

Gramene meeting April 19th

Palitha Dharmawardhana

Use of Gramene resources in analyzing large-scale gene expression data

- Data source: A comprehensive *Brachypodium* abiotic stress gene expression dataset from Mockler lab (250 Affy arrays)
- Treatments: Salt, cold, heat, PEG, photoperiod, light quality

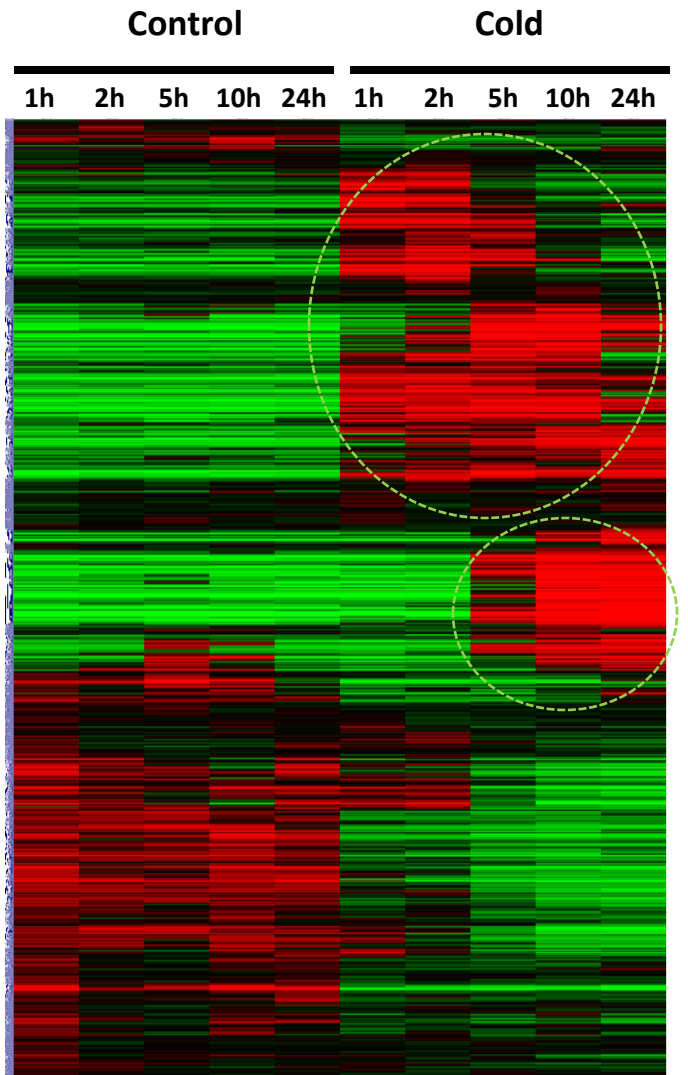
Method in brief

- Differentially expressed genes during salt, cold, heat and drought stress conditions were identified
- The genes were clustered based on expression pattern to identify co-regulated groups of genes
- Co-regulated gene clusters were analyzed using Gramene resources
 - Gene Ontology information
 - Pathway information
 - Protein and orthology information

Brachypodium cold response

- Sampling intervals following cold treatment
 - 1h, 2h, 5h, 10h, 24h,
- >2K genes were regulated during cold stress
- Slightly over half the genes are up regulated during salt treatment with clear early and late responding genes

