

ómica

A stylized graphic on the right side of the word 'ómica'. It features a white DNA double helix structure. The top part of the helix is composed of a series of white dots of varying sizes, arranged in a spiral pattern. The bottom part of the helix is composed of a series of white lines, also arranged in a spiral pattern. The entire graphic is set against a solid green background.

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Identification of rice genes which respond to saline stress from co-expression networks analysis

Camila Riccio Rengifo

In-silico

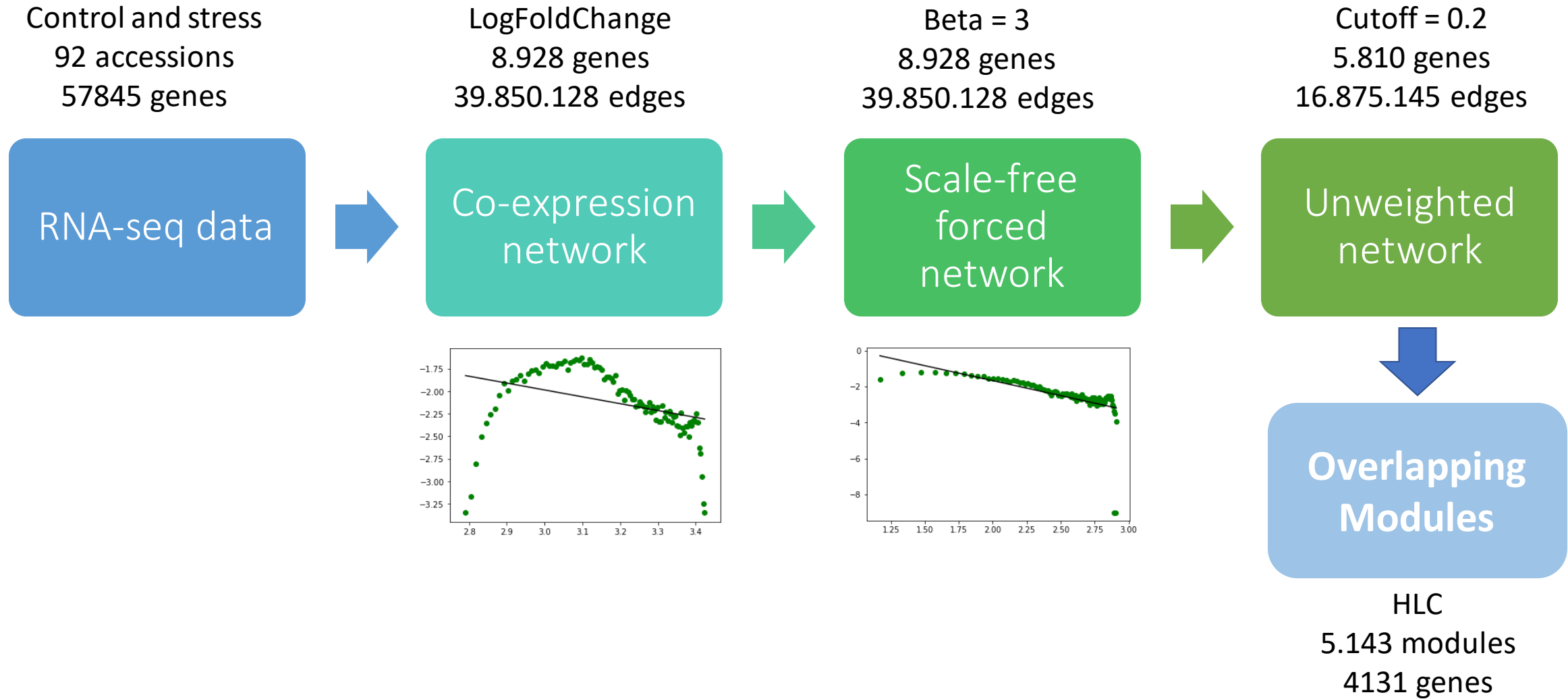


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Network construction



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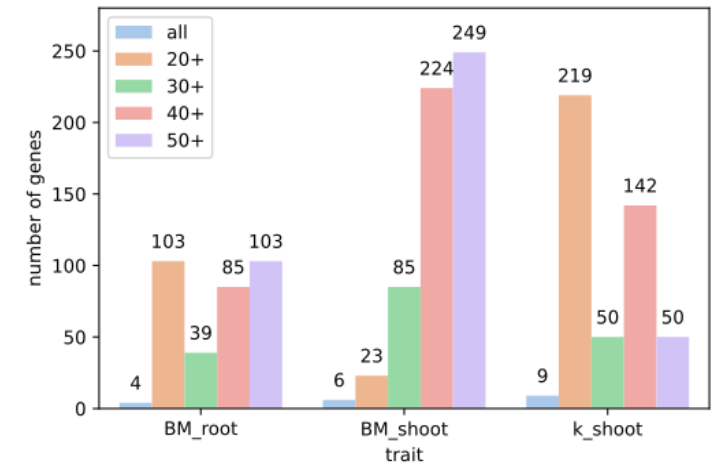
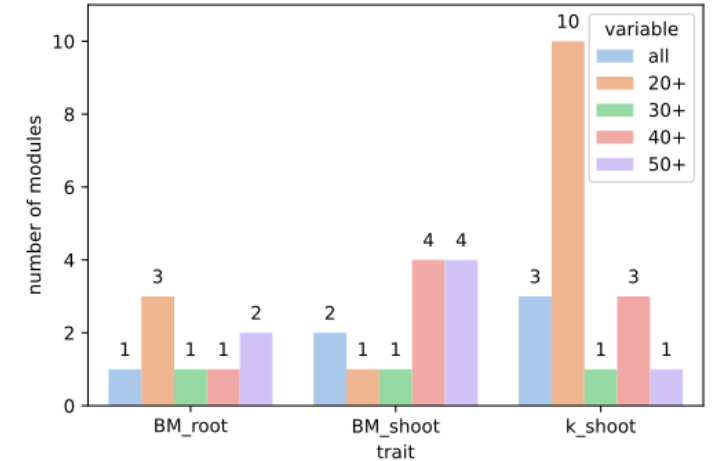
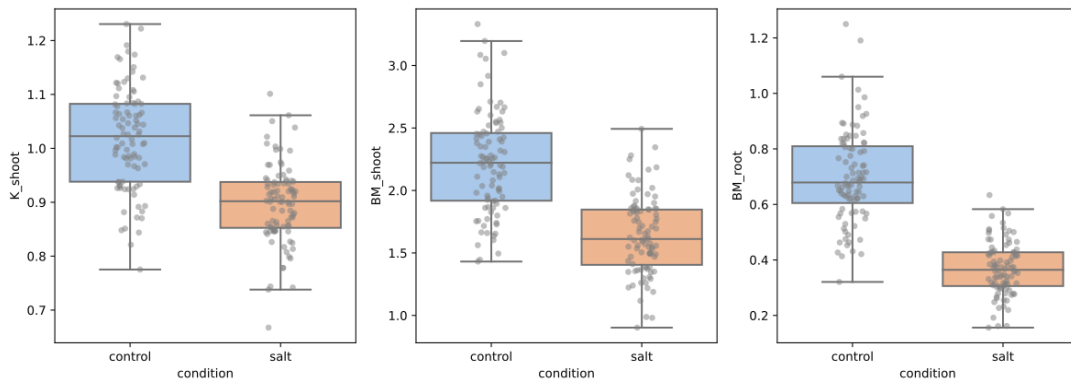
Modules selection

Phenotypic data

Log2FC PCA

genotype	K shoot	BM shoot	BM root	Module 1	...	Module 5143
101	0.92277	1.331149	0.445581	-1.772555		5.628090
105	0.83132	0.925433	0.226476	1.444241		3.260164
...
4	1.06181	2.306094	1.043257	-1.364746		-1.689424
9	0.94060	1.866801	0.586201	-2.122829		2.862661

