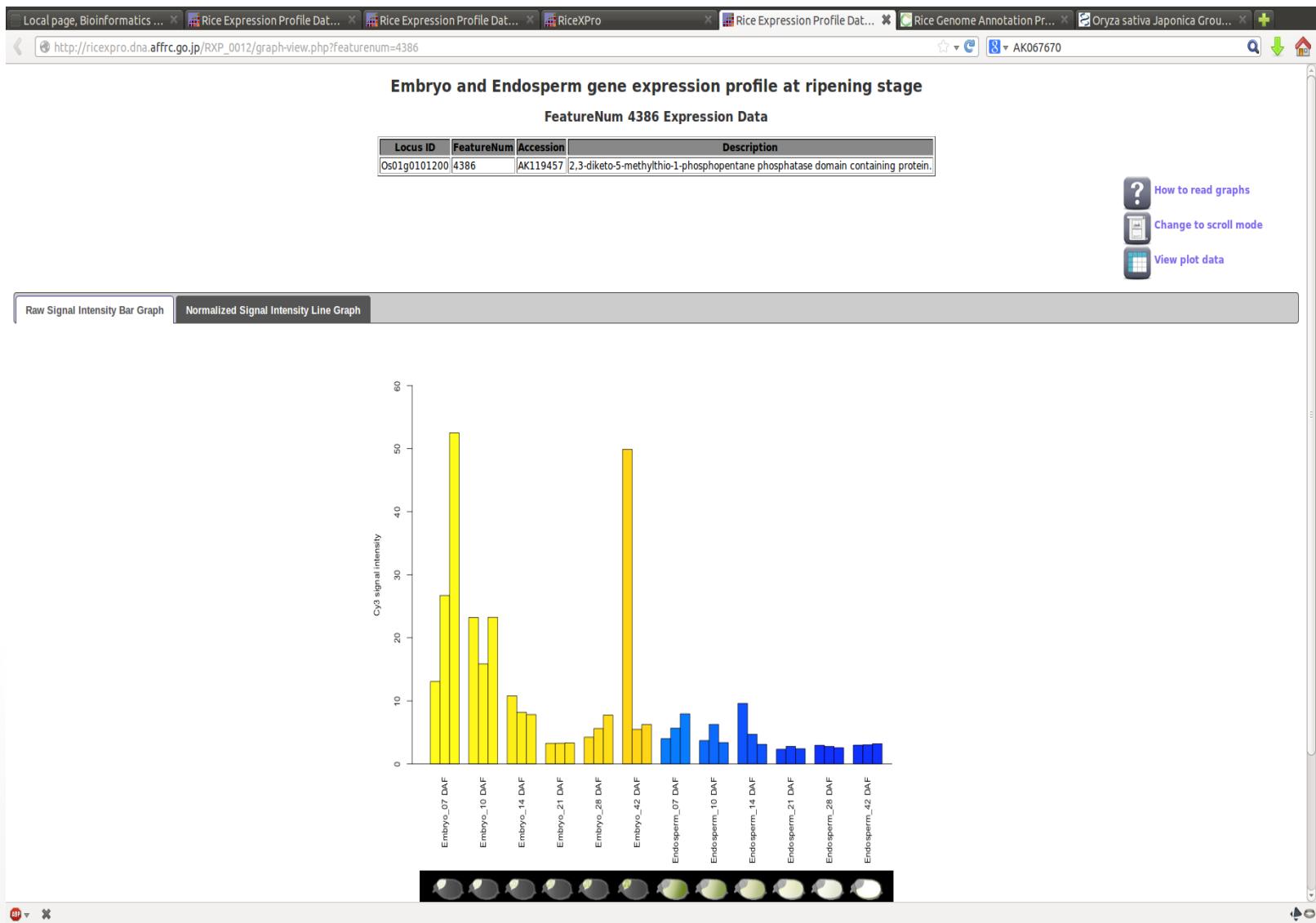
A screenshot of the RiceXPro interface showing field development results for Feature 4386. The top navigation bar includes links for HOME, GLOBAL PROFILE, DATA SETS, EXP\_BLAST, and ExProFlip. A dropdown menu indicates the Data Category is set to "Field / Development". Below this, a table displays the Locus ID (Os01g0101200), FeatureNum (4386), Accession (AK119457), and a brief Description of the protein. There are buttons for "Select All" and "Download selected graph", and a "Clear graph" link. The main content area is titled "Field / Development" and features a grid of icons representing different growth conditions: Leaf\_sunrise, Leaf\_diurnal, Leaf\_sunset, Leaf\_daytime, Root\_diurnal, Leaf\_nighttime, Root\_daytime, and Root\_nighttime. Below this grid, there are two additional sections: "Reproductive organs" and "Spatio-temporal profile", each with its own icon and a small image of rice plants. The background of the page features a stylized illustration of rice plants at various stages of growth.

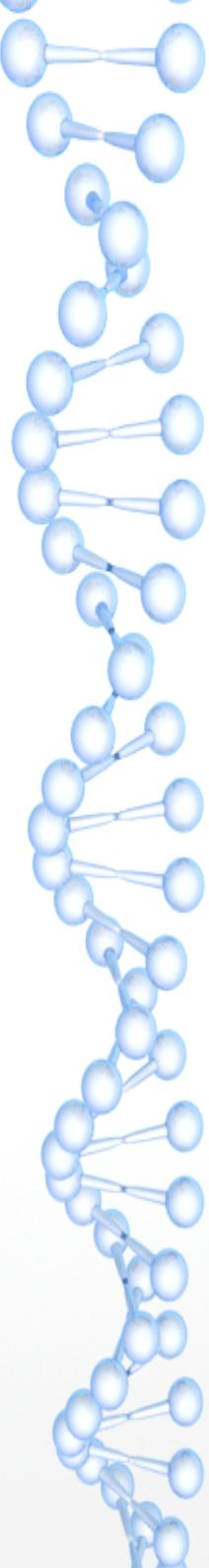


# What is the expression profile at various stages of grain ripening?

- Selecting grain ripening, I am taken to a new window that shows me the gene expression data for Os01g0101200 at various stages of grain ripening.
- The first tab is a chart of the raw signal intensity at various stages of the rice grain's development as an embryo, transitioning to an endosperm.
- The second tab shows the same data normalized.

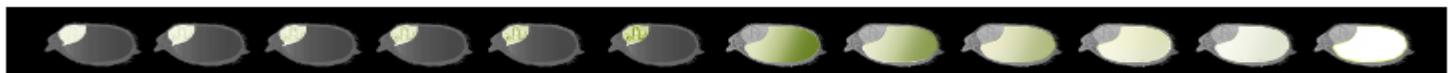
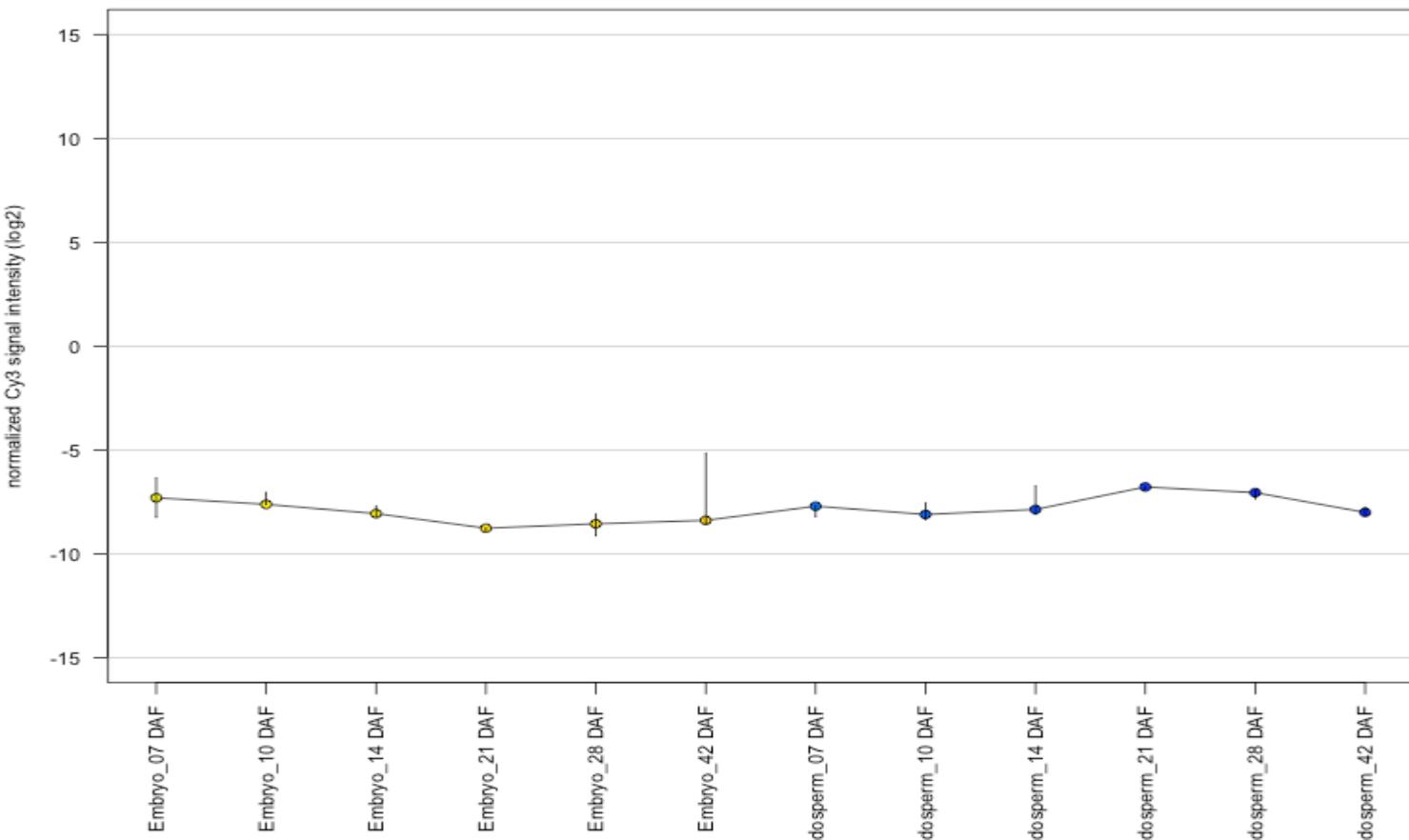
# Expression Data Raw Signal Intensity

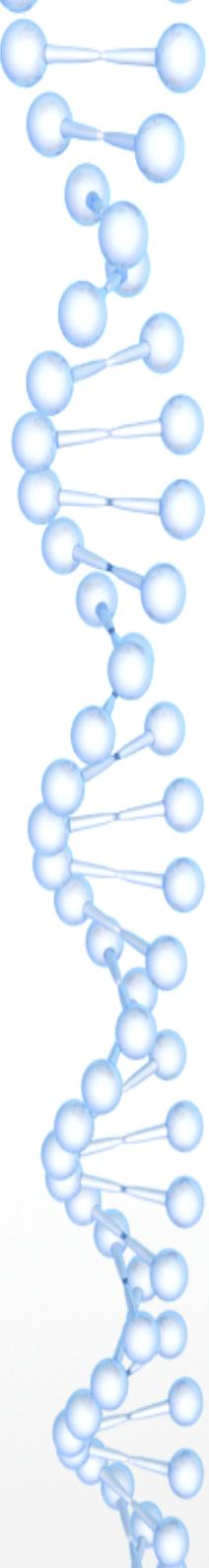




# Expression Data Normalized

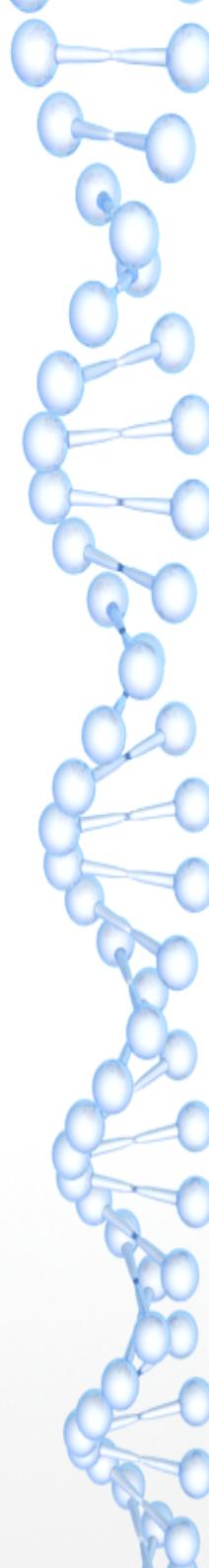
[change Y-scale of lineplot]