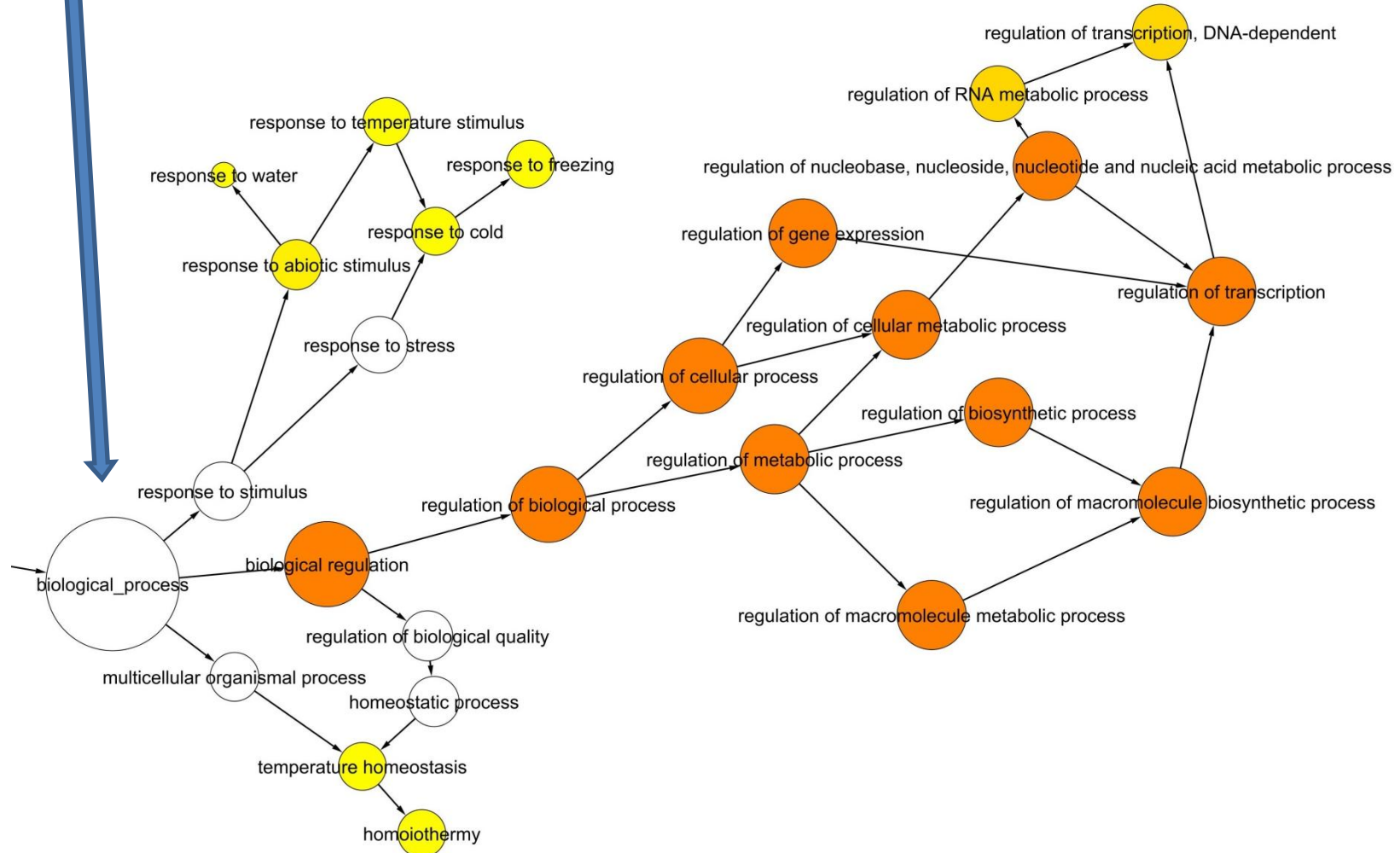
Gene expression pattern of cold regulated genes illustrated as a cluster diagram



