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VERSATILE SEARCH INTERFACE & PAN-GENOME SITES

- ### Highlights
- Gramene's homepage has been reimplemented for easy deployment across our sites.
 - Search results integrate six data types as embedded views: Location, Expression, Homology, Pathways, Papers & Cross-References.
 - The Homology view allows zooming in (Multi-alignment view) and out (Neighborhood conservation) from the Alignment Overview of a gene family tree.
 - Integration of gene functions described in the literature (354 Z. mays, 4006 O. sativa, 7184 A. thaliana), see Papers tab.

Updated layout

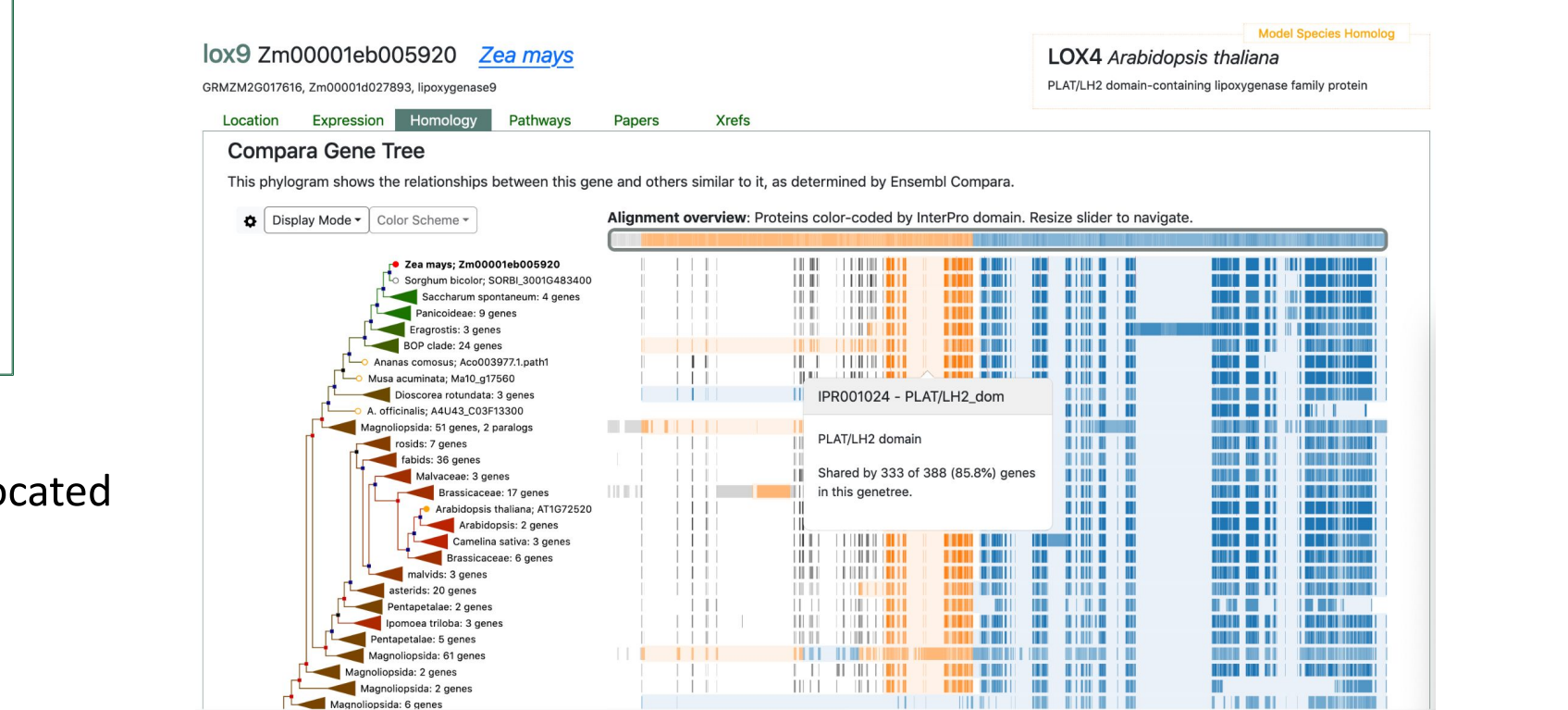
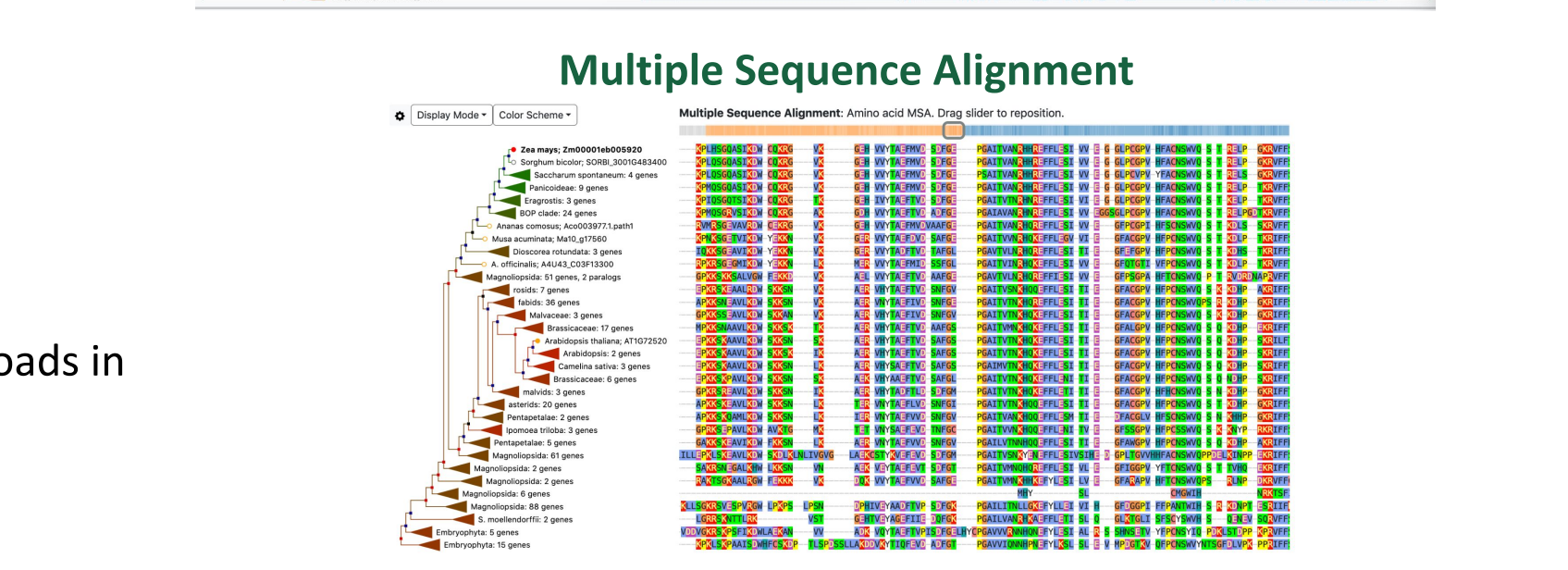
New Papers tab. More control over search filters, automatically pruned species tree, relocated configuration button for choosing genomes of interest