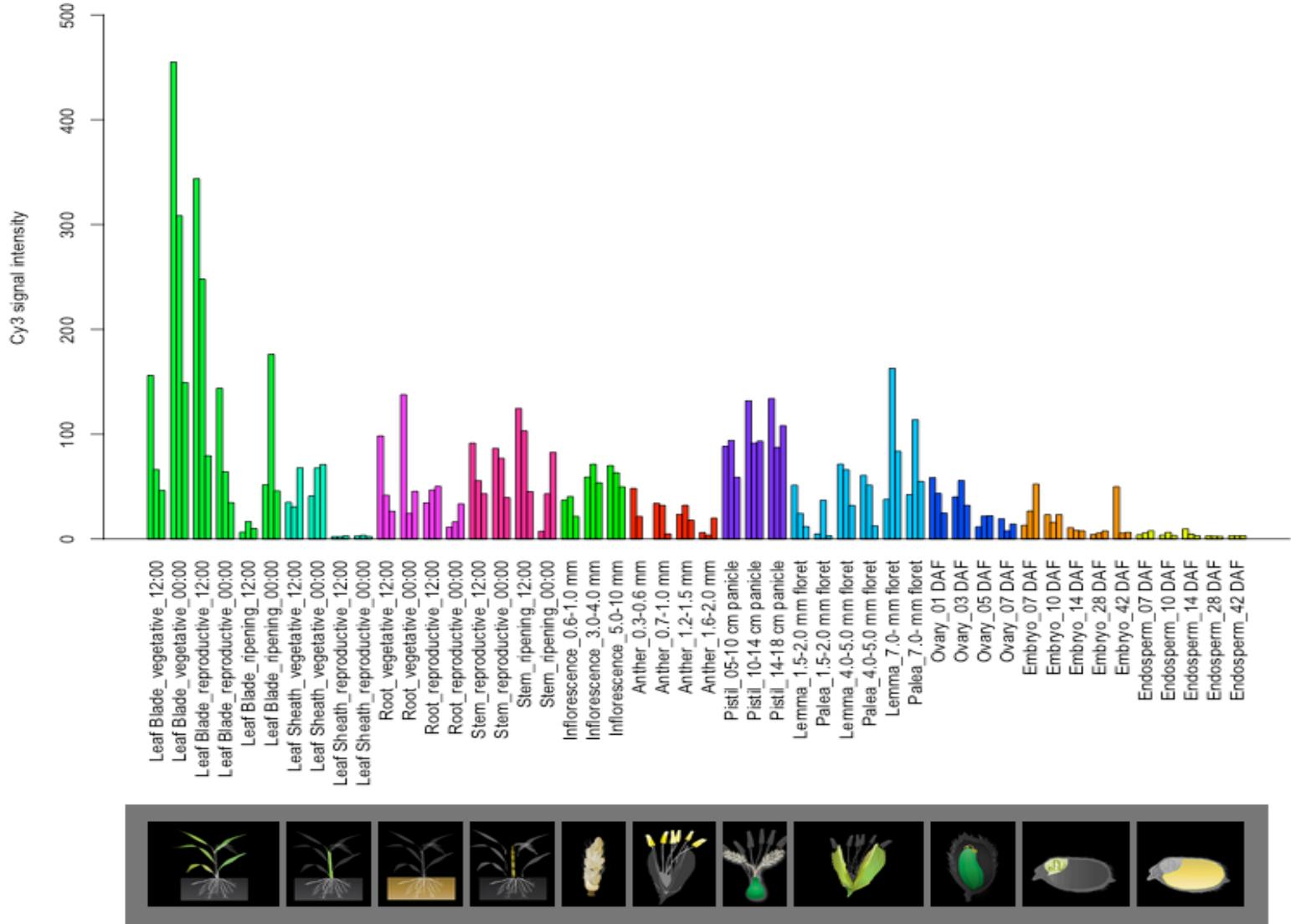


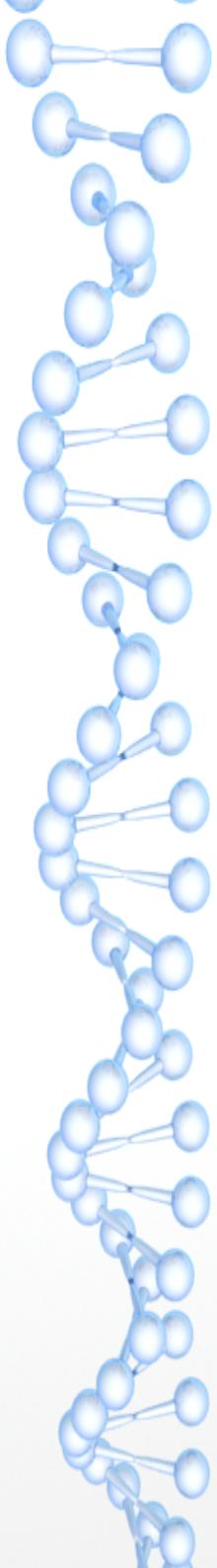
# What about across the entire plant?

- Going back to our results, we can view a spatio-temporal profile for a more complete picture of where, and at what time, expression occurs within the plant.
- Spatio-temporal data will display results from samples taken from all major parts of the plant.

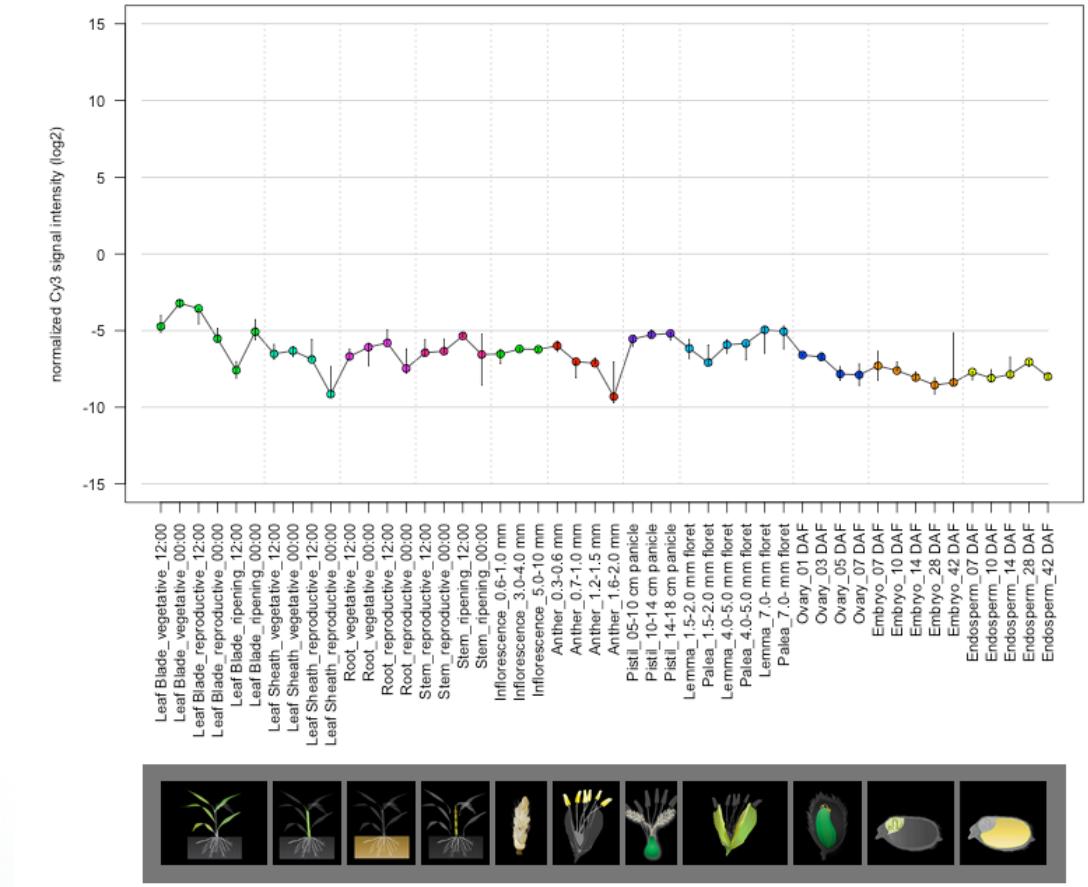


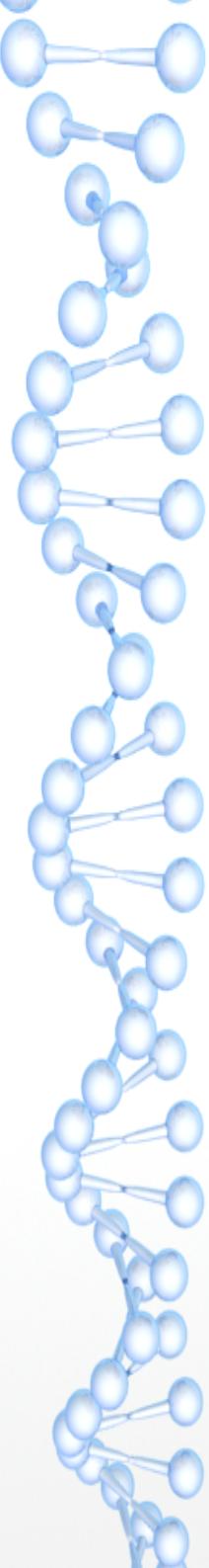
# Spatio-Temporal Profile Raw Signal Intensity





# Spatio-Temporal Profile Normalized

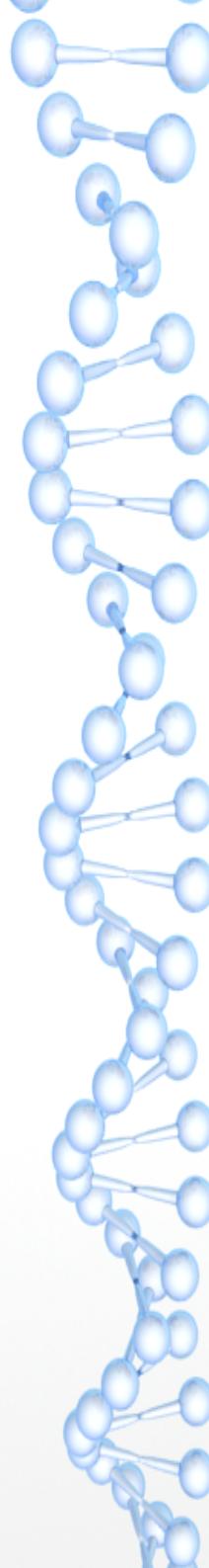




# Hormone Response

- The expression profile of all genes in root and shoot from rice seedlings treated with six plant hormones
  - abscisic acid (ABA), gibberellic acid (GA3), indole-3-acetic acid (IAA), brassinolide (BL) trans-zeatin (tZ) and jasmonic acid (JA)
- Seeds were germinated and grown hydroponically in a growth chamber at 28°C under continuous light. Seven-day old seedlings were transferred in culture solution containing the hormone and in culture solution without hormone to serve as control (mock treatment).
- Samples were collected after 15 min, 30 min, 1 h, 3 h and 6 h incubation for root with three replicates
- Samples collected 1 h, 3 h, 6 h and 12 h incubation for shoot with two replicates.
- RNA isolated from a total of 138 samples were labeled with Cy3 (mock treatment) and Cy5 (hormone treatment), and used for hybridization using the Agilent two-color microarray analysis system
- Time-course expression profile for each gene is shown as the log-ratio of signal intensity ( $\log_2 \text{Cy5/Cy3}$ ).

# Plant Hormone DB Search



**RiceXPro** RICE X PRO

Global gene expression profile in response to plant hormones

An overview of the expression profile of all genes in root and shoot from rice seedlings treated with six plant hormones, namely, abscisic acid (ABA), gibberellic acid (GA3), indole-3-acetic acid (IAA), brassinolide (BL), trans-zeatin (Z), and jasmonic acid (JA). Seeds of japonica rice cultivar Nipponbare were germinated and grown hydroponically in a growth chamber at 28°C under continuous light. Seven-day old seedlings were transferred in culture solution containing the hormone and in culture solution without hormone to serve as control (mock treatment). Samples were collected after 15 min, 30 min, 1 h, 3 h and 6 h in incubation for root with three replicates, and after 1 h, 3 h, 6 h and 12 h in incubation for shoot with two replicates ([Details of methods](#)). The RNA isolated from a total of 138 samples were labeled with Cy3 (mock treatment) and Cy5 (hormone treatment), and used for hybridization using the Agilent two-color microarray analysis system ([Sample list](#)). The time-course expression profile for each gene is shown as the log-ratio of signal intensity ( $\log_2 \text{Cy5/Cy3}$ ). Search options include keyword search for individual RAP-DB locus ID, MSU Osa1 Rice locus, and accession number, or chromosome search to get a list of all genes for each chromosome.