Cold induced genes

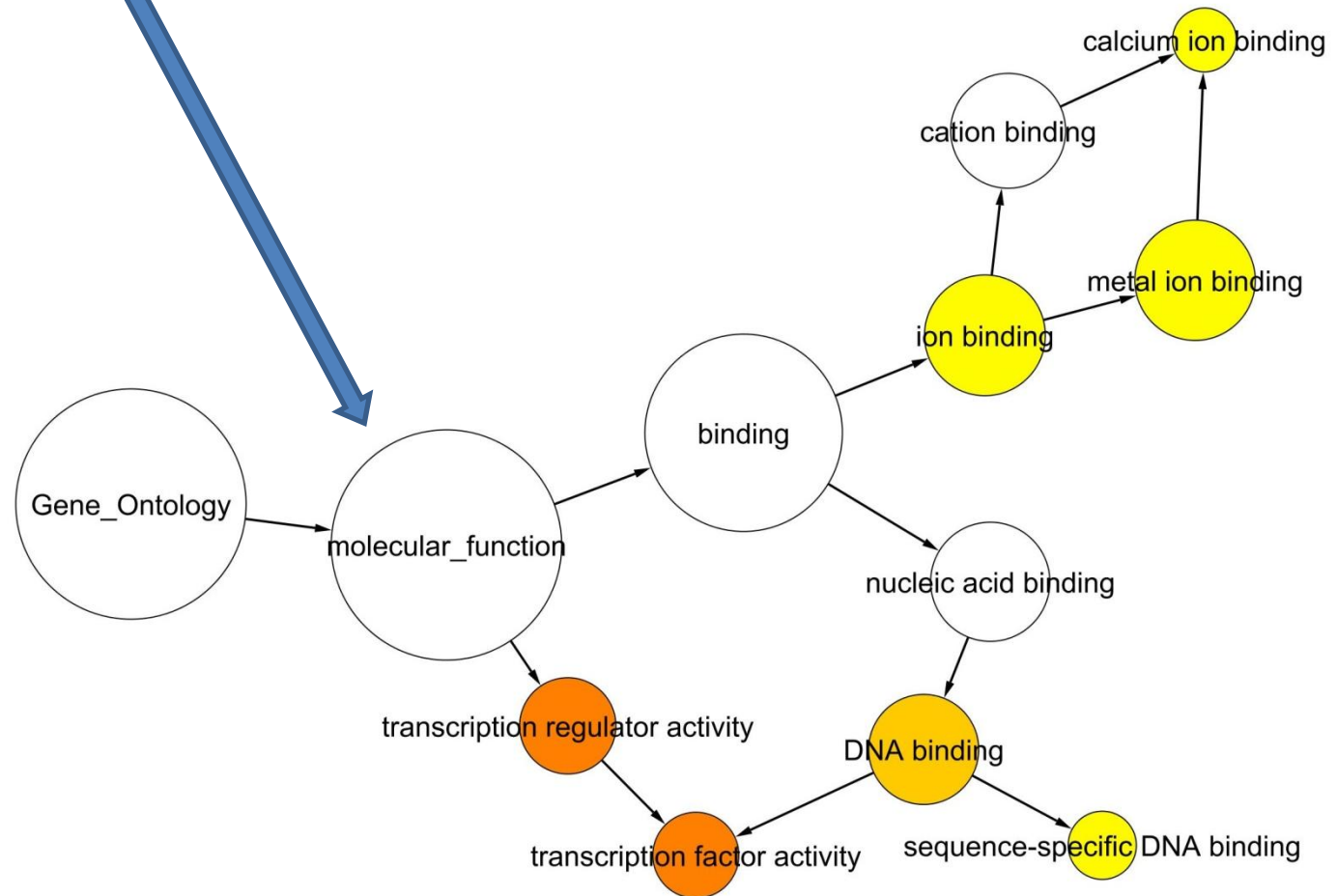
Cold induced genes

GO category enrichment analysis: biological process



Cold induced genes

GO category enrichment analysis: molecular function



Pathway representation analysis using BrachyCyc















[Pathways Home](#) | [Search Pathways](#) | [Omics Viewer](#) | [Omics Validator](#) | [Download RiceCyc & SorghumCyc](#) | [Help](#) | [Tutorial](#) | [FAQs](#) | [Release notes](#)