Shows the reactions and pathways that a gene takes part in and offers links to data downloads in

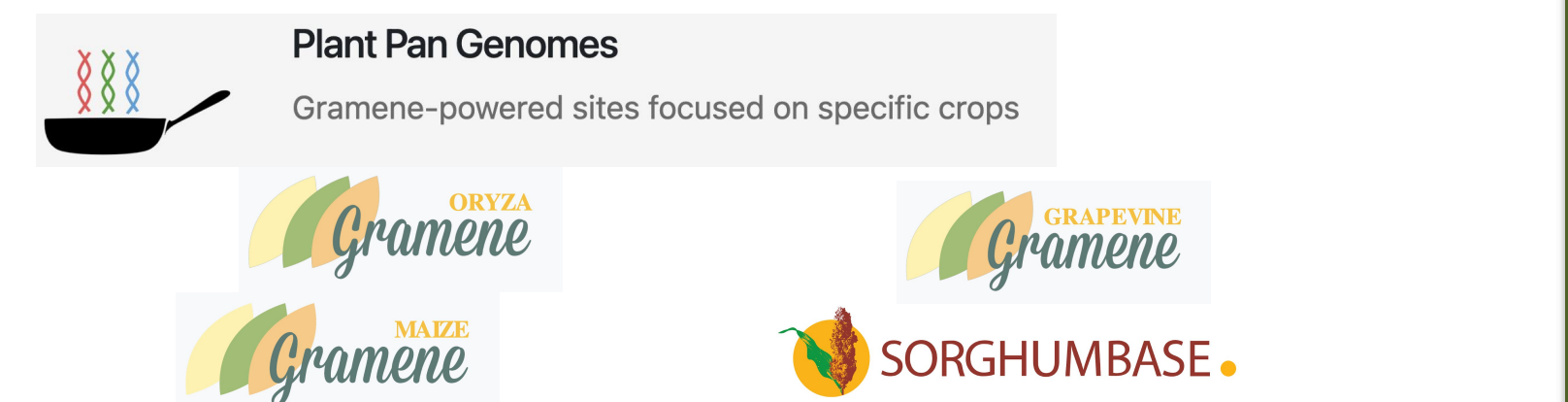
Homology view

Shows inferred evolutionary histories from Compara, integrated with functional domain information from InterPro.