LASSO



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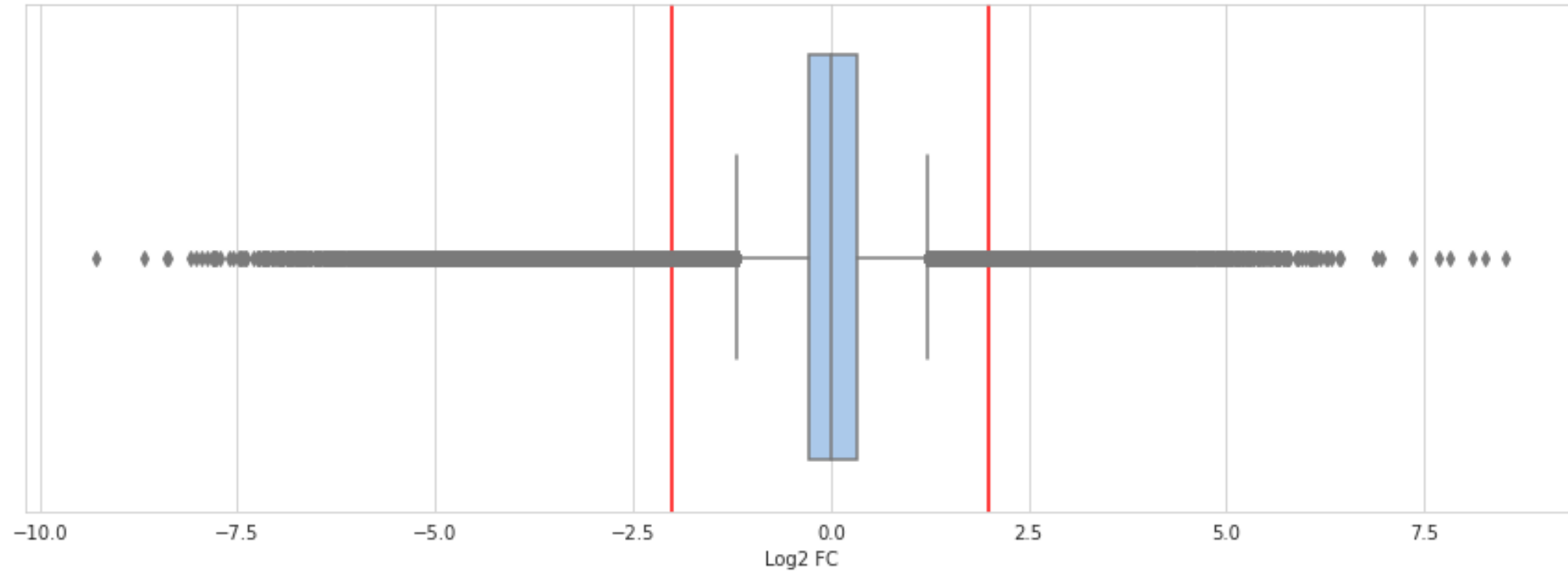