Plant Metabolic Pathways

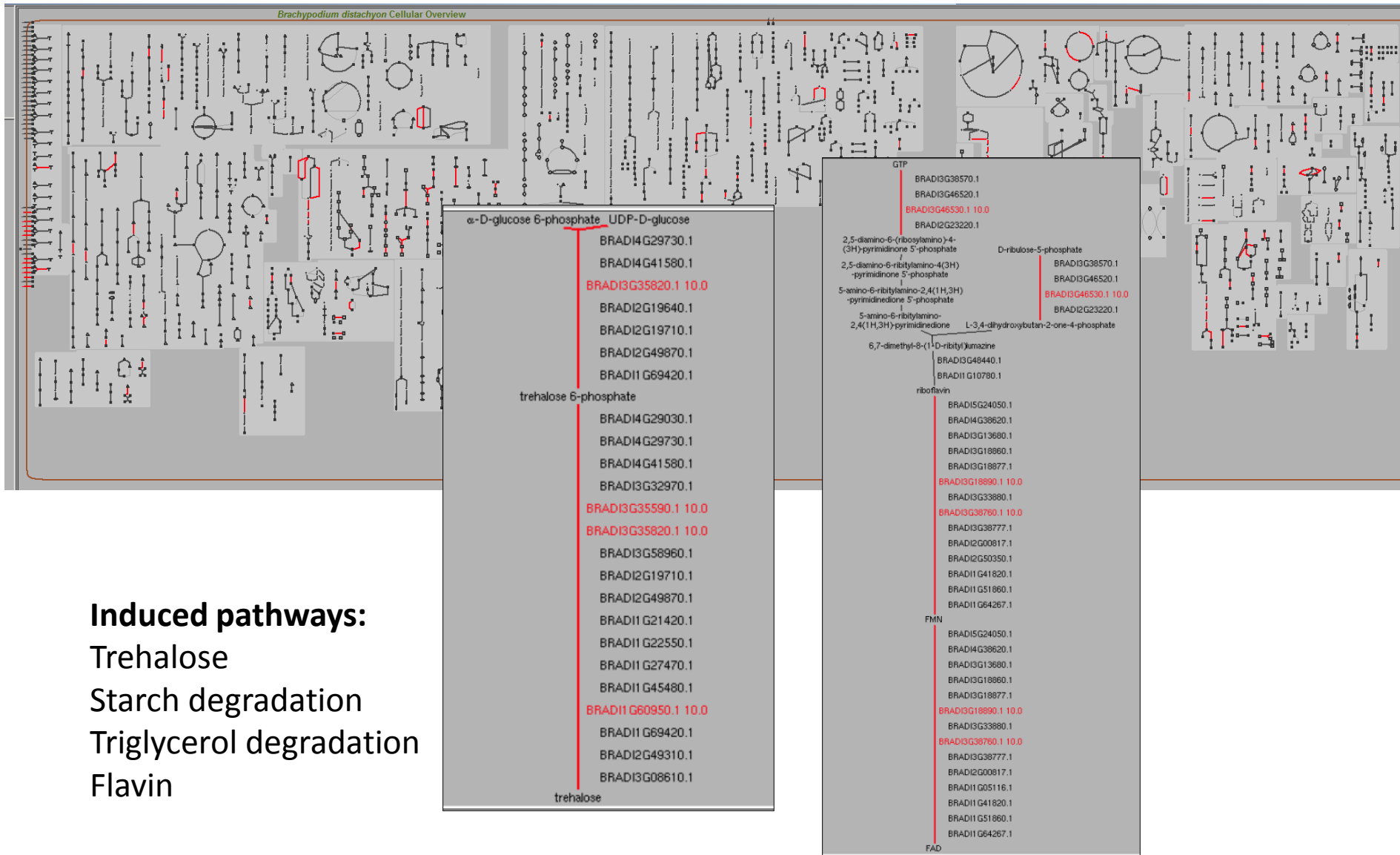
Pathways section in the Gramene databases is home for the RiceCyc and the SorghumCyc, the pathway databases for rice and Sorghum respectively. It also provides mirrors of pathway databases from *Arabidopsis*, tomato, potato, pepper, coffee, *Medicago*, *E. coli* and the MetaCyc reference database. In addition to search and browse functions, the database allows users to find genes mapped to respective reactions and pathways and draw intraspecific comparison between the pathways.

Pathways Browse and Other Options

Click on the species specific links such as **browse** to go through the list of pathways; **summary** to get a summarized overview. Click on the **more info** link to learn more details on the respective pathway database.

RiceCyc ver 3.0 <i>Oryza sativa japonica</i> Strain: Nipponbare Browse Summary More info		AraCyc * ver 6.0 <i>Arabidopsis thaliana</i> Strain: Columbia Browse Summary More info		EcoCyc * ver 13.5 <i>Escherichia coli</i> Strain: K-12 MG1655 Browse Summary More info	
SorghumCyc ver 1.0 <i>Sorghum bicolor</i> Strain: BTx623 Browse Summary More info		MediCyc * ver 1.0 <i>Medicago truncatula</i> , Barreldlover Strain: n/a Browse Summary More info		MetaCyc * ver 13.5 Reference Pathway Database Strain: not applicable Browse Summary More info	
MaizeCyc ** ver 1.2beta <i>Zea mays</i> Strain: B73 Browse Summary More info		PoplarCyc * ver 1.0 <i>Populus trichocarpa</i> (and other <i>Populus</i> species and hybrids) Strain: not applicable Browse Summary More info		PlantCyc * ver 3.0 Plant Metabolic Pathway Database Strain: not applicable Browse Summary More info	
BrachyCyc ** ver 1.2beta <i>Brachypodium distachyon</i> Strain: Bd21 Browse Summary More info		CapCyc * ver 1.0.1.1 <i>Capsicum annuum</i> , Pepper Strain: n/a Browse Summary More info			
		PotatoCyc * ver 1.0.1.1 <i>Solanum tuberosum</i> , Potato Strain: n/a Browse Summary More info			
		CoffeaCyc * ver 1.1.1 <i>Coffea canephora</i> , Coffee Strain: n/a Browse Summary More info			
		LycCyc * ver 2.0.1.1 <i>Solanum lycopersicum</i> , Tomato Strain: n/a Browse Summary More info			