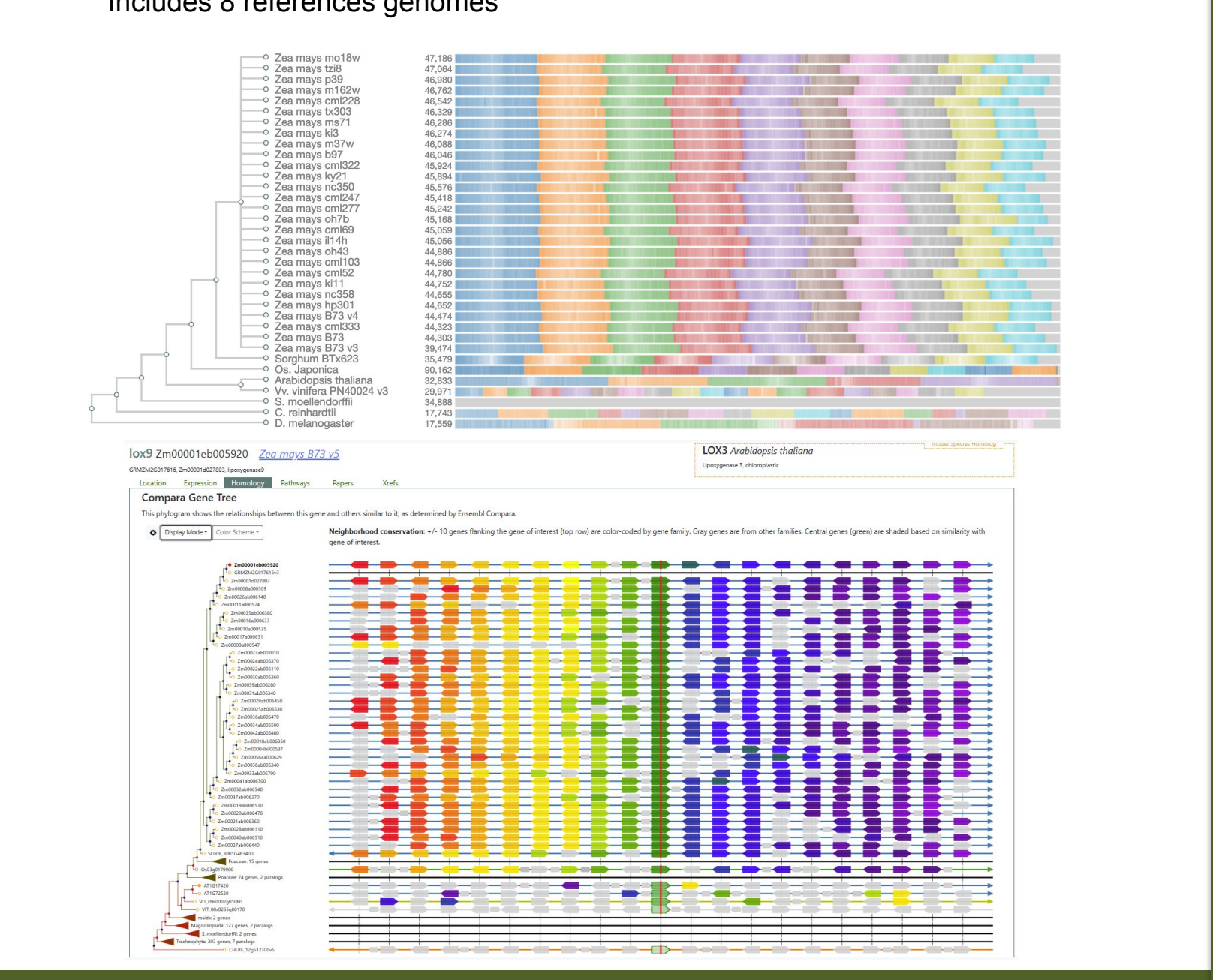
Plant Pan Genomes

Gramene-powered sites focused on specific crops



Crop	Current release (date)	Genomes *	Gene Families
sorghum	R6 (June 2023)	37	44K
maize	R3 (Mar 2023)	43	31K
rice	R6 (Jan 2023)	28	38K
grapevine	R3 (May 2022)	18	28K