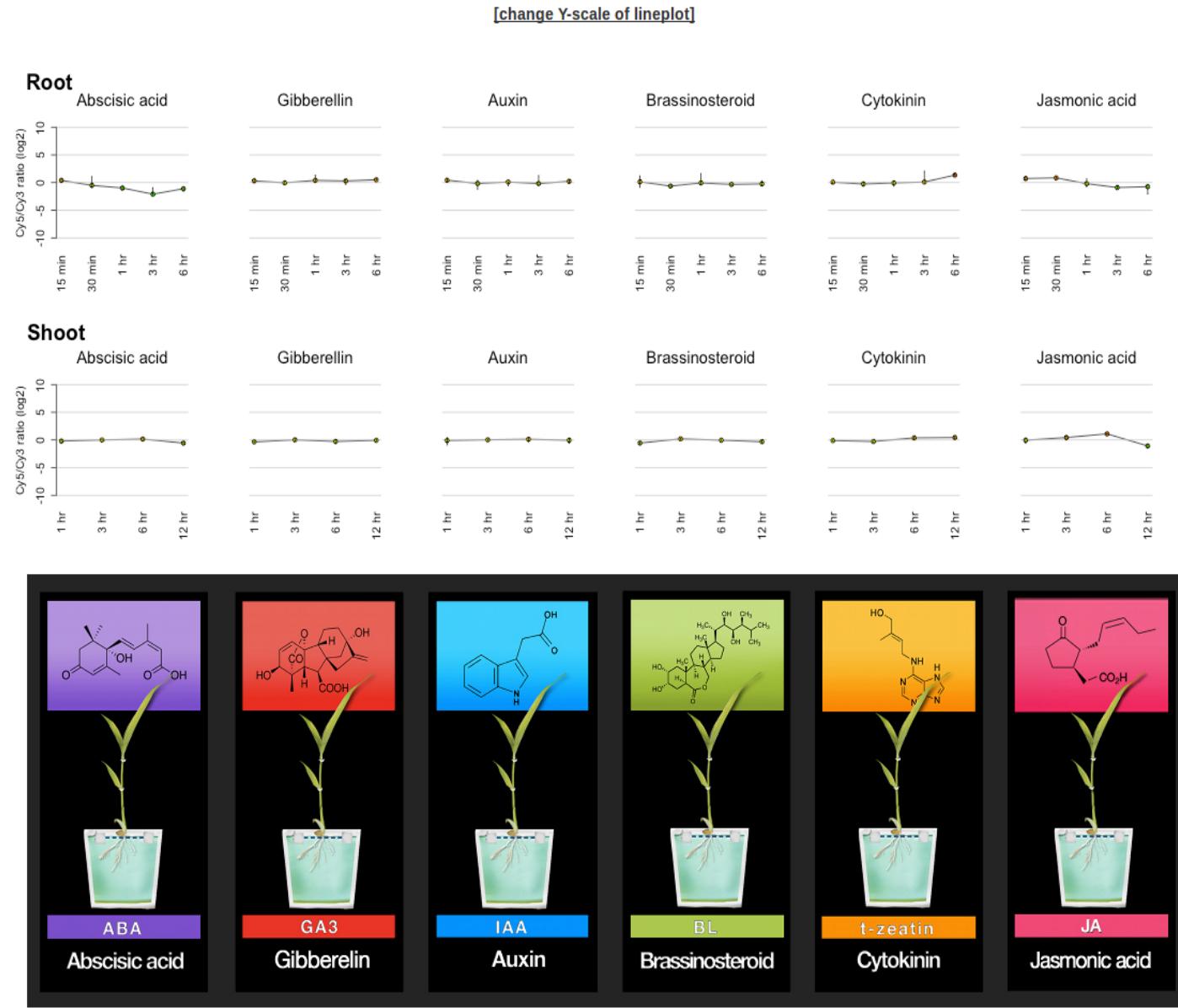
**Keyword search** [Help](#)  
Enter RAP locus ID, MSU ID, Accession number, or gene name.

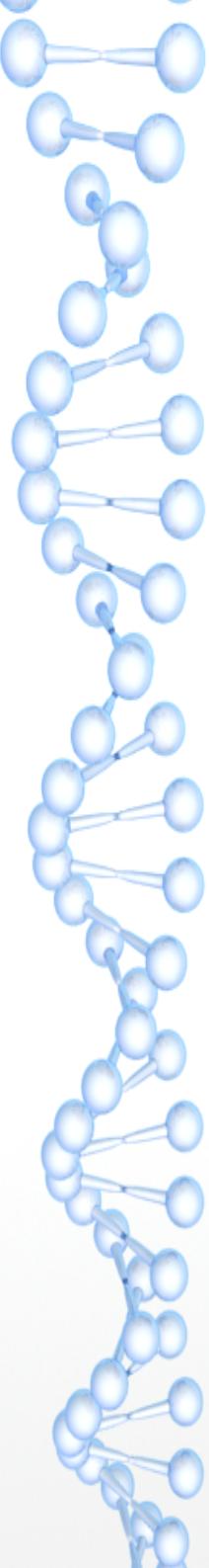
**Chromosome / Region search**  
Click a chromosome to get a tabular list of all genes in sequential order.  
[01](#) [02](#) [03](#) [04](#) [05](#) [06](#) [07](#) [08](#) [09](#) [10](#) [11](#) [12](#)

Search genes located in between two loci [Example](#)

[http://ricexpro.dna.affrc.go.jp/RXP\\_1000/index.php](#)

# Plant Hormone Search Results





# Cross-Linked Sites

- RiceXPro also provides links to various other sites to determine more information about a particular gene of interest.
  - RiceFrend
  - Rice TOGO
  - Salad
- These various resources can be accessed from the results menu when you mouse over the result link

# Link Menu

Local page, ... | Rice Express... | Rice Express... | RiceXPro | RiceXPro | Rice TOGO B... | http://...01200 | Pfam: Help | Rice Express... | Rice Genom... | Rice Express... | Rice Express... | +

<http://ricexpro.dna.affrc.go.jp/field-development.php?featurenum=4386>

RiceXPro RICEYIELD

HOME GLOBAL PROFILE DATA SETS EXP\_BLAST ExProFlip

Data Category Field / Development

Field / Development

Growth condition

Locus ID	FeatureNum	Accession	Description
Link: Plant Homolog	AK119457		2,3-diketo-5-methylthio-1-phosphopentane phosphatase domain containing protein.
Link: RiceFREN			
Link: Rice TOGO Brow			Selected graph
Link: RAP-DB			
Link: SALAD ver3.0			
Link: FIT-DB			

[Clear graph](#)

Leaf\_sunrise  

Leaf\_diurnal  

Leaf\_sunset  

Leaf\_daytime  

Root\_diurnal  

Leaf\_nighttime  

Root\_daytime  

Root\_nighttime  

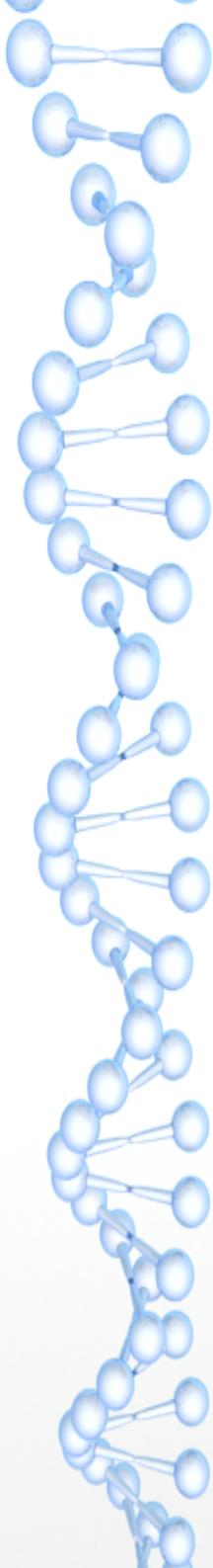


Spatio-temporal profile 

Reproductive organs  

Grain\_early stage  

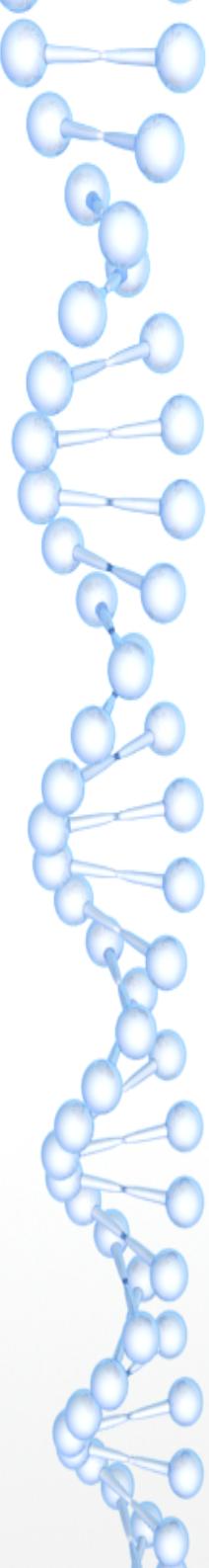
Grain ripening  

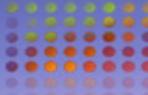


# Laser Micro-dissection

- The final DB, is the laser micro-dissection database.
- It covers the expression profile of all genes in different developmental stages along the longitudinal axis and distinct tissue types along the radial axis of a rice crown root.
- Searching this DB is performed through the same interface as the previous two databases.

# Root gene expression



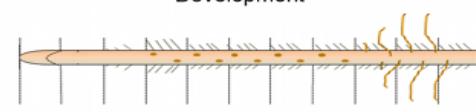
**RiceXPro** 

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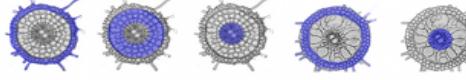
***Root gene expression profile covering various developmental stages and tissue-types***

An overview of the expression profile of all genes in different developmental stages along the longitudinal axis and distinct tissue types along the radial axis of a rice crown root. Using laser microdissection, the crown root of 10 day old seedlings was separated into 8 sections with different developmental stages from the root tip to the basal zone for 'development sub-dataset' and 3 distinct radial tissue types at 2 different developmental stages for 'tissue-type sub-dataset' ([Details of methods](#)). The RNAs isolated from a total of 13 samples ([Sample list](#)) in 3 replicates were labeled with Cy3, and used for hybridization using the Agilent one-color microarray analysis system. The expression profile for each gene is shown as raw signal intensity, normalized signal intensity (log2) and relative expression value (log2).

**Development**



**Tissue-type**

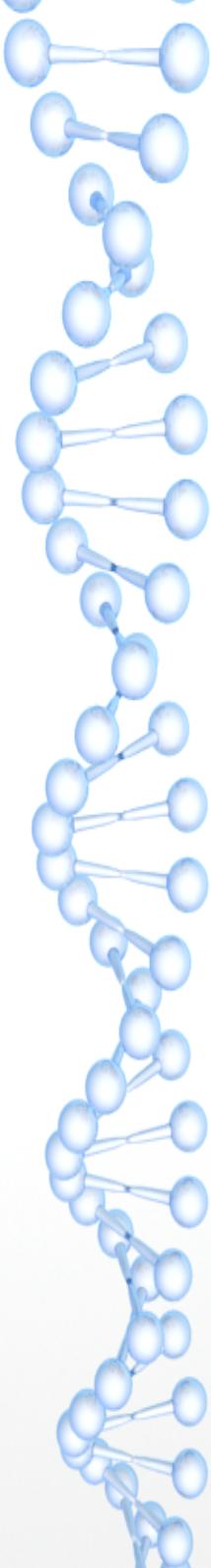


**Keyword search** [Help](#)  
Enter RAP locus ID, MSU ID, Accession number, or gene name.

**Chromosome / Region search**  
Click a chromosome to get a tabular list of all genes in sequential order.

[01](#) [02](#) [03](#) [04](#) [05](#) [06](#) [07](#) [08](#) [09](#) [10](#) [11](#) [12](#)

Search genes located in between two loci   
Locus 1  Locus 2



# Additional Result Data

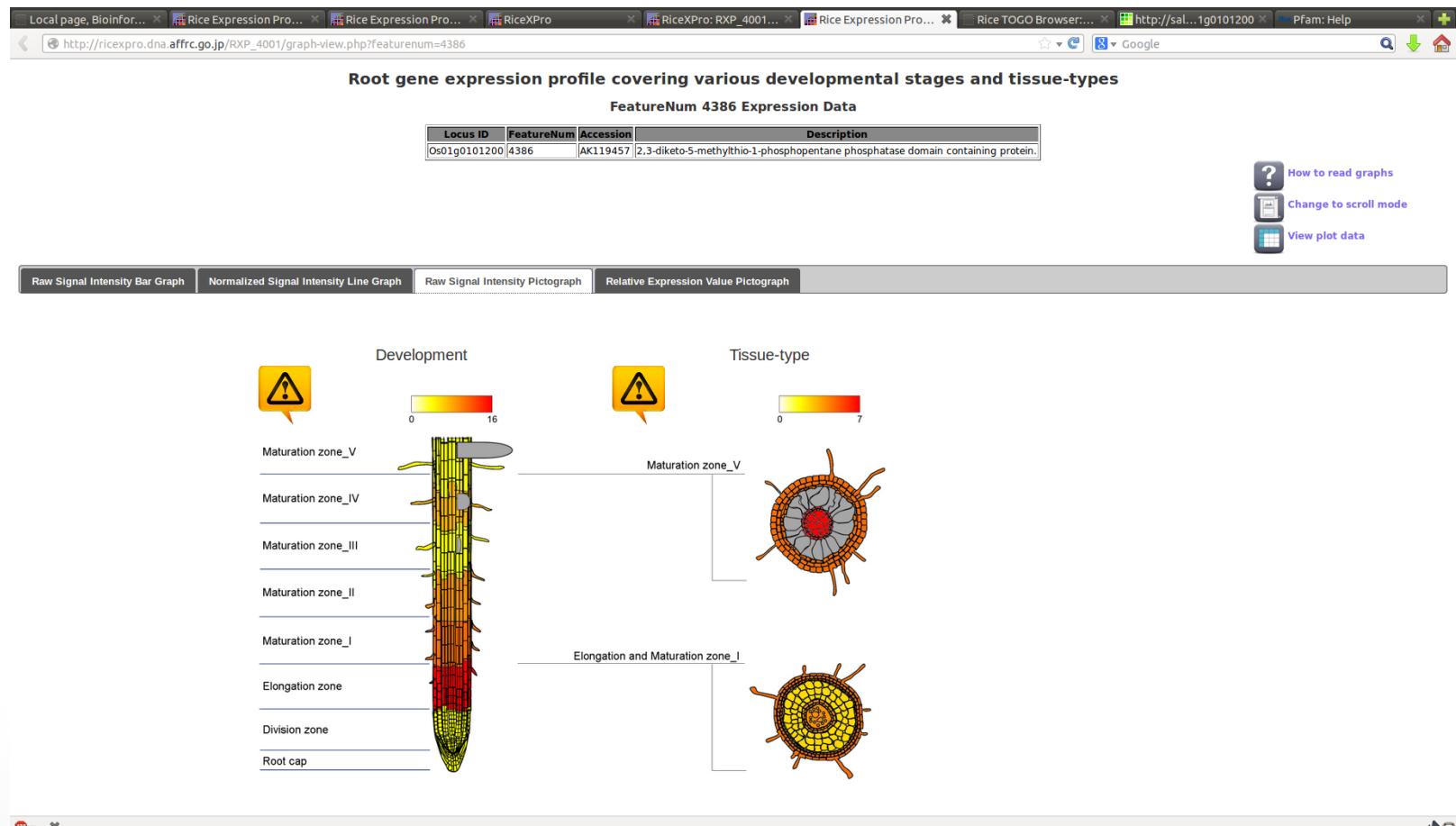
- On the next slide notice the warning graphics, denoting low signal intensity. Mousing over the warning explains the meaning of the warning in detail.
  - The raw signal intensities for these results all had median values of less than 50, generating a warning in the upper left of the graph.
- There are also pictograph tabs available, showing raw signal and expression data in relation to the location of a sample on the root.