240 genes out of the 1078 cold induced genes map to Brachypodium pathways



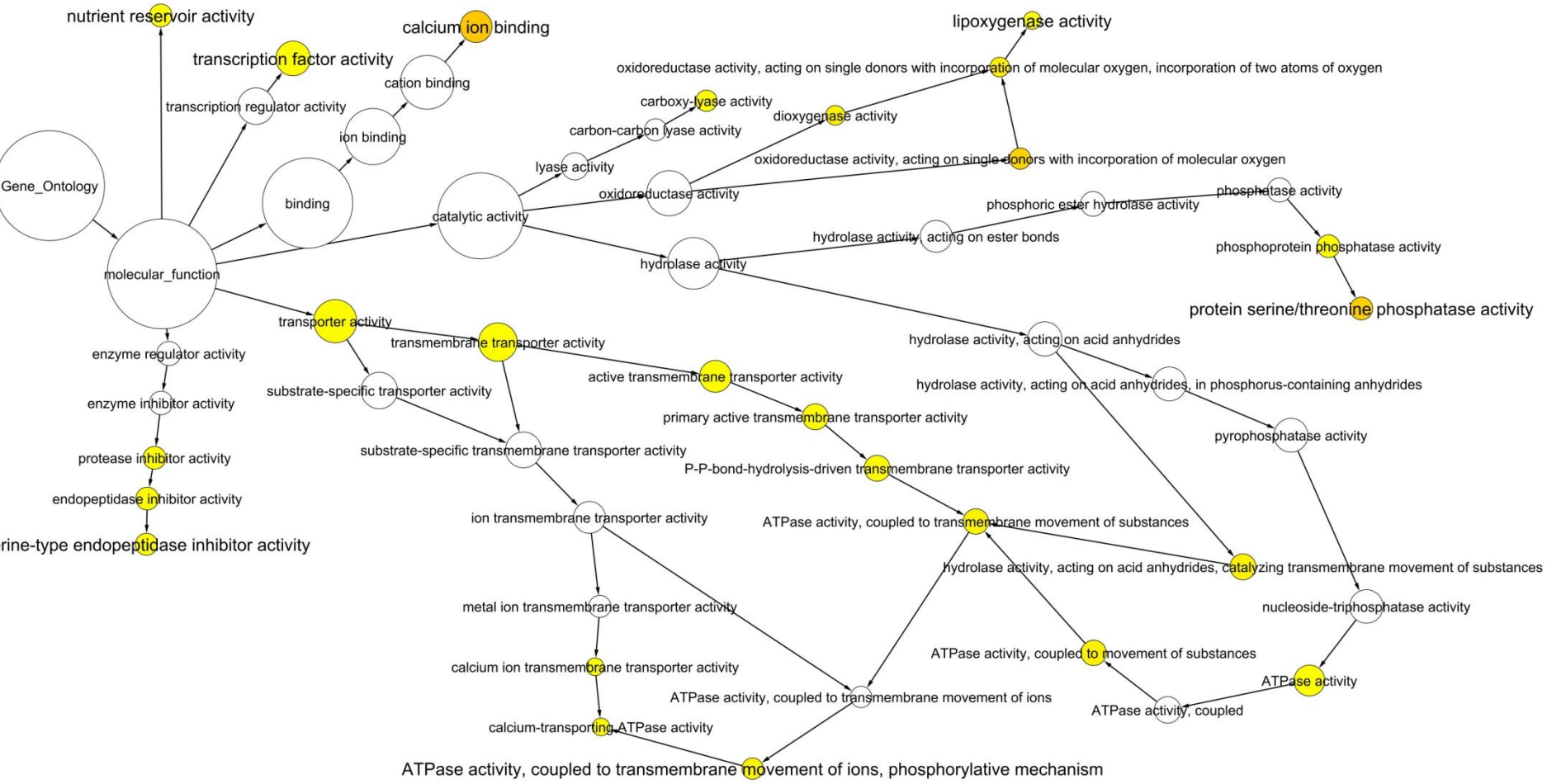
Brachypodium salt response

- >1500 genes are regulated during salt stress
- Slightly over half the genes are down regulated during salt treatment with the rest being upregulated to various degrees

The heatmap displays gene expression data across two conditions: Control and Salt, with time points at 1h, 2h, 5h, 10h, and 24h. The color scale ranges from -2 (blue) to 2 (red). A dashed blue circle highlights a cluster of genes that are upregulated in the Salt condition at 10h and 24h.