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DGE analysis



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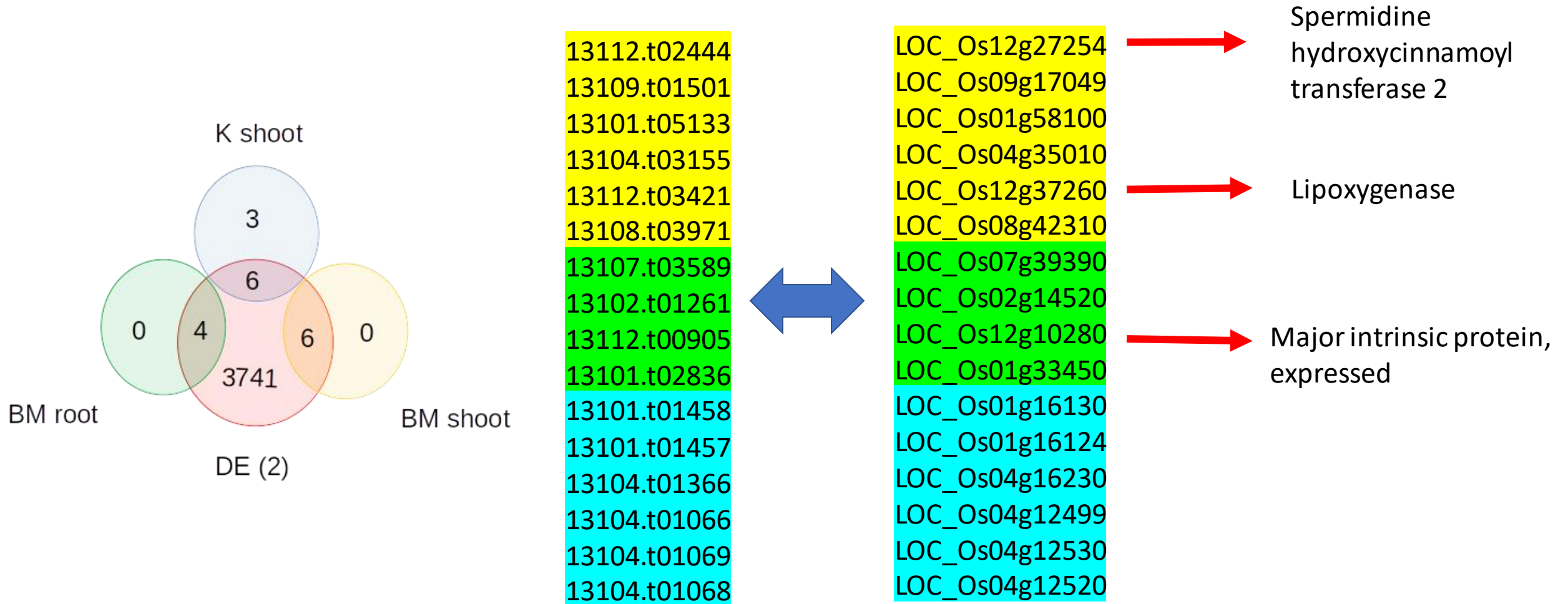


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Genes intersection



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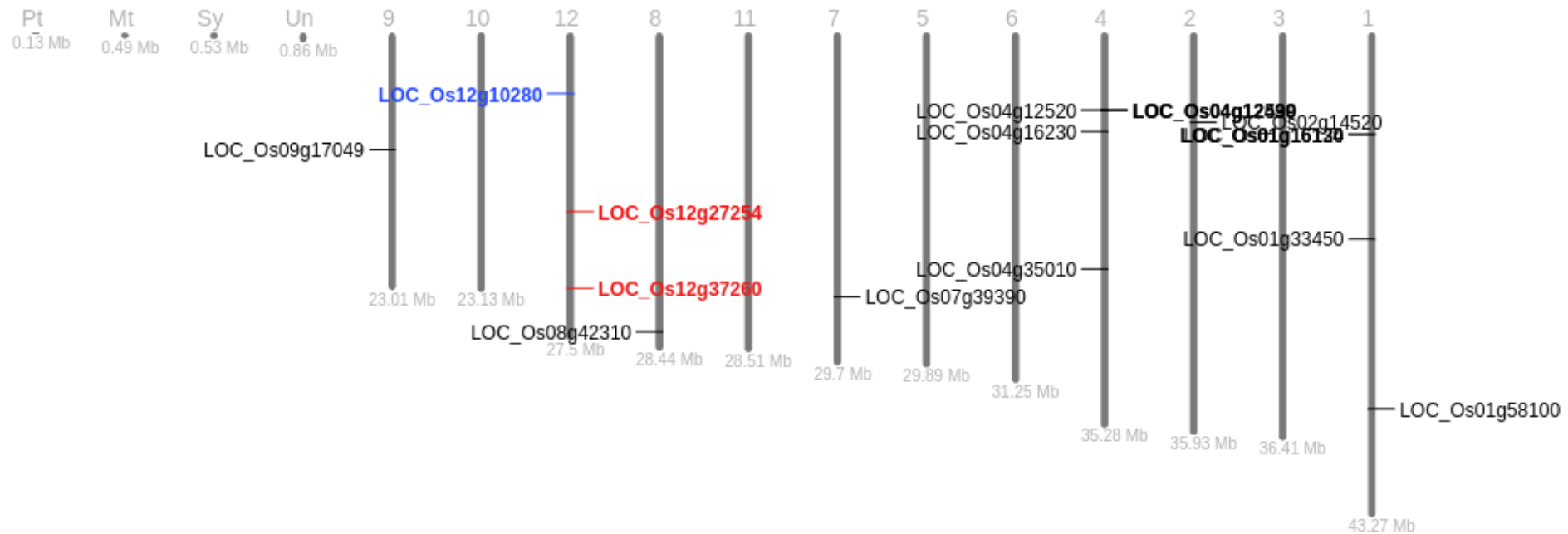
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Chromosome Viewer eFP-Browser