# Results for root gene expression

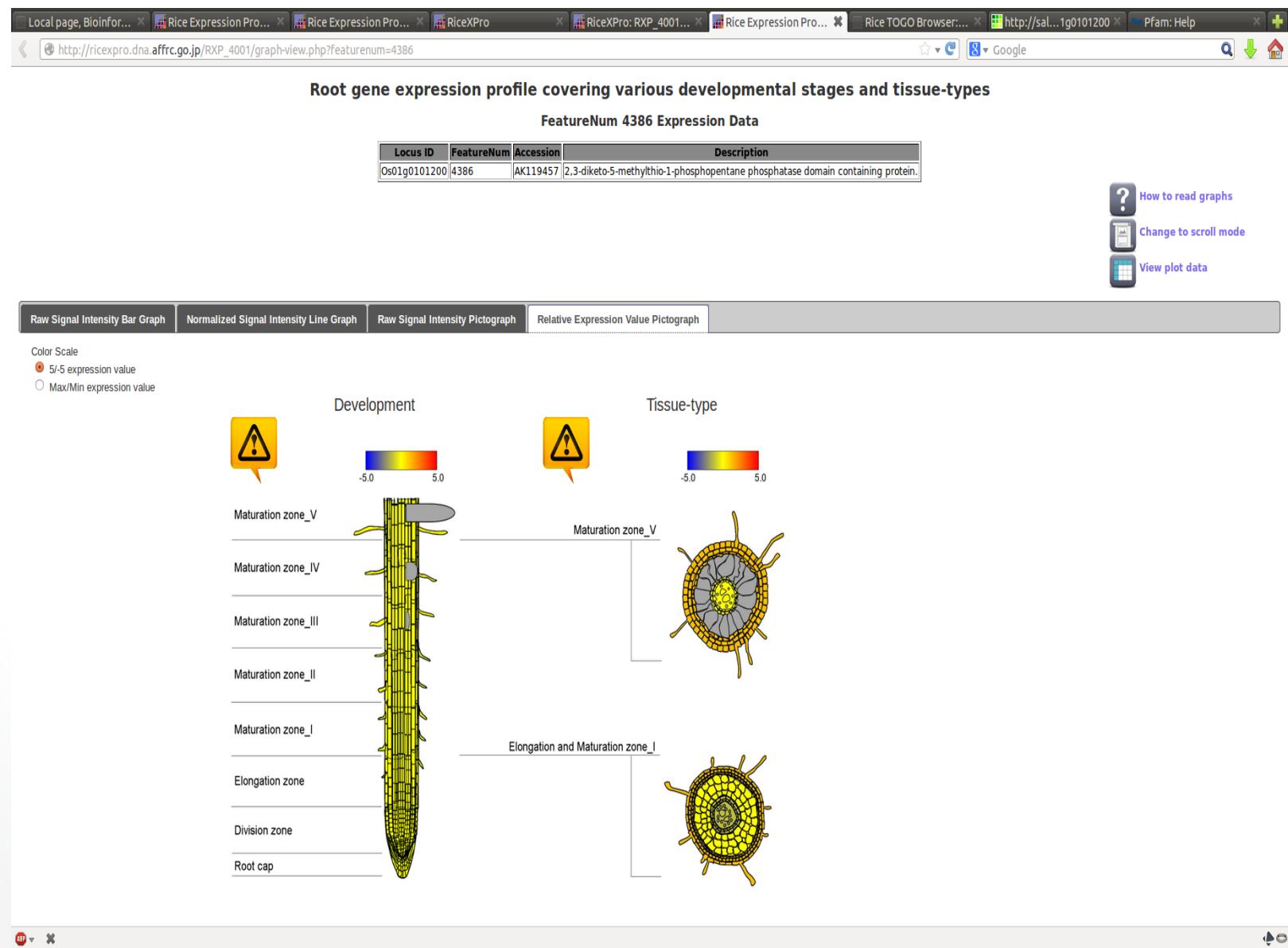
## Raw Signal Intensity

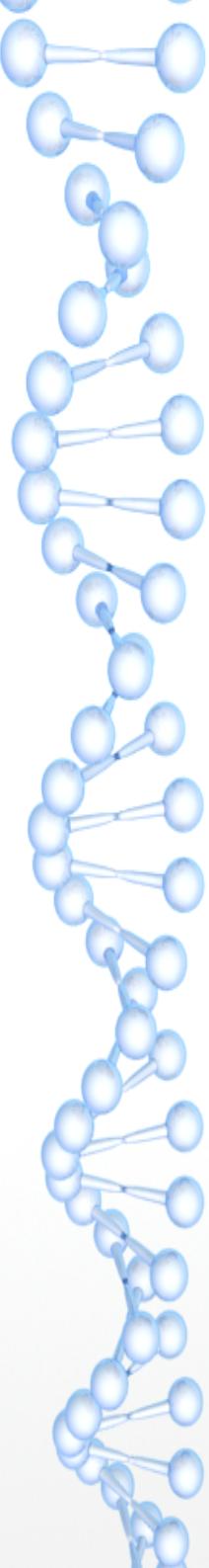


# Raw Signal Intensity Pictograph



# Relative Expression





# ExProFlip

- One of the neat features available is ExProFlip, which allow you to query several databases (or all databases) at once and then flip through the resulting data as a slide-show in the browser.
- I found this feature to be useful when examining various aspects of a gene
- Field/Development, Hormone response and Laser Dissection results could be viewed as a whole with a single search!

# ExProFlip (continued)

**RiceXPro**

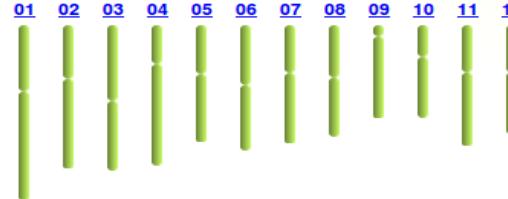
HOME GLOBAL PROFILE DATA SETS EXP\_BLAST ExProFlip

## ExProFlip

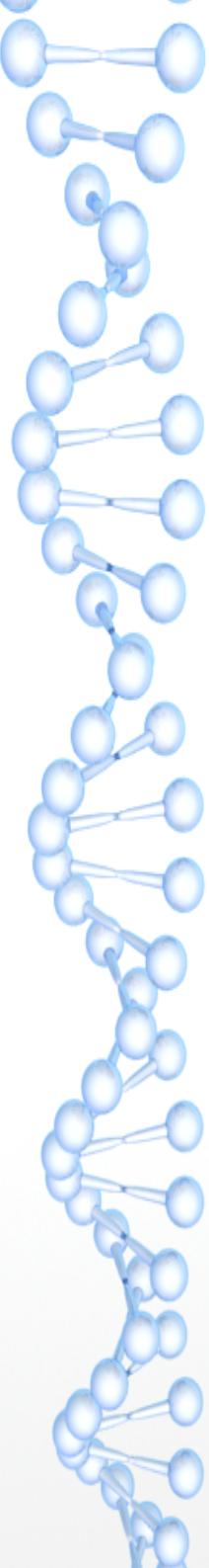
The ExProFlip function allows the user to effectively survey a number of expression profiles across different dataset(s) and/or gene(s) by flipping view of graph. Preferred dataset(s) can be selected and ExProFlip is initiated from the search options such as keyword search and chromosome/region search.

<b>Field / Development</b> <input type="checkbox"/> All select <input type="checkbox"/> RXP_0001 <a href="#">Spatio-temporal profile</a> <input type="checkbox"/> RXP_0002 <a href="#">Leaf diurnal</a> <input type="checkbox"/> RXP_0003 <a href="#">Leaf daytime</a> <input type="checkbox"/> RXP_0004 <a href="#">Leaf nighttime</a> <input type="checkbox"/> RXP_0005 <a href="#">Leaf sunrise</a> <input type="checkbox"/> RXP_0006 <a href="#">Leaf sunset</a> <input type="checkbox"/> RXP_0007 <a href="#">Root daytime</a> <input type="checkbox"/> RXP_0008 <a href="#">Root nighttime</a> <input type="checkbox"/> RXP_0009 <a href="#">Root diurnal</a> <input type="checkbox"/> RXP_0010 <a href="#">Reproductive organs</a> <input type="checkbox"/> RXP_0011 <a href="#">Grain early stage</a> <input type="checkbox"/> RXP_0012 <a href="#">Grain ripening</a>	<b>Plant Hormone</b> <input type="checkbox"/> All select <input type="checkbox"/> RXP_1000 <a href="#">Hormones</a> <input type="checkbox"/> RXP_1001 <a href="#">Abscisic acid_root</a> <input type="checkbox"/> RXP_1006 <a href="#">Abscisic acid_shoot</a> <input type="checkbox"/> RXP_1002 <a href="#">Gibberellin_root</a> <input type="checkbox"/> RXP_1007 <a href="#">Gibberellin_shoot</a> <input type="checkbox"/> RXP_1003 <a href="#">Auxin_root</a> <input type="checkbox"/> RXP_1008 <a href="#">Auxin_shoot</a> <input type="checkbox"/> RXP_1004 <a href="#">Brassinosteroid_root</a> <input type="checkbox"/> RXP_1009 <a href="#">Brassinosteroid_shoot</a> <input type="checkbox"/> RXP_1005 <a href="#">Cytokinin_root</a> <input type="checkbox"/> RXP_1010 <a href="#">Cytokinin_shoot</a> <input type="checkbox"/> RXP_1011 <a href="#">Jasmonic acid_root</a> <input type="checkbox"/> RXP_1012 <a href="#">Jasmonic acid_shoot</a>	<b>Cell- and Tissue-Type (Laser Microdissection)</b> <input type="checkbox"/> RXP_4001 <a href="#">LM_Root development</a>
---	---	---

**Keyword search** [Help](#)  
Enter RAP locus ID, MSU ID, Accession number, or gene name.

**Chromosome / Region search**  
Click a chromosome to get a tabular list of all genes in sequential order.  
  
 [Example](#)  
Locus 1  Locus 2

# More ExProFlip



**RiceXPro**

HOME GLOBAL PROFILE DATA SETS EXP\_BLAST ExProFlip

## Search Result: ExProFlip

[\[Back to search page\]](#)

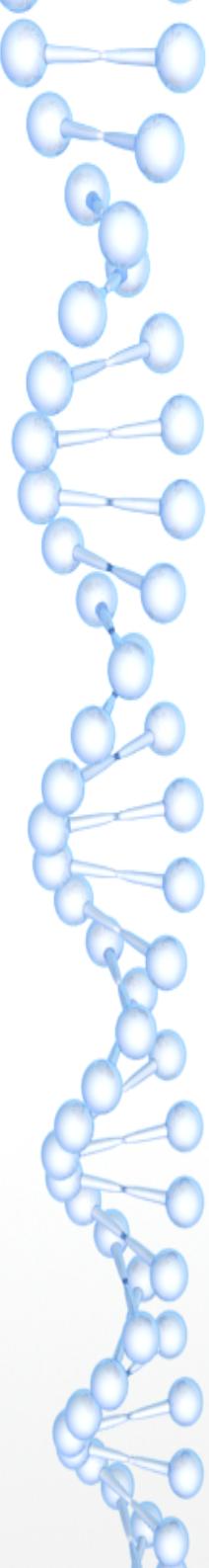
Search dataset:[RXP\_0001,RXP\_0002,RXP\_0003,RXP\_0004,RXP\_0005,RXP\_0006,RXP\_0007,RXP\_0008,RXP\_0009,RXP\_0010,RXP\_0011,RXP\_0012]  
Search keyword:["os01g0102700" OR "loc\_os01g01070" OR "ak067670"]  
3 loci found 1-3 listed of 3

[ExProFlip start](#)

Locus ID / Links	FeatureNum (Link to graph)	Accession	Probe Sequence ID (Link to SeqInfo)	Description	MSU ID
<a href="#">Os01g0100</a>	<a href="#">Os01g0100800</a>	AK122012	<a href="#">S-18431</a> (unique)	Protein of unknown function DUF1664 family protein.	<a href="#">LOC_Os01g01070</a>
<a href="#">Os01g0102</a>	Link: Field / Development Link: Plant Hormone Link: RiceFREN Link: Rice TOGO Browser	AK063774	<a href="#">S-14818</a> (unique)	Translocon-associated beta family protein.	<a href="#">LOC_Os01g01307</a>
<a href="#">Os01g0102</a>	Link: RAP-DB Link: SALAD ver3.0 Link: FIT-DB	AK099081 AK099360 AK067670	<a href="#">S-16540</a> (unique) <a href="#">S-29011</a> (unique) <a href="#">S-17781</a> (unique)	Translocon-associated beta family protein. Translocon-associated beta family protein. Light regulated Lir1 family protein.	<a href="#">LOC_Os01g01307</a> <a href="#">LOC_Os01g01307</a> <a href="#">LOC_Os01g01340</a>