*Includes 8 reference genomes

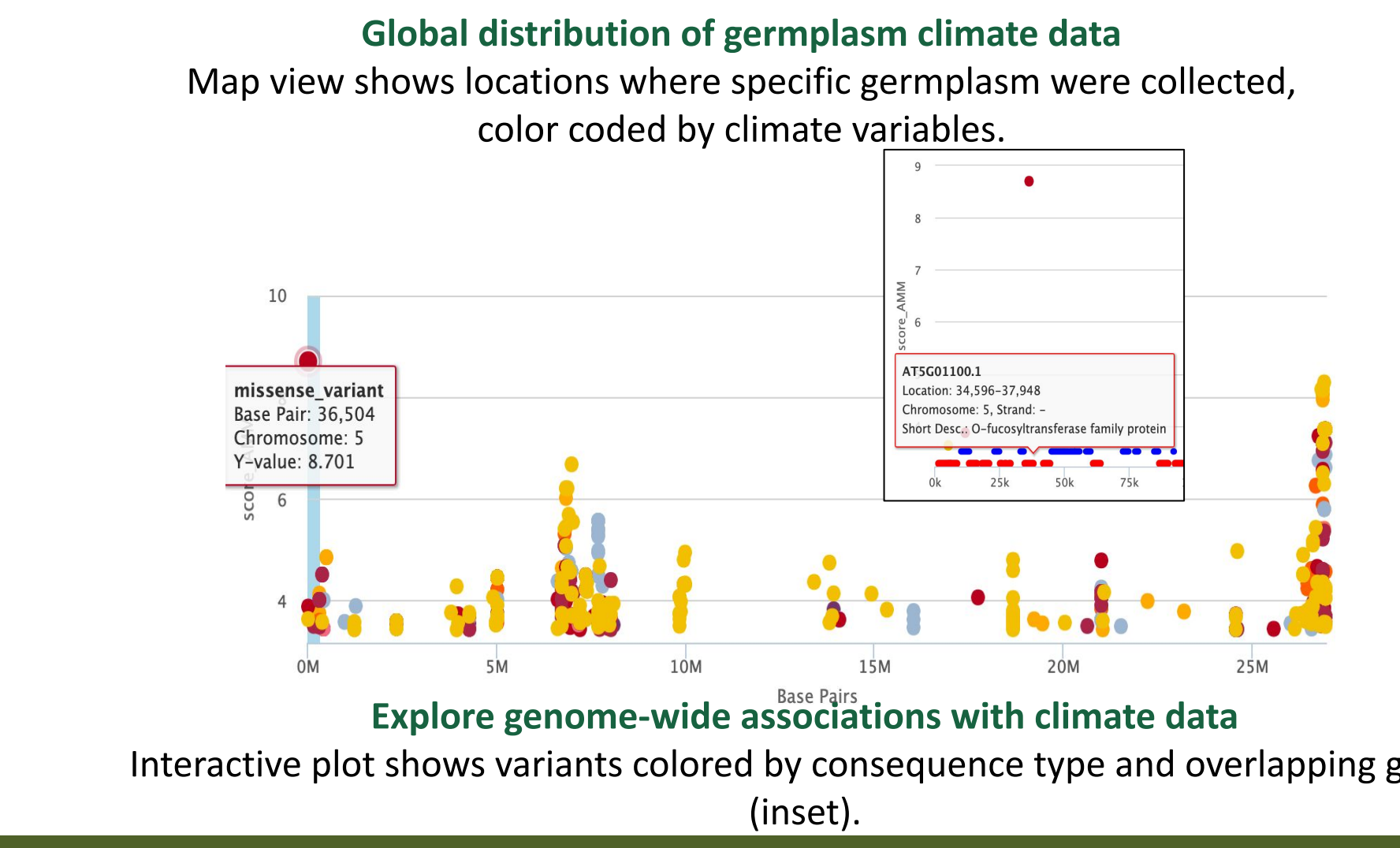
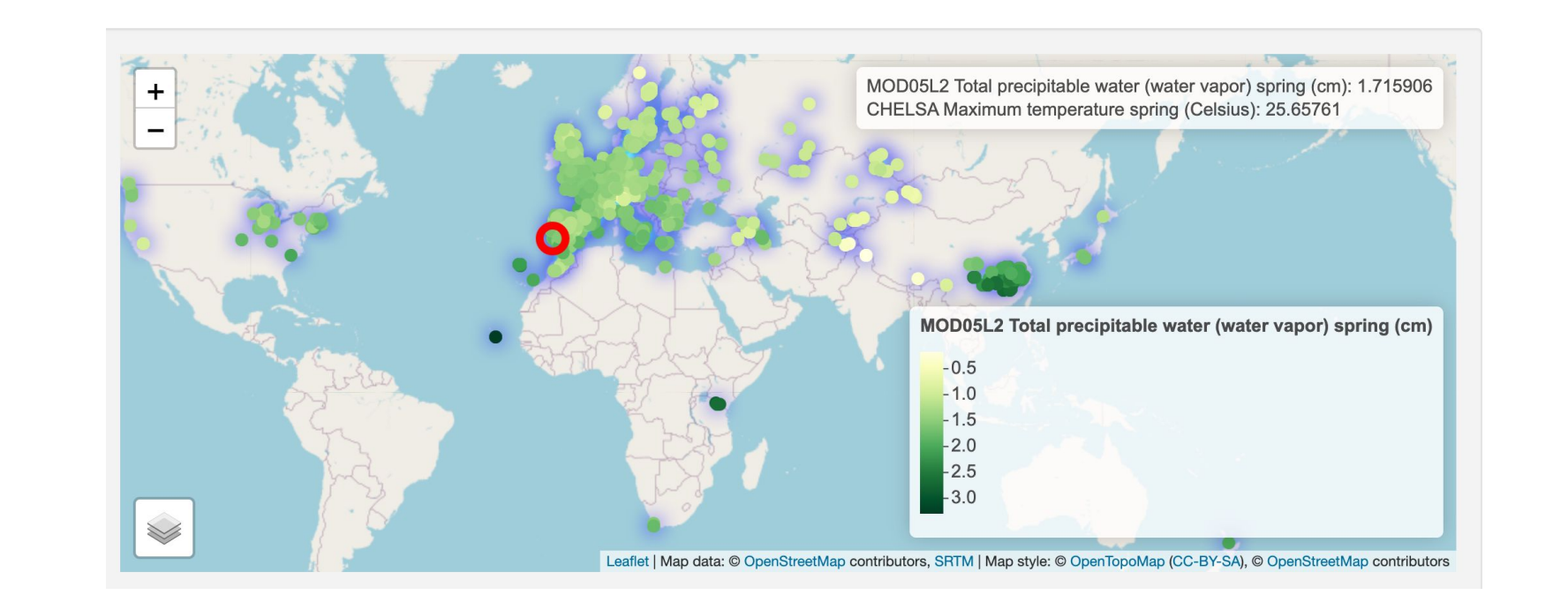