Chromosome Viewer



This image was generated with the Chromosome Viewer at bar.utoronto.ca/eplant by Waese et al. 2017

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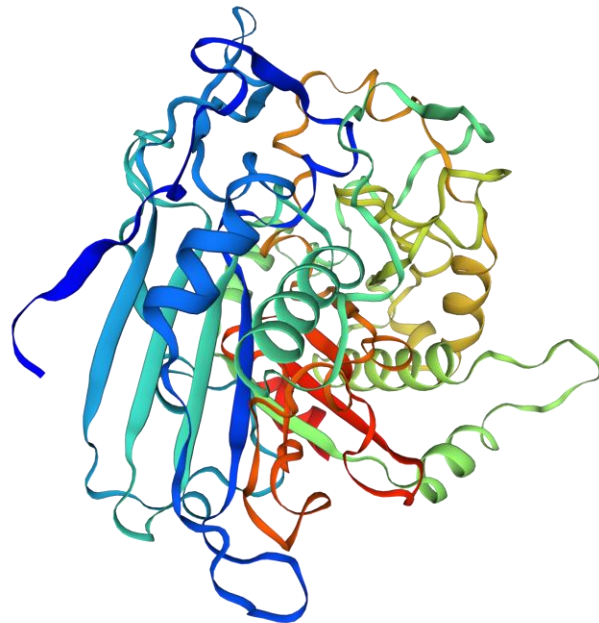
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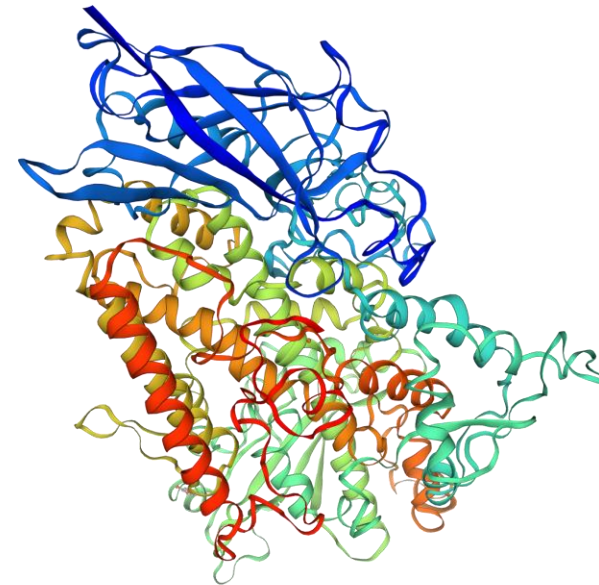


Named genes protein structure

Spermidine hydroxycinnamoyl
transferase 2 (SHT2)



Lipoxygenase



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Spermidine hydroxycinnamoyltransferase 2 (BM shoot)

Function:

Hydroxycinnamoyl transferase that catalyzes the transfer of an acyl from p-coumaroyl-CoA to spermidine, to produce coumaroyl spermidine. Can use feruloyl-CoA as acyl donor. Contributes to the natural variation of spermidine-based phenolamides in rice cultivars.