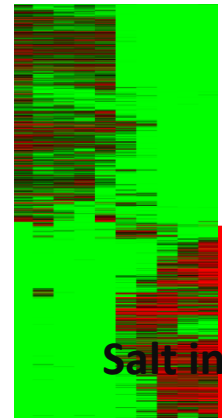
Salt induced genes

Salt in

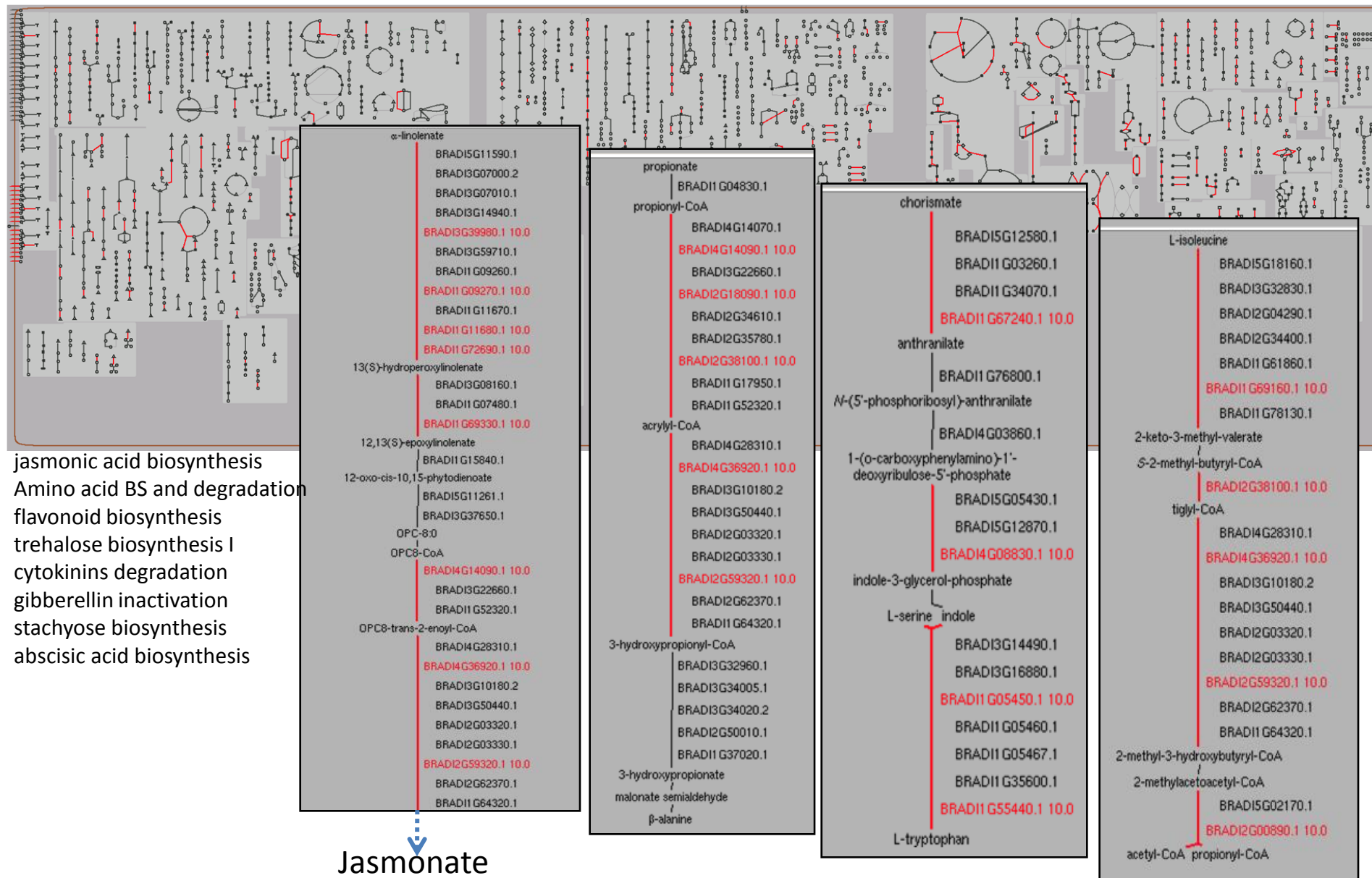


Salt in

Salt in



276 salt induced genes map to Brachypodium pathways



In-depth analysis of affected pathways and genes using other Gramene data modules