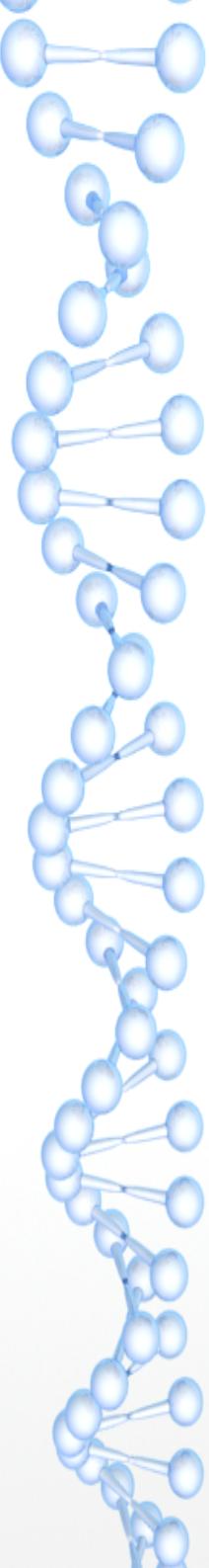
# What clicking ExProFlip will do





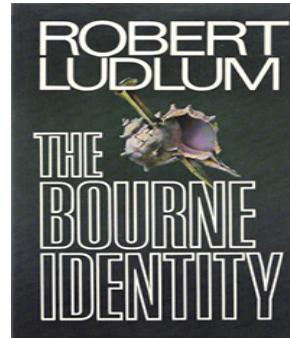
# Analysis Tools

- RiceXPro provides information on co-expressed genes
- Co-expression data based on calculation of Pearson's correlation coefficients ( $r$ -values) of the normalized signal intensities ( $\log_2$ ) in each data set
- T-test & fold change (FC) analysis
- Heatmap toolkit

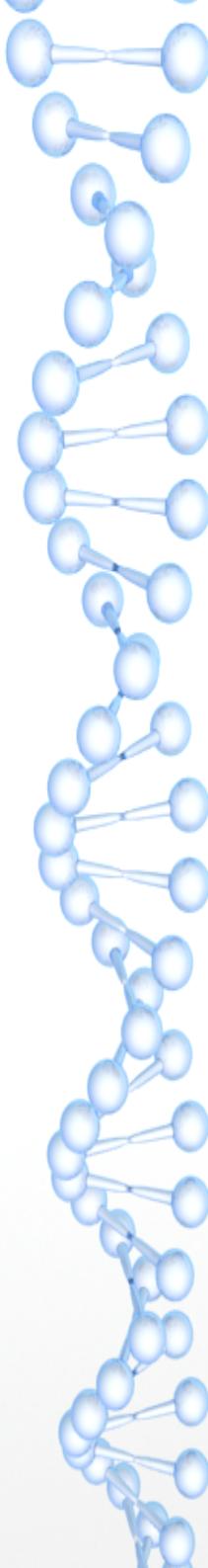


# More on Pearson

- The Pearson correlation
- Not to be confused with:

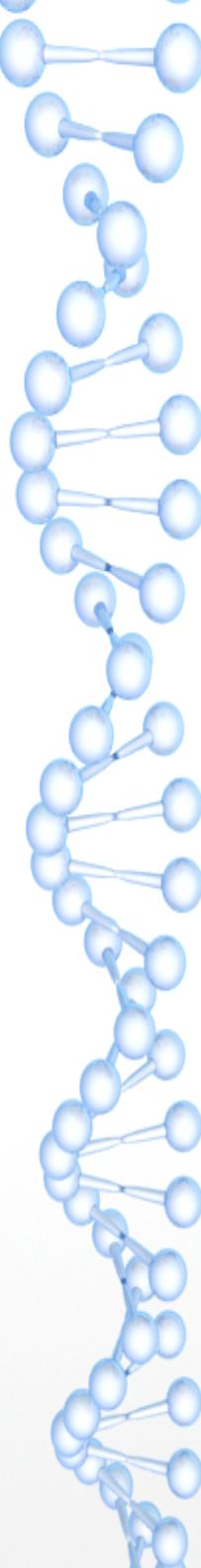


- +1 in the case of a perfect positive (increasing) linear relationship (correlation)
- -1 in the case of a perfect decreasing (negative) linear relationship (anti-correlation)
- some value between -1 and 1 in all other cases, indicating the degree of linear dependence between the variables.
- As it approaches zero there is less of a relationship (closer to uncorrelated). The closer the coefficient is to either -1 or 1, the stronger the correlation between the variables.



# Searching a specific dataset

- Previously we utilized Global profile
- We can also get more in depth information by querying a distinct dataset
- Selecting datasets from the main page let's choose a particular dataset to query.



## Data Sets

This database provides an overview of the expression pattern of all rice genes in specific tissues/organs at various stages of growth and development under normal field conditions, rice plants treated with various phytohormones, and cell/tissue types isolated by laser microdissection( LMD) . The gene expression profiles are presented as data sets from specific samples, experiments, or treatment conditions. The Data Table includes a list of samples used for microarray analysis and other relevant information that maybe useful in interpretation of gene expression levels.

### Field / Development

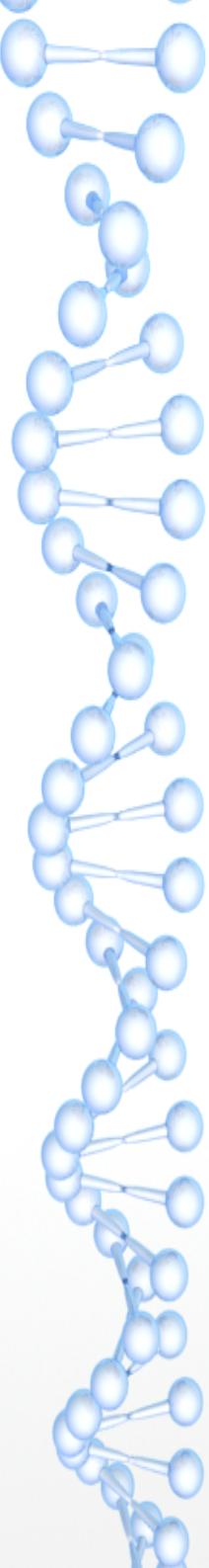
<a href="#">RXP_0001</a>	Spatio-temporal gene expression of various tissues/organs throughout entire growth in the field	<a href="#">Sample list</a>
<a href="#">RXP_0002</a>	Diurnal and circadian gene expression profile of leaf throughout entire growth	<a href="#">Sample list</a>
<a href="#">RXP_0003</a>	Leaf gene expression profile throughout entire growth in the field (12:00)	<a href="#">Sample list</a>
<a href="#">RXP_0004</a>	Leaf gene expression profile throughout entire growth in the field (00:00)	<a href="#">Sample list</a>
<a href="#">RXP_0005</a>	Leaf gene expression profile during sunrise	<a href="#">Sample list</a>
<a href="#">RXP_0006</a>	Leaf gene expression profile during sunset	<a href="#">Sample list</a>
<a href="#">RXP_0007</a>	Root gene expression profile throughout entire growth in the field (12:00)	<a href="#">Sample list</a>
<a href="#">RXP_0008</a>	Root gene expression profile throughout entire growth in the field (00:00)	<a href="#">Sample list</a>
<a href="#">RXP_0009</a>	Diurnal and circadian gene expression profile of root	<a href="#">Sample list</a>
<a href="#">RXP_0010</a>	Gene expression profile during reproductive organ development	<a href="#">Sample list</a>
<a href="#">RXP_0011</a>	Grain gene expression profile at early developmental stage	<a href="#">Sample list</a>
<a href="#">RXP_0012</a>	Embryo and Endosperm gene expression profile at ripening stage	<a href="#">Sample list</a>

### Plant Hormone

Hormones	<a href="#">RXP_1000</a>	Global gene expression profile in response to plant hormones	<a href="#">Sample list</a>
Abscisic acid	<a href="#">RXP_1001</a>	Root gene expression profile in response to abscisic acid	<a href="#">Sample list</a>
	<a href="#">RXP_1006</a>	Shoot gene expression profile in response to abscisic acid	<a href="#">Sample list</a>
Gibberellin	<a href="#">RXP_1002</a>	Root gene expression profile in response to gibberellin	<a href="#">Sample list</a>
	<a href="#">RXP_1007</a>	Shoot gene expression profile in response to gibberellin	<a href="#">Sample list</a>
Auxin	<a href="#">RXP_1003</a>	Root gene expression profile in response to auxin	<a href="#">Sample list</a>
	<a href="#">RXP_1008</a>	Shoot gene expression profile in response to auxin	<a href="#">Sample list</a>
Brassinosteroid	<a href="#">RXP_1004</a>	Root gene expression profile in response to brassinosteroid	<a href="#">Sample list</a>
	<a href="#">RXP_1009</a>	Shoot gene expression profile in response to brassinosteroid	<a href="#">Sample list</a>
Cytokinin	<a href="#">RXP_1005</a>	Root gene expression profile in response to cytokinin	<a href="#">Sample list</a>
	<a href="#">RXP_1010</a>	Shoot gene expression profile in response to cytokinin	<a href="#">Sample list</a>
Jasmonic acid	<a href="#">RXP_1011</a>	Root gene expression profile in response to jasmonic acid	<a href="#">Sample list</a>
	<a href="#">RXP_1012</a>	Shoot gene expression profile in response to jasmonic acid	<a href="#">Sample list</a>

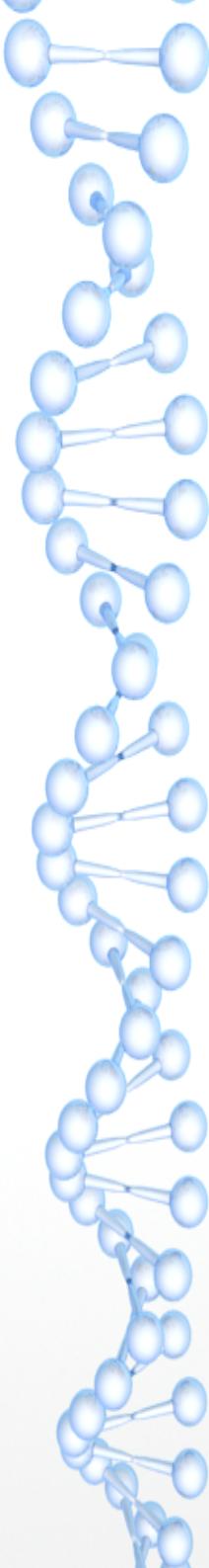
### Cell- and Tissue-Type (Laser Microdissection)

<a href="#">RXP_4001</a>	Root gene expression profile covering various developmental stages and tissue-types	<a href="#">Sample list</a>
--------------------------	---	-----------------------------



# Co-expression Analysis

- Choosing datasets and then selecting **RXP\_0001** we get taken to a similar search page as before
- Clicking on analysis tools takes us to more options



## Analysis Tools

[\[Back to search page\]](#)

### Correlation analysis

Enter a RAP locus ID or accession number and click submit. Please wait for about a few seconds for the results.

Os01g0100100

Submit

### T-test & fold change (FC) analysis

Select a data as control and another data to be used for comparison by clicking the corresponding radio buttons from the list of samples. Then specify the p-value and fold change from the pull-down menu, and click submit. Please wait for a few seconds for the results.

p-value

< 0.01

FC

> 10

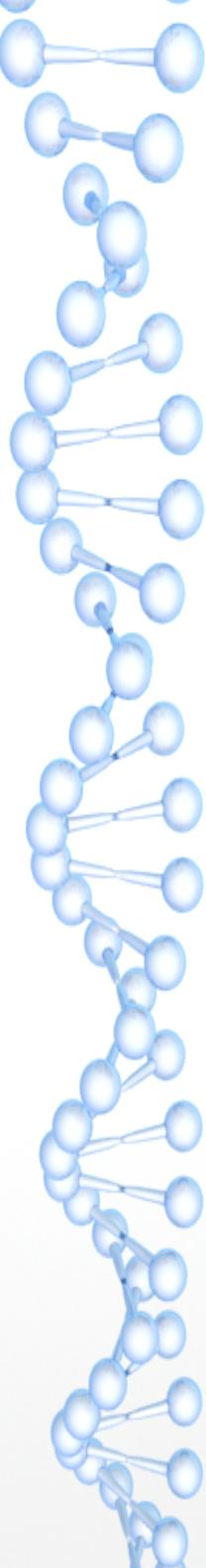
= 3.32 (log<sub>2</sub> scale)