Salinity tolerance evidence:

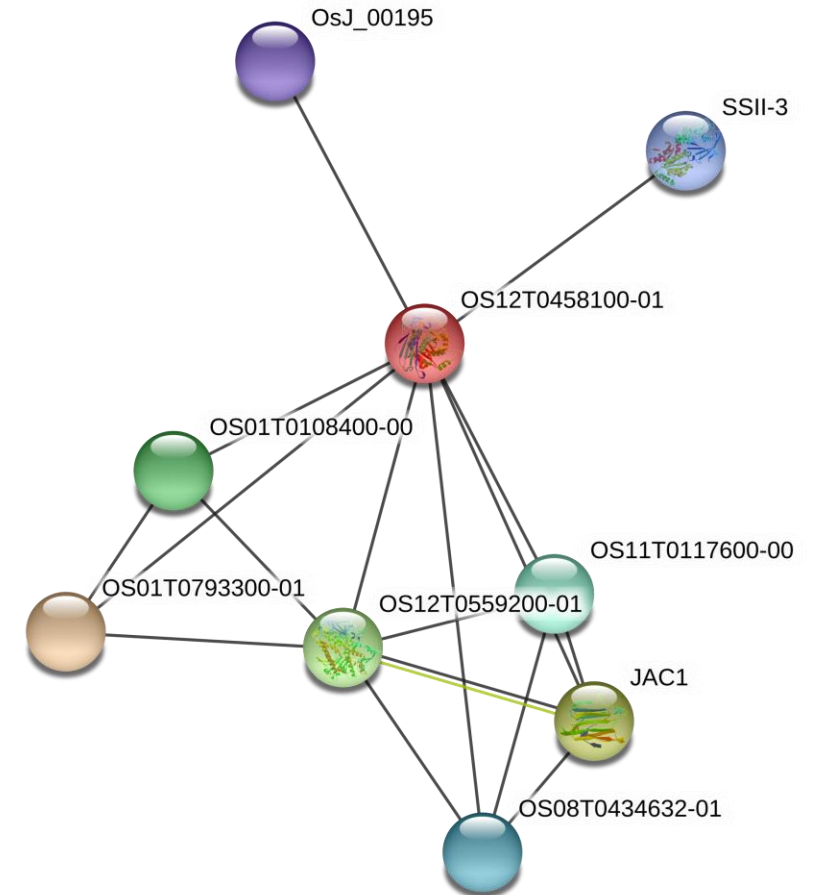
- (Roychoudhury, 2011)
- (Peng, 2019)
- (Gupta, 2013)

Annotations (4):

Molecular functions (4):

- transferase activity, transferring acyl groups
- transferase activity
- transferase activity, transferring acyl groups other than amino-acyl groups
- hydroxycinnamoyltransferase activity

Stress eFP: LOC_Os12g27254



STRING

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Lipoxygenase (BM shoot)

Function:

Plant lipoxygenase may be involved in a number of diverse aspects of plant physiology including growth and development, pest resistance, and senescence or responses to wounding.

Salinity tolerance evidence:

- (Hou, 2015)
- (Mitova, 2002)