CLIMTOOLS



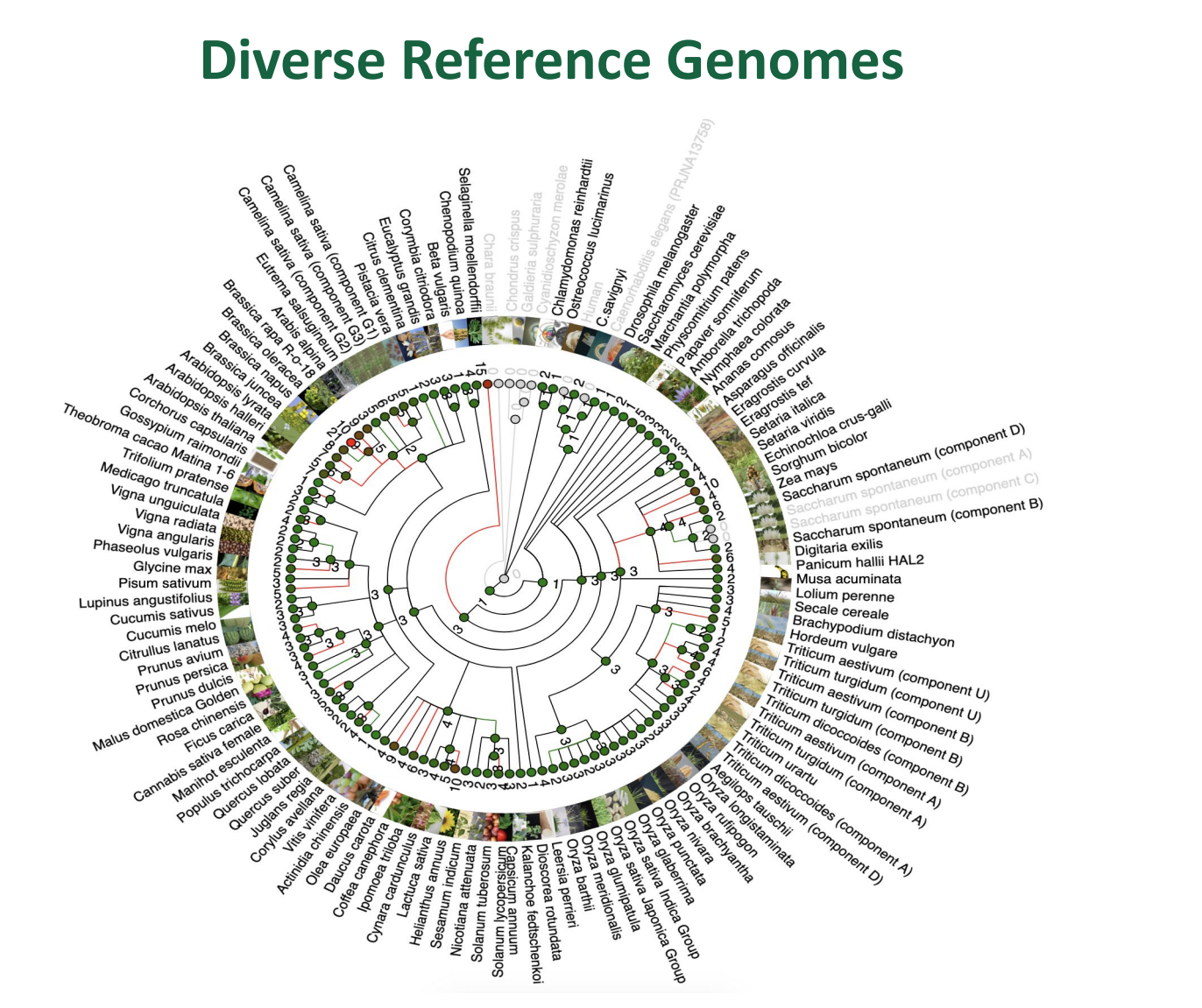
<https://gramene.org/CLIMtools>

CLIMtools is a set of interactive web-based databases of the environment x genome associations and correlations between the local environment and a pool of curated phenotypes.