Submit

Reset

Sample ID	Control	Test
Leaf blade_vegetative_12:00	<input checked="" type="radio"/>	<input type="radio"/>
Leaf blade_vegetative_00:00	<input type="radio"/>	<input checked="" type="radio"/>
Leaf blade_reproductive_12:00	<input type="radio"/>	<input type="radio"/>
Leaf blade_reproductive_00:00	<input type="radio"/>	<input type="radio"/>
Leaf blade_ripening_12:00	<input type="radio"/>	<input type="radio"/>
Leaf blade_ripening_00:00	<input type="radio"/>	<input type="radio"/>
Leaf sheath_vegetative_12:00	<input type="radio"/>	<input type="radio"/>
Leaf sheath_vegetative_00:00	<input type="radio"/>	<input type="radio"/>
Leaf sheath_reproductive_12:00	<input type="radio"/>	<input type="radio"/>
Leaf sheath_reproductive_00:00	<input type="radio"/>	<input type="radio"/>
Root_vegetative_12:00	<input type="radio"/>	<input type="radio"/>
Root_vegetative_00:00	<input type="radio"/>	<input type="radio"/>
Root_reproductive_12:00	<input type="radio"/>	<input type="radio"/>
Root_reproductive_00:00	<input type="radio"/>	<input type="radio"/>
Stem_reproductive_12:00	<input type="radio"/>	<input type="radio"/>
Stem_reproductive_00:00	<input type="radio"/>	<input type="radio"/>
Stem_ripening_12:00	<input type="radio"/>	<input type="radio"/>
Stem_ripening_00:00	<input type="radio"/>	<input type="radio"/>
Inflorescence_0.6-1.0 mm	<input type="radio"/>	<input type="radio"/>
Inflorescence_3.0-4.0 mm	<input type="radio"/>	<input type="radio"/>
Inflorescence_5.0-10.0 mm	<input type="radio"/>	<input type="radio"/>
Anther_0.3-0.6 mm	<input type="radio"/>	<input type="radio"/>
Anther_0.7-1.0 mm	<input type="radio"/>	<input type="radio"/>
Anther_1.2-1.5 mm	<input type="radio"/>	<input type="radio"/>

Sample ID	Control	Test
Anther_1.6-2.0 mm	<input type="radio"/>	<input type="radio"/>
Pistil_5-10 cm panicle	<input type="radio"/>	<input type="radio"/>
Pistil_10-14 cm panicle	<input type="radio"/>	<input type="radio"/>
Pistil_14-18 cm panicle	<input type="radio"/>	<input type="radio"/>
Lemma_1.5-2.0 mm floret	<input type="radio"/>	<input type="radio"/>
Palea_1.5-2.0 mm floret	<input type="radio"/>	<input type="radio"/>
Lemma_4.0-5.0 mm floret	<input type="radio"/>	<input type="radio"/>
Palea_4.0-5.0 mm floret	<input type="radio"/>	<input type="radio"/>
Lemma_7.0 mm floret	<input type="radio"/>	<input type="radio"/>
Palea_7.0 mm floret	<input type="radio"/>	<input type="radio"/>
Ovary_01 DAF	<input type="radio"/>	<input type="radio"/>
Ovary_03 DAF	<input type="radio"/>	<input type="radio"/>
Ovary_05 DAF	<input type="radio"/>	<input type="radio"/>
Ovary_07 DAF	<input type="radio"/>	<input type="radio"/>
Embryo_07 DAF	<input type="radio"/>	<input type="radio"/>
Embryo_10 DAF	<input type="radio"/>	<input type="radio"/>
Embryo_14 DAF	<input type="radio"/>	<input type="radio"/>
Embryo_28 DAF	<input type="radio"/>	<input type="radio"/>
Embryo_42 DAF	<input type="radio"/>	<input type="radio"/>
Endosperm_07 DAF	<input type="radio"/>	<input type="radio"/>
Endosperm_10 DAF	<input type="radio"/>	<input type="radio"/>
Endosperm_14 DAF	<input type="radio"/>	<input type="radio"/>
Endosperm_28 DAF	<input type="radio"/>	<input type="radio"/>
Endosperm_42 DAF	<input type="radio"/>	<input type="radio"/>



# Searching data for significance

- Entering the Locus of interest and selecting data sets as control and test
- In statistical significance testing, the **p-value** is the probability of obtaining a test statistic at least as extreme as the one that was actually observed.
- A researcher will often "reject the null hypothesis" when the p-value turns out to be less than a certain significance level, often 0.05 or 0.01. Such a result indicates that the observed result would be highly unlikely under the null hypothesis (that is, the observation is highly unlikely to be the result of random chance alone)
- **Fold change** is a measure describing how much a quantity changes going from an initial to a final value. For example, an initial value of 30 and a final value of 60 corresponds to a fold change of 2, or in common terms, a two-fold increase. Fold change is calculated simply as the ratio of the final value to the initial value

# T-Test & fold change (FC) Analysis Results: Spatio-temporal gene expression of various tissues/organs throughout entire growth in the field

[Back to Analysis Tools]

Search: p-value<0.01, FC>10, control:Leaf blade\_vegetative\_12:00, test:Leaf blade\_vegetative\_00:00

1-100 listed of 180

[First](#) [1](#) [2](#) [Last](#)

Download graph

Construct a heatmap

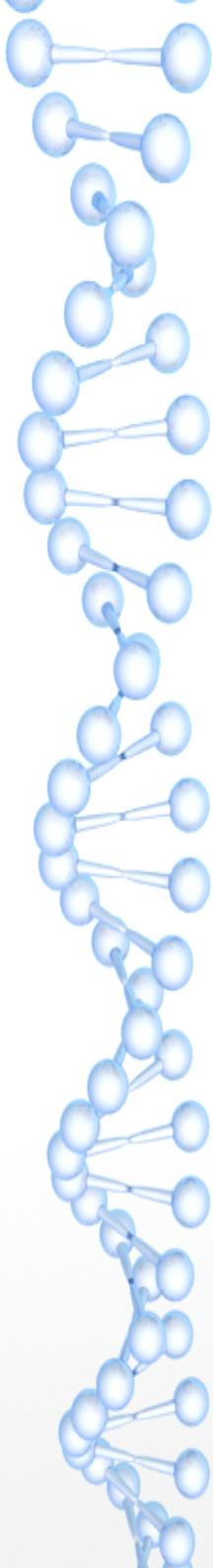
All Select

Download sequences

[\[help\]](#)

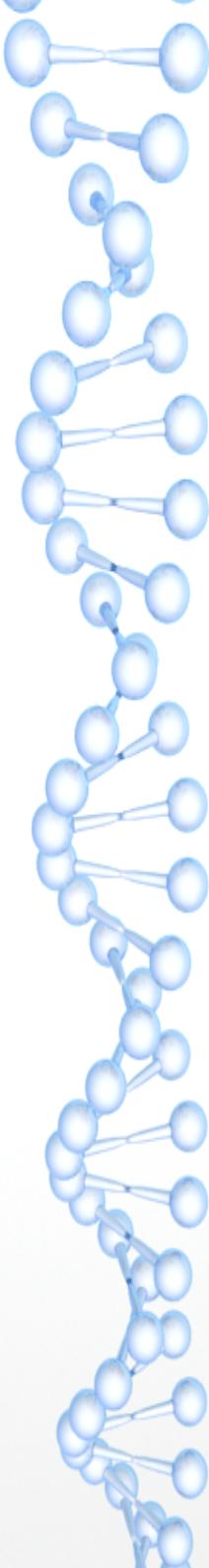
Result download

Locus ID / Links	FeatureNum (Link to graph)	Select	Accession	Probe Sequence ID (Link to SeqInfo)	Description	Fold Change	T-Test p-value	MSU ID
<a href="#">Os04g0583900</a>	<a href="#">41367</a>	<input type="checkbox"/>	AK101209	<a href="#">S-33320</a> (unique)	Similar to LHY protein.	767.409	0.0000112	<a href="#">LOC_Os04g49450</a>
<a href="#">Os08g0520700</a>	<a href="#">34368</a>	<input checked="" type="checkbox"/>	AK060548	<a href="#">S-28044</a> (unique)	Conserved hypothetical protein.	602.480	0.0004010	<a href="#">LOC_Os08g40919</a>
<a href="#">Os10g0565200</a>	<a href="#">17363</a>	<input type="checkbox"/>	CI411567	<a href="#">S-14560</a> (unique)	Similar to Beta-amylase PCT-BMYI (EC 3.2.1.2).	577.648	0.0000706	<a href="#">LOC_Os10g41550</a>
<a href="#">Os04g0119000</a>	<a href="#">23888</a>	<input checked="" type="checkbox"/>	AK062143	<a href="#">S-19829</a> (unique)	Conserved hypothetical protein.	214.249	0.0001046	<a href="#">LOC_Os04g02880</a>
<a href="#">Os02g0685200</a>	<a href="#">2161</a>	<input type="checkbox"/>	AK111726	<a href="#">S-1686</a> (unique)	Homeodomain-like containing protein.	199.399	0.0000007	<a href="#">LOC_Os02g46030</a>
<a href="#">Os04g0119000</a>	<a href="#">23634</a>	<input checked="" type="checkbox"/>	AK120328	<a href="#">S-19639</a> (unique)	Conserved hypothetical protein.	184.070	0.0005601	<a href="#">LOC_Os04g02880</a>
<a href="#">Os10g0330400</a>	<a href="#">33415</a>	<input type="checkbox"/>	AK109353	<a href="#">S-18017</a> (non-unique)	Protein of unknown function DUF179 family protein.	160.849	0.0000947	<a href="#">LOC_Os10g18370</a>
<a href="#">Os10g0330400</a>	<a href="#">21921</a>	<input type="checkbox"/>	AK099421	<a href="#">S-18244</a> (unique)	Protein of unknown function DUF179 family protein.	159.781	0.0000438	<a href="#">LOC_Os10g18370</a>
<a href="#">Os10g0330400</a>	<a href="#">21643</a>	<input type="checkbox"/>	AK105880	<a href="#">S-18017</a> (non-unique)	Protein of unknown function DUF179 family protein.	144.206	0.0002055	<a href="#">LOC_Os10g18370</a>
<a href="#">Os10g0330400</a>	<a href="#">3188</a>	<input type="checkbox"/>	AK061323	<a href="#">S-2579</a> (unique)	Protein of unknown function DUF179 family protein.	105.441	0.0000439	<a href="#">LOC_Os10g18370</a>
<a href="#">Os06g0298200</a>	<a href="#">9812</a>	<input type="checkbox"/>	AK072192	<a href="#">S-8326</a> (unique)	Similar to Oryza sativa (indica cultivar-group) Hd1.	96.637	0.0000072	<a href="#">LOC_Os06g19444</a>
<a href="#">Os06g0298200</a>	<a href="#">27899</a>	<input type="checkbox"/>	AK121630	<a href="#">S-23017</a> (non-unique)	Similar to Oryza sativa (indica cultivar-group) Hd1.	87.142	0.0001651	<a href="#">LOC_Os06g19444</a>
<a href="#">Os03g0765400</a>	<a href="#">12398</a>	<input type="checkbox"/>	AK065267	<a href="#">S-10474</a> (unique)	Conserved hypothetical protein.	81.304	0.0000867	<a href="#">LOC_Os03g55670</a> <a href="#">LOC_Os03g55660</a>
<a href="#">Os06g0298200</a>	<a href="#">29312</a>	<input type="checkbox"/>	AK098865	<a href="#">S-23017</a> (non-unique)	Similar to Oryza sativa (indica cultivar-group) Hd1.	77.326	0.0012570	<a href="#">LOC_Os06g19444</a>
<a href="#">Os01g0702000</a>	<a href="#">17469</a>	<input type="checkbox"/>	AK065414	<a href="#">S-14639</a> (unique)	Protein of unknown function DUF151 domain containing protein.	54.579	0.0026313	<a href="#">LOC_Os01g50622</a>
<a href="#">Os04g0583200</a>	<a href="#">7118</a>	<input type="checkbox"/>	AK073181	<a href="#">S-6013</a> (unique)	Conserved hypothetical protein.	52.553	0.0002772	<a href="#">LOC_Os04g49370</a>
<a href="#">Os08g0520700</a>	<a href="#">33511</a>	<input type="checkbox"/>	AK122042	<a href="#">S-27369</a> (unique)	Conserved hypothetical protein.	51.974	0.0009084	<a href="#">LOC_Os08g40919</a>
<a href="#">Os02g0724000</a>	<a href="#">34449</a>	<input type="checkbox"/>	AB001888	<a href="#">S-28106</a> (unique)	Zinc finger, B-box domain containing protein.	51.893	0.0002090	<a href="#">LOC_Os02g49230</a>
<a href="#">Os02g0724000</a>	<a href="#">40607</a>	<input type="checkbox"/>	AK071630	<a href="#">S-32754</a> (unique)	Zinc finger, B-box domain containing protein.	49.476	0.0005284	<a href="#">LOC_Os02g49230</a>
<a href="#">Os08g0520700</a>	<a href="#">31904</a>	<input type="checkbox"/>	AK060618	<a href="#">S-26120</a> (unique)	Conserved hypothetical protein.	35.491	0.0039811	<a href="#">LOC_Os08g40919</a>
<a href="#">Os01g0303800</a>	<a href="#">10646</a>	<input type="checkbox"/>	AK060078	<a href="#">S-9016</a> (unique)	Universal stress protein (Usp) family protein.	34.716	0.0017933	<a href="#">LOC_Os01g19820</a>
<a href="#">Os07g0489800</a>	<a href="#">39970</a>	<input type="checkbox"/>	AK068191	<a href="#">S-32271</a> (unique)	Ferredoxin domain containing protein.	34.571	0.0000081	<a href="#">LOC_Os07g30670</a>
<a href="#">Os01g0966200</a>	<a href="#">37328</a>	<input type="checkbox"/>	AK098935	<a href="#">S-30310</a> (unique)	Protein of unknown function YGGT family protein.	34.417	0.0000544	<a href="#">LOC_Os01g73540</a>



# Examining multiple genes

- Constructing a heatmap to view various predicted conserved hypothetical proteins
- Download zip file of relevant graphs
- Download heatmap as a pdf file



## Construct a heatmap

This option facilitates the construction of a heatmap for selected multiple locus IDs or feature IDs. The heatmap is constructed based on a customized order, or alternatively, based on clustering of correlation distance and complete linkage of each gene using heatmap.2 in the "gplots" package of R program. The expression level for each gene is normalized by shifting the baseline of median value to zero for each gene across all data within a dataset. The heatmap can be downloaded as PDF.