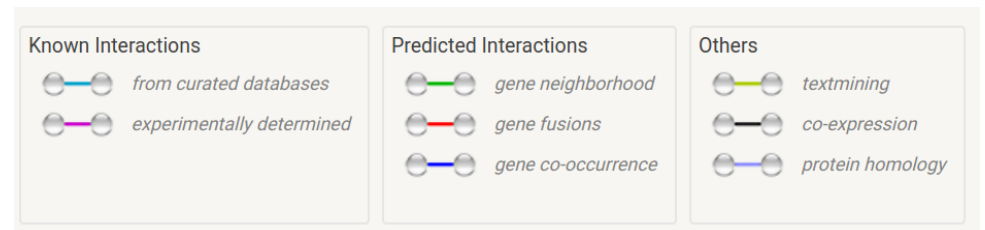
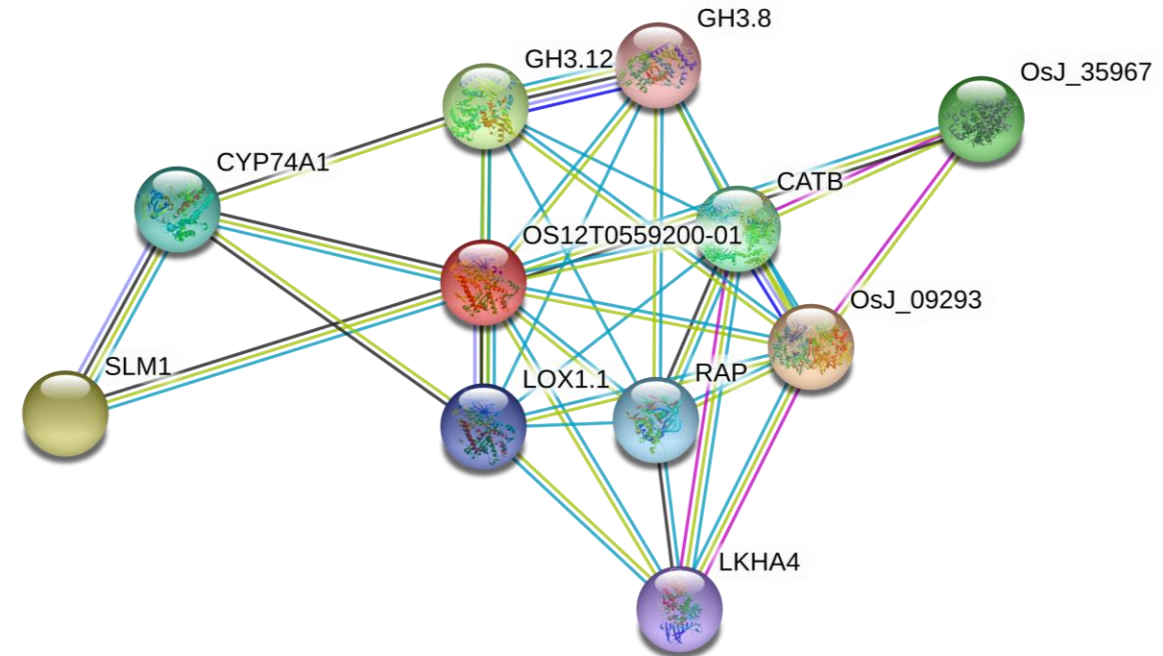
Annotations (17):

Molecular functions (8):

- oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen
- metal ion binding

Biological process (9):

- lipid oxidation
- oxidation-reduction process
- fatty acid biosynthetic process
- lipid metabolic process
- oxylipin biosynthetic process



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A network of rice genes associated with stress response and seed development

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Edited by Frederick M. Ausubel, Harvard Medical School, Boston, MA, and approved February 10, 2003 (received for review December 12, 2002)

We used a systematic approach to build a network of genes associated with developmental and stress responses in rice by identifying interaction domains for 200 proteins from stressed and developing tissues, by measuring the associated gene expression changes in different tissues exposed to a variety of environmental, biological, and chemical stress treatments, and by localizing the cognate genes to regions of stress-tolerance trait genetic loci. The integrated data set suggests that similar genes respond to environmental cues and stresses, and some may also regulate development. We demonstrate that the data can be used to correctly predict gene function in monocots and dicots. As a result, we have identified five genes that contribute to disease resistance in *Arabidopsis*.

Plant disease response often mimics certain normal developmental processes. For example, plants respond to fungal gibberellic acid and fusaric acid similarly to the way they respectively respond to plant-produced gibberellin and auxin (1, 2). The same can be said for abiotic stress responses and certain stages of plant development. Leaf cells undergoing dehydration stress express some of the same genes that embryonic cells express during development or seed desiccation (3, 4). Because systematic regulation of gene expression drives developmental processes and stress responses (5, 6), it is likely that there is a broader overlapping set of genes and their cognate proteins involved in such responses.

dough, hard dough, and germinating), callus, and panicles late in development (10–20 cm). More than five million bait/prey pairs were tested in reactions with each library. The inserted cDNA in each DNA-binding and activation domain vector that allowed for selective yeast growth was sequenced. The amino acid coordinates of interacting baits and prey can be found in Table 1, which is published as supporting information on the PNAS web site, www.pnas.org. The protein sequences (Table 2, which is published as supporting information on the PNAS web site), and the DNA sequences (Table 3, which is published as supporting information on the PNAS web site), were compared by BLAST (12) to sequences in GenBank. Protein sequences for which BLAST could not provide a functional annotation were searched with the SAM-T99 software package (13) against a library of 6,296 hidden Markov models representing all protein chains in the Protein Data Bank (14) to find remote homologs at the Structural Classification of Proteins superfamily level (15, 16). Interactions were confirmed by transforming paired constructs into naïve yeast cells and performing liquid culture β -galactosidase assays.