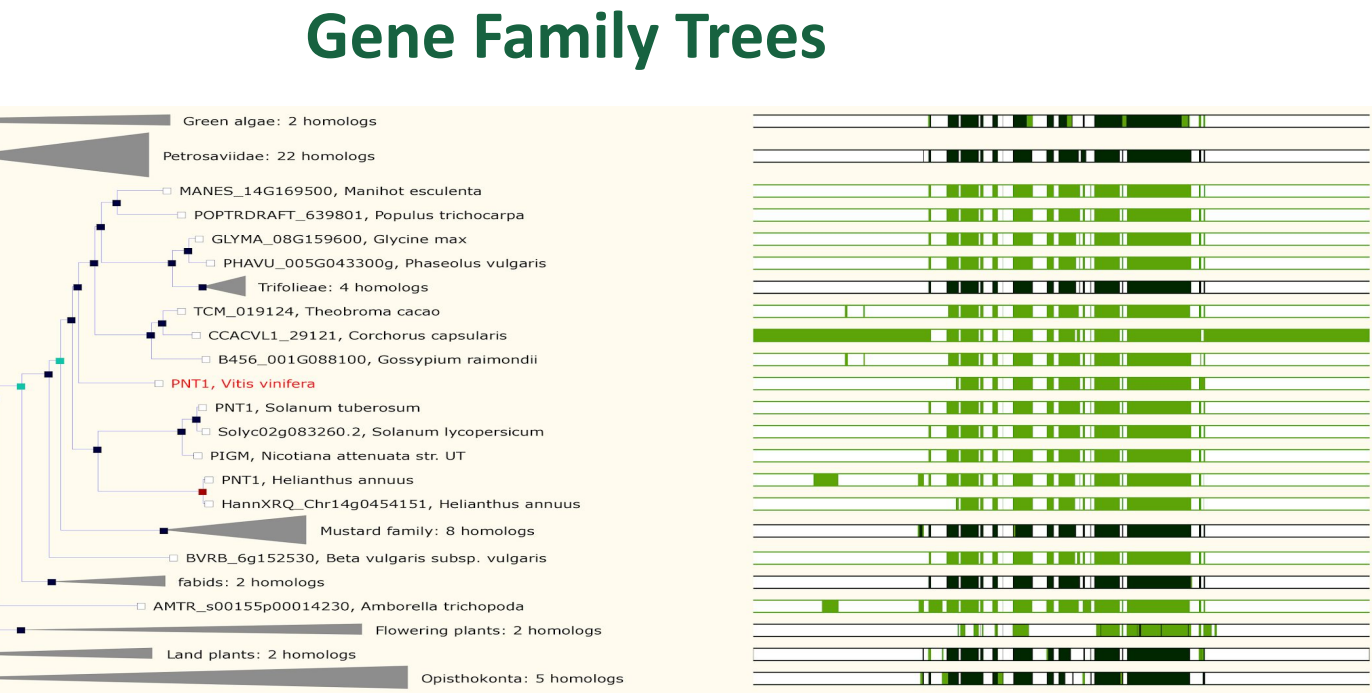


GENOMES, PATHWAYS & EXPRESSION

Diverse Reference Genomes