### Heatmap construction option

#### Ordering

- Customized ordering
- Clustering

#### Scale

max(abs)

#### Enter title

I hope I get an A on this

[download](#)

For customized ordering, rearrange the locus\_feature IDs by drag and drop.

↔  Os04g0119000\_23634

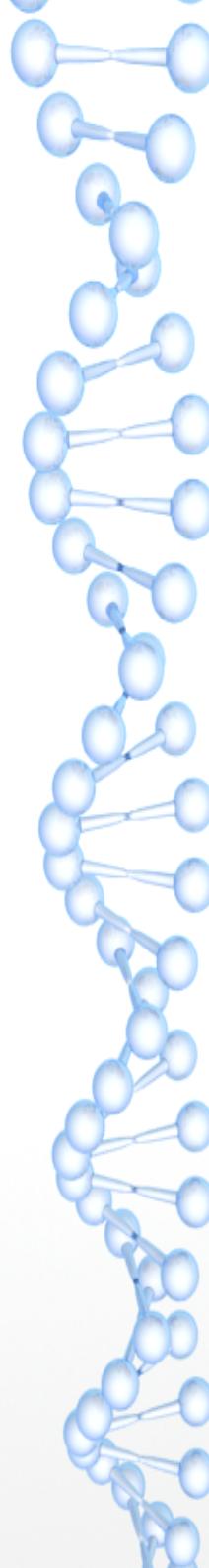
Conserved hypothetical protein.

↔  Os04g0119000\_23888

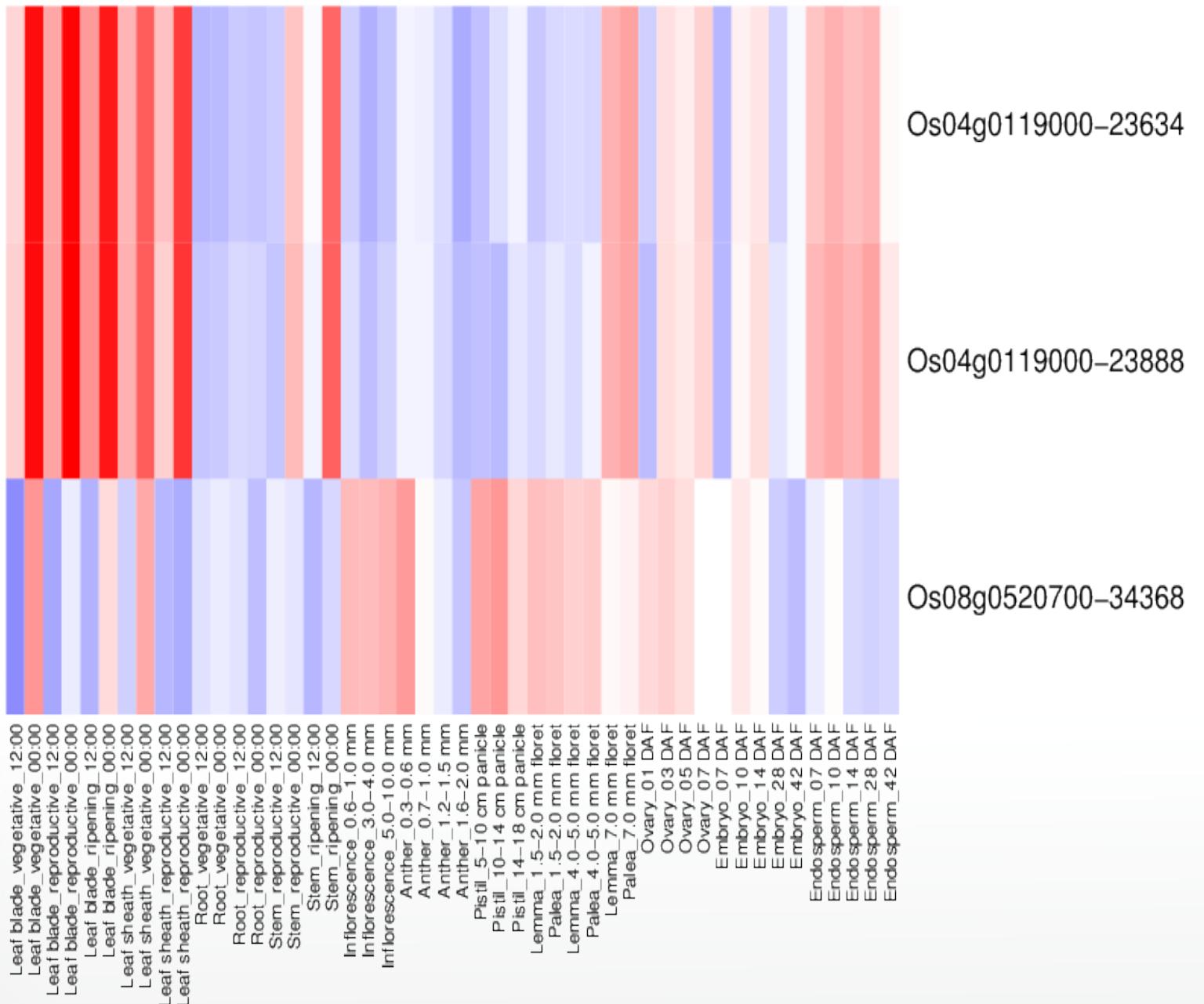
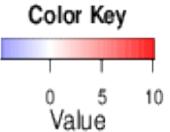
Conserved hypothetical protein.

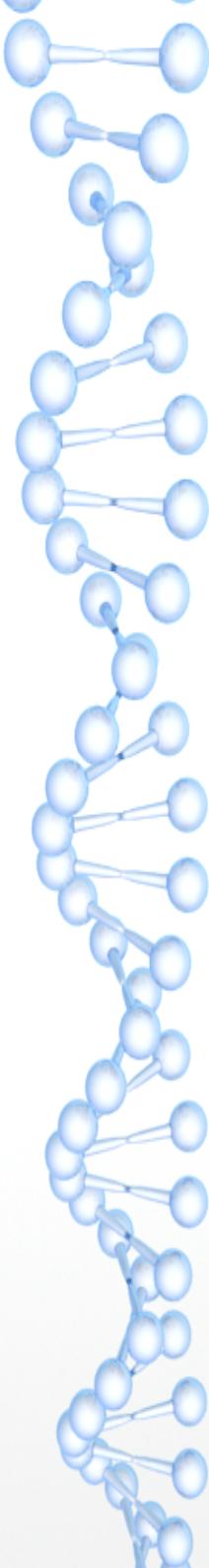
↔  Os08g0520700\_34368

Conserved hypothetical protein.



I hope I get an A on this

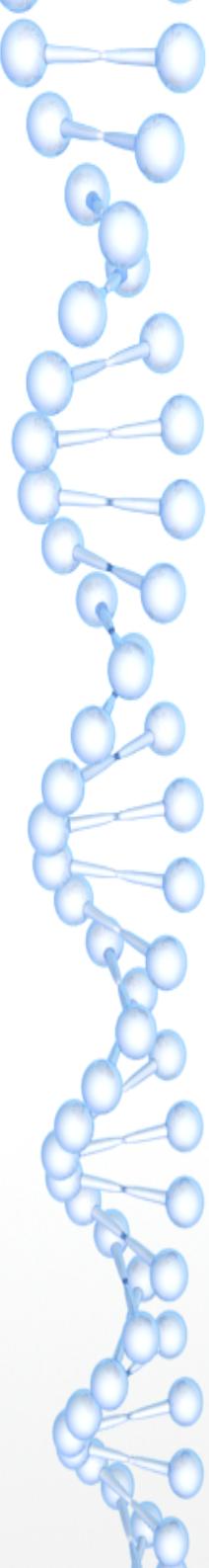




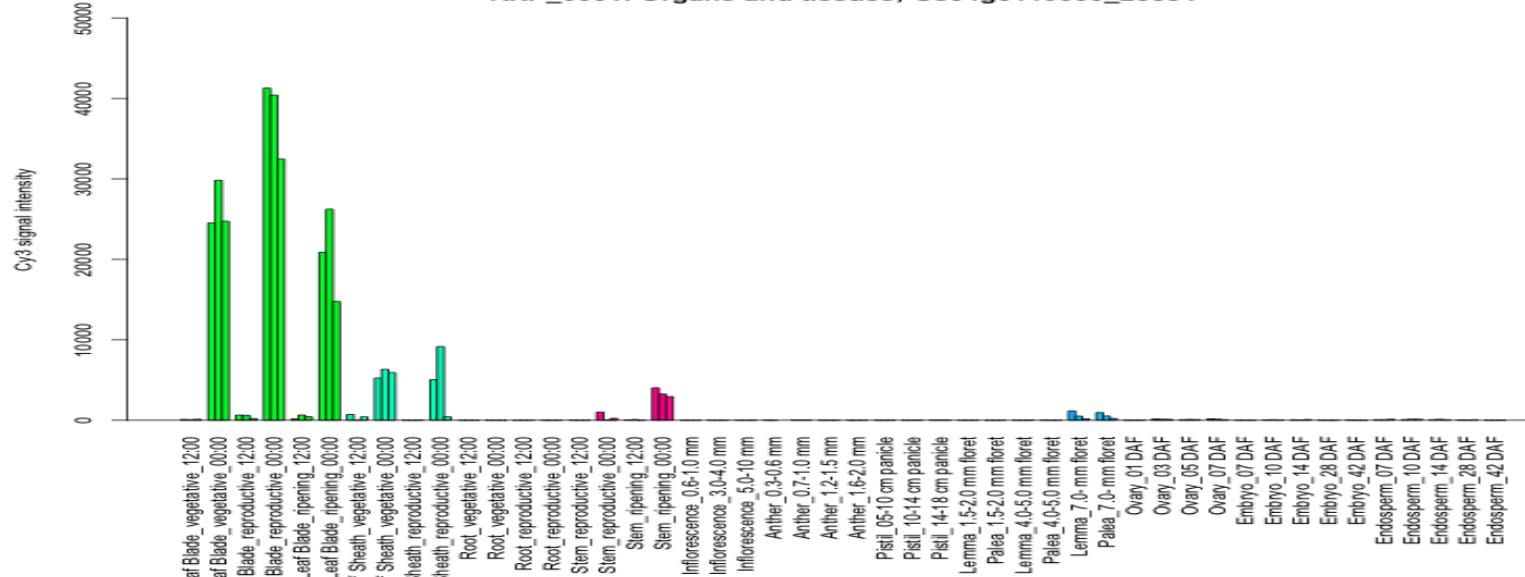
# Downloading the graphs

- Downloading the graphs we get a zip file containing the relevant data
- Unzipping it gives us png formatted bar (Raw) and line (Normalized) graphs

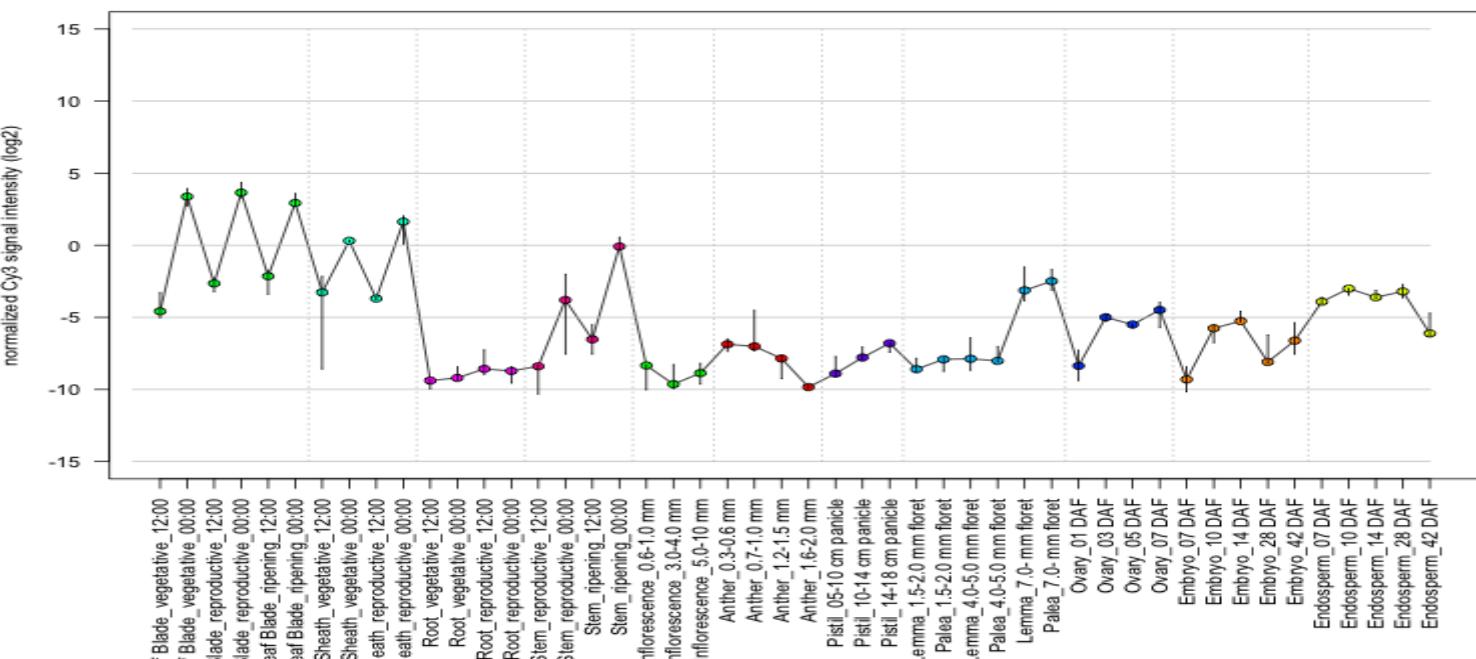
```
zeon:Journal(1509)$ unzip GGEP-graph.zip
Archive: GGEP-graph.zip
  inflating: RXP_0001-0s08g0520700-34368_bar.png
  inflating: RXP_0001-0s08g0520700-34368_line.png
  inflating: RXP_0001-0s04g0119000-23888_bar.png
  inflating: RXP_0001-0s04g0119000-23888_line.png
  inflating: RXP_0001-0s04g0119000-23634_bar.png
  inflating: RXP_0001-0s04g0119000-23634_line.png
```