Gene Expression. We compared the gene sequences of the baits and preys with the gene fragments represented on our GeneChip Rice Genome Array (Affymetrix, Santa Clara, CA) and experimentally determined expression as previously described (17,

PLANT BIOLOGY

Yeast Two-Hybrid (Y2H)
Protein-protein interactions

Differential Gene Expression (DGE)
various plant tissues
various stresses

QTLs mapping
contribution of a locus to variation
in continuous traits

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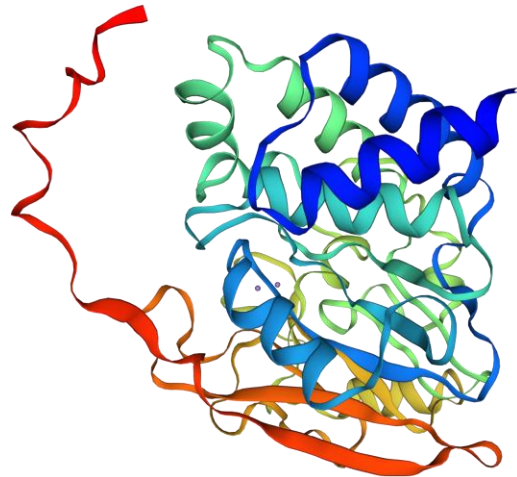
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Salt-stress responsive gene: PP2A-3

Function:

Catalytic activity



Annotations (9):

Molecular functions (5):

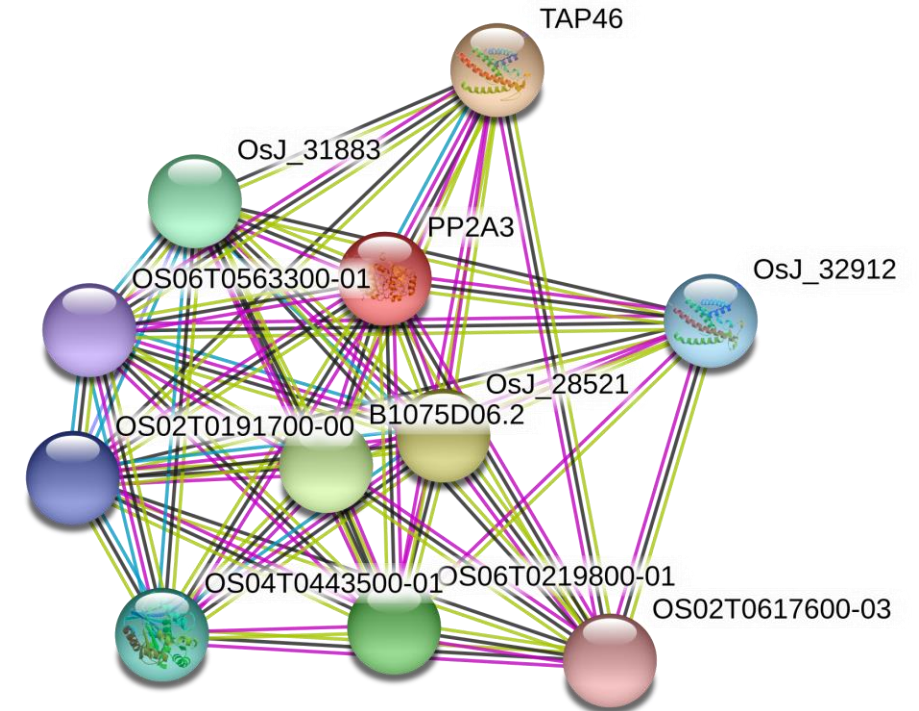
- metal ion binding
- hydrolase activity
- phosphoprotein phosphatase activity

Biological process (2):

- protein dephosphorylation

Cellular component (2):

- Cytoplasm



Known Interactions

- from curated databases
- experimentally determined

Predicted Interactions

- gene neighborhood
- gene fusions
- gene co-occurrence

Others

- textmining
- co-expression
- protein homology

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Aliados



Apoyan



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