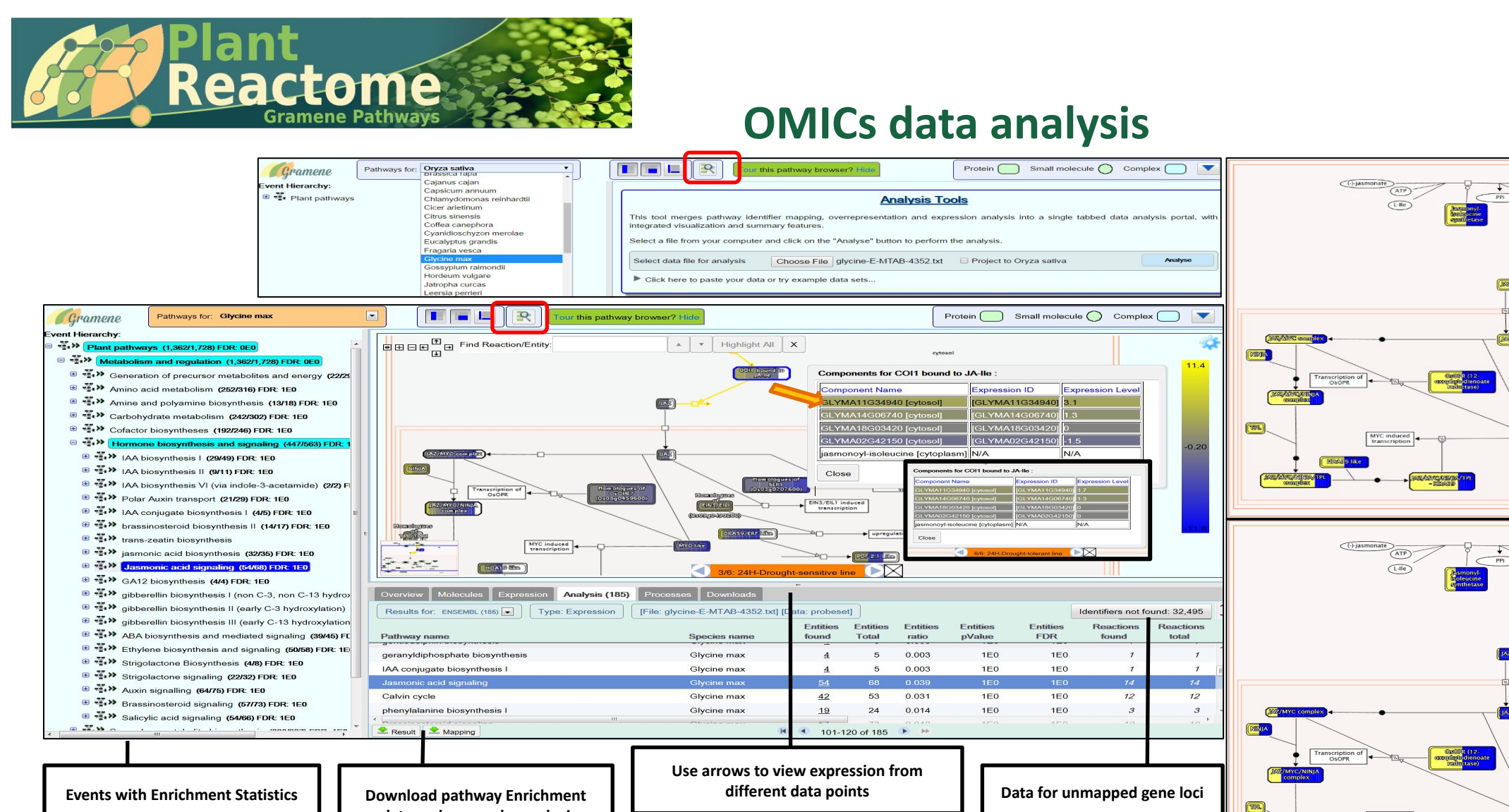


Gene Family Trees



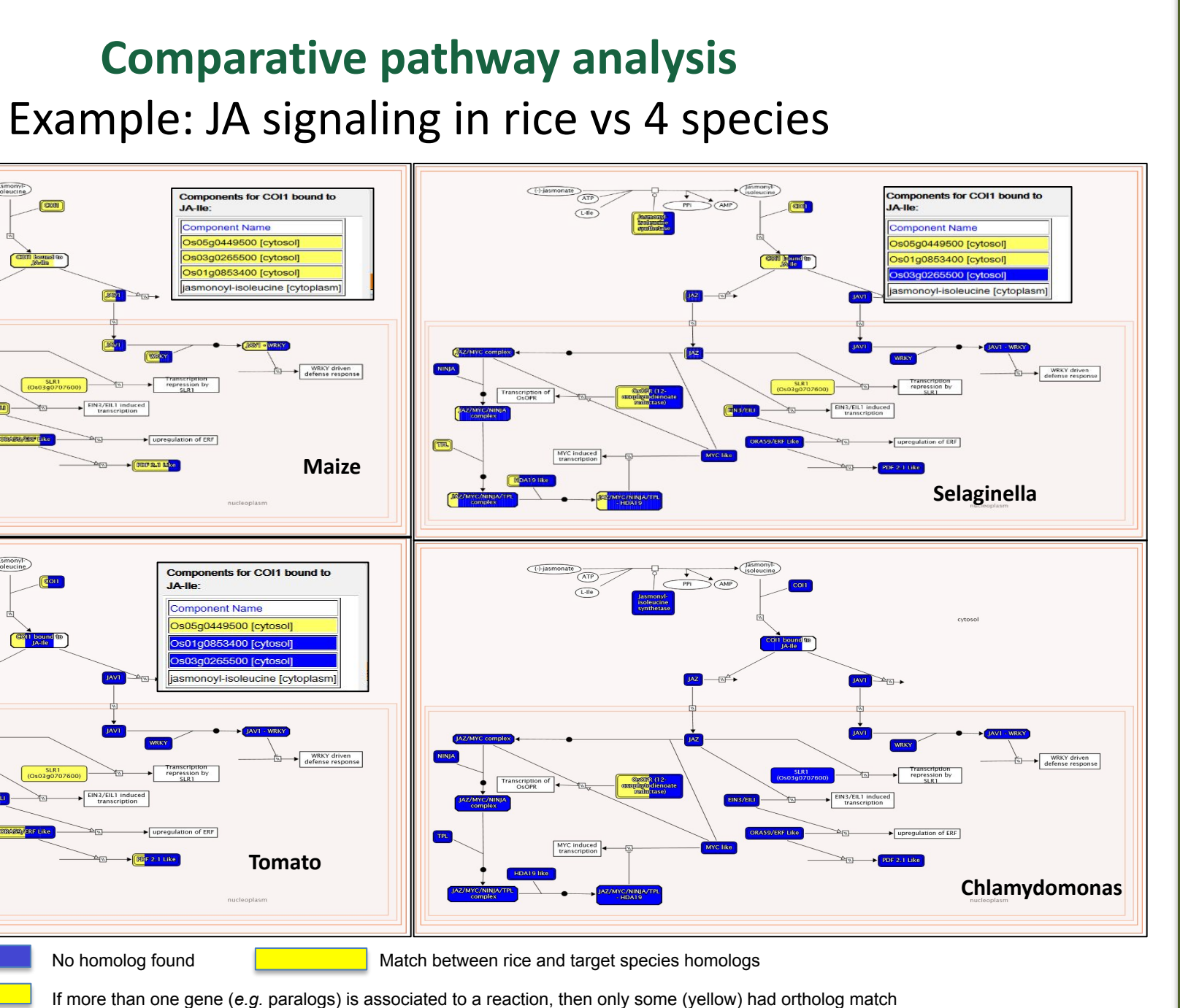