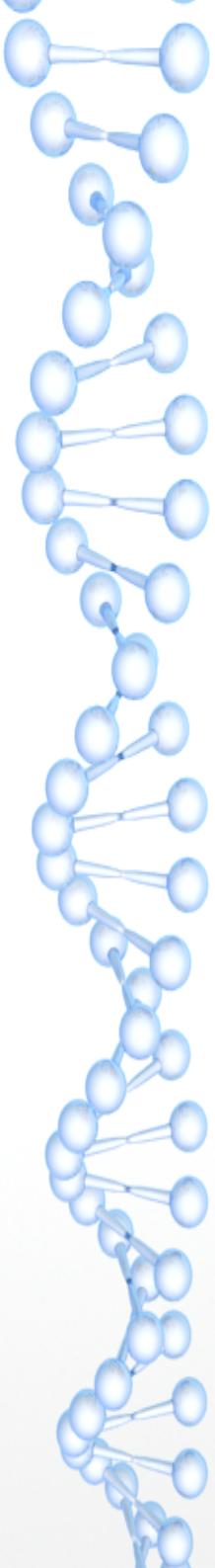


RXP\_0001: Organs and tissues; Os04g0119000\_23634



RXP\_0001: Organs and tissues; Os04g0119000\_23634

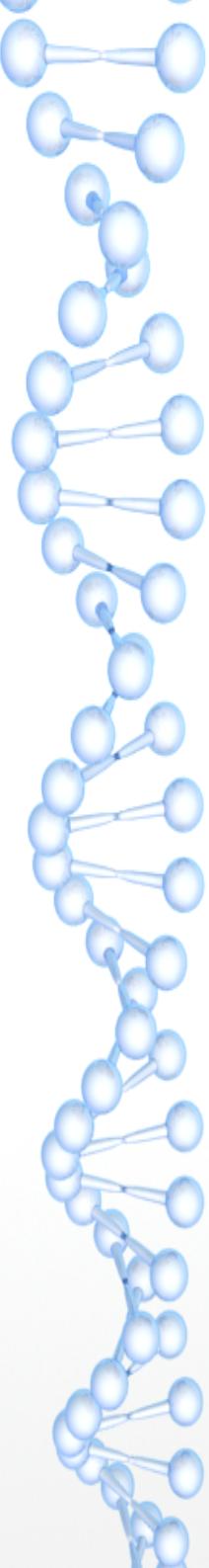




# We can't have a Bioinformatics website without BLAST!

- Similarity comparisons can be carried out via the EXP\_BLAST link on the top menu bar
- 3 different types of similarity queries can be made:
  - Blastn – Nucleotide vs. DB Nucleotide blast
  - Tblastn – Protein vs. DB Translated Nucleotide
  - Tblastx – Translated Nucleotide vs.DB Translated Nucleotide

# EXP\_BLAST



The RiceXPro logo is located at the top left of the page, featuring the text "RiceXPro" in a stylized font with a color gradient from blue to red, accompanied by a background of colored dots.

HOME GLOBAL PROFILE DATA SETS EXP\_BLAST ExProFile

## EXP\_BLAST

The EXP\_BLAST provides the opportunity to explore expression profile of a gene/genes with similarity to a query sequence. The users can extract a gene/genes by blastn, tblastn, or tblastx against coding sequence (CDS) of genes with probes in Rice 4x44K Microarray.

**CDS sequence search**

Select blast program

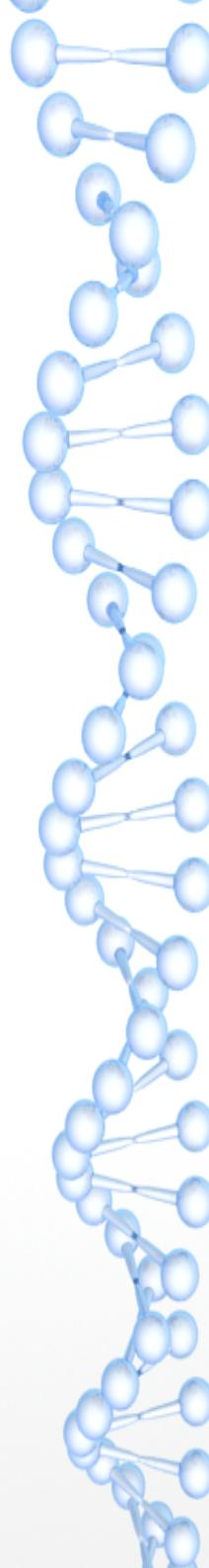
blastn – Query:Nucleotide vs. DB:Nucleotide

Query sequence Example

```
ATGTCGTGGCCGGGCAAGACAACGGAGATACCGCTGGGACTACATCAAGTG  
GATGTGCGCGCCGGTGGCGTGGGCGCCATGGCCAACCTCAGCGCGCG  
TTGGCTCCCTCGTCCGTGACATTGGCGACCCCTGCCTAACCCATCCCCGTTAAG  
GGGAGCAAATGCTAAACCGGAAAAATGGCA
```

Submit Reset





# Blastn Results

**RiceXPro**

HOME GLOBAL PROFILE DATA SETS EXP\_BLAST ExProFlip

## EXP\_BLAST result

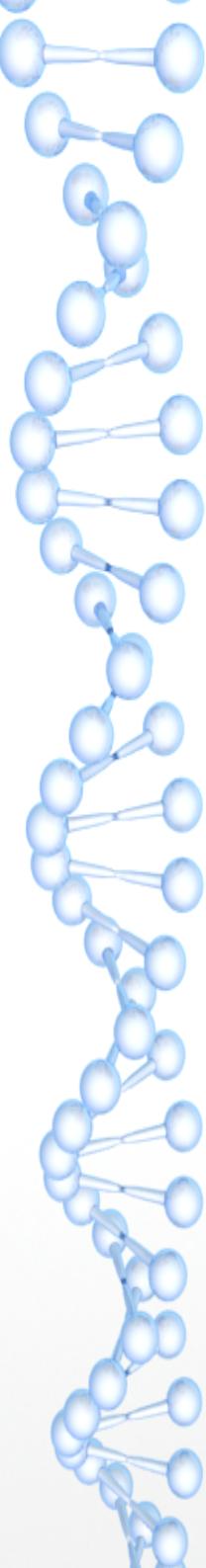
---

Program: BLASTN 2.2.21 [Jun-14-2009] [Citation](#)

Query Length: 200 letters

[Go to keyword search](#)

Locus	Description	Score(bits)	E value
<input type="checkbox"/> <a href="#">Os01g0100100</a>	RabGAP/TBC domain containing protein.	396	e-110
<input type="checkbox"/> <a href="#">Os03g0845600</a>	Glycoside hydrolase, family 17 protein.	36	0.067
<input type="checkbox"/> <a href="#">Os01g0194000</a>	Conserved hypothetical protein.	36	0.067



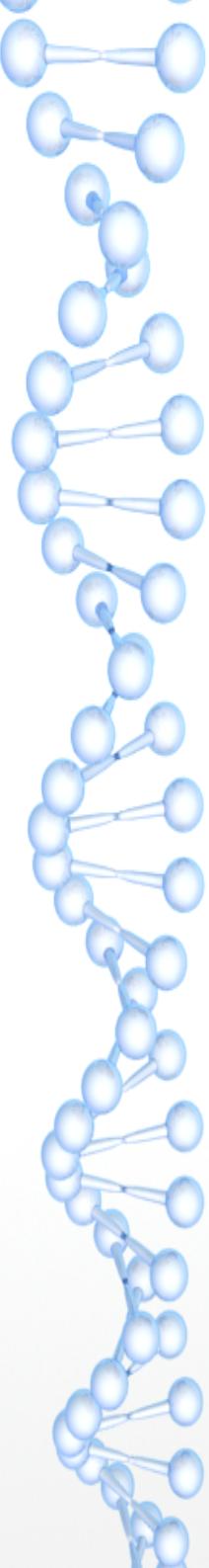
# What I like about RiceXPro

- RiceXPro provides a wealth of genome expression data regarding *Oryza Sativa Japonica Nipponbare*.
- Co-expression analysis can be conducted across this broad data set to find significant co-expressed genes.
  - Heatmaps are useful for visualizing and interpreting the results of this analysis
- The site is easily navigated and links to search various other rice genome databases are easily accessed.
- The site contains a consistent and straight-forward user interface and design.
- The ExProFlip feature is well thought out and provides a way to browse large amounts of graphical data quickly and easily.

# What I didn't like

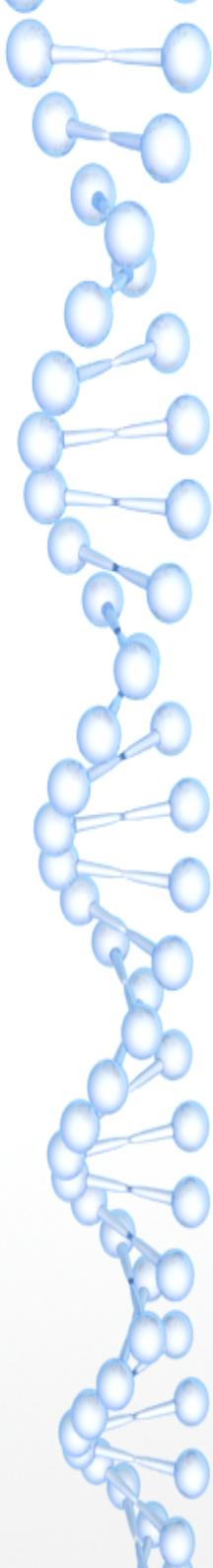
- “I've got a problem with the pop-ups.”  
“The pop-ups?”  
“Yeah, you know, the pop-ups.”





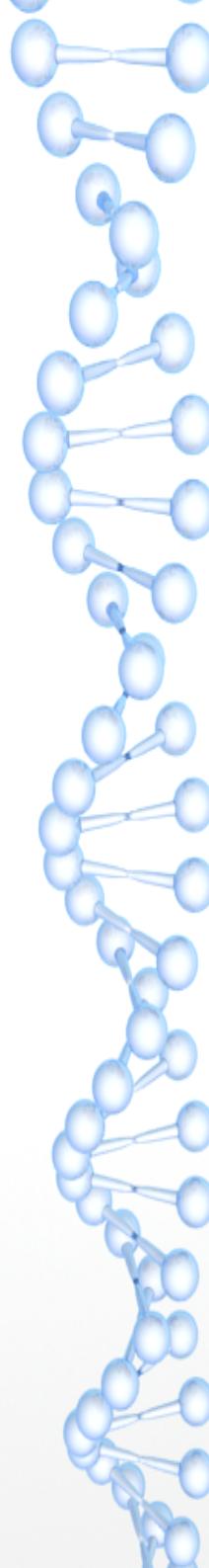
# More on the Pop-ups

- The mouse over function is a nice touch, however it would have been better implemented if the small preview windows disappeared after a short delay when the mouse moved off the target.
  - The mouse over menus do this, so we have the technology!



# References and other Rice Bioinformatics Websites

- <http://www.ncbi.nlm.nih.gov/pubmed/11935017>
- <http://www.goldenrice.org/>
- <http://www.ricediversity.org/>
- <http://ricefrend.dna.affrc.go.jp/>
- <http://agri-trait.dna.affrc.go.jp/>
- <http://rice.plantbiology.msu.edu/index.shtml>

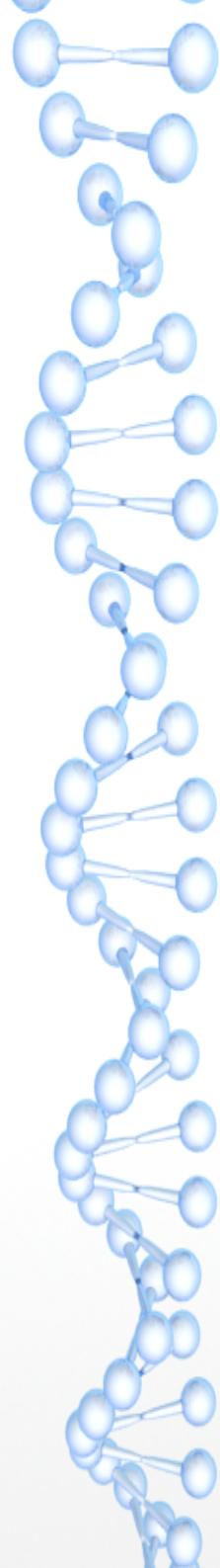


# Questions?



# Comments?





完了