Plant Reactome

OMICs data analysis

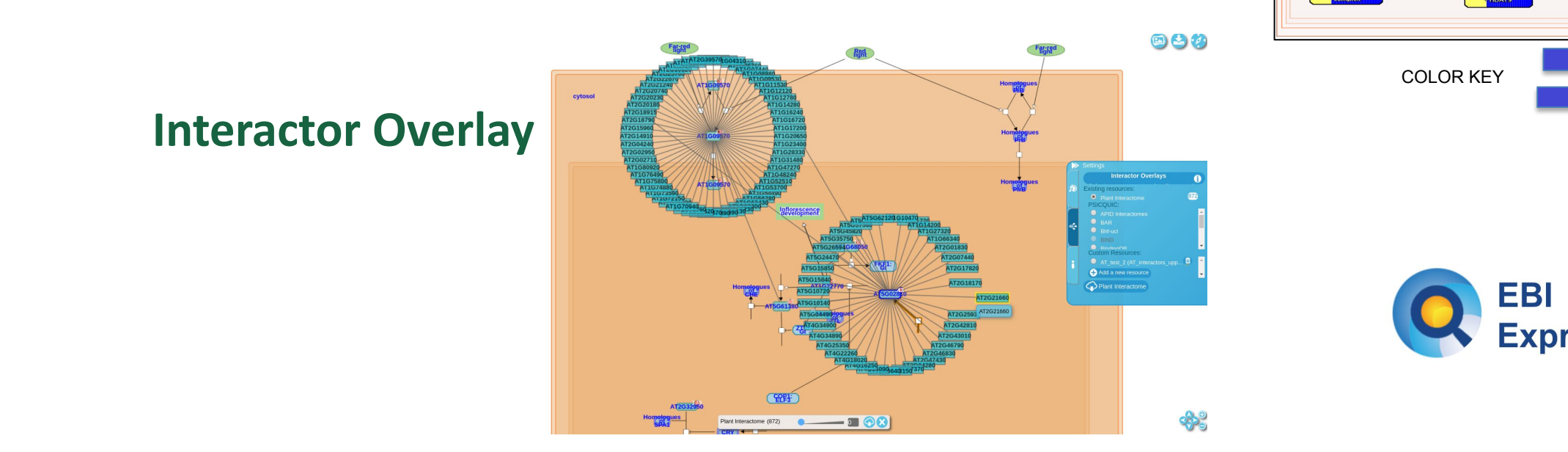


Comparative pathway analysis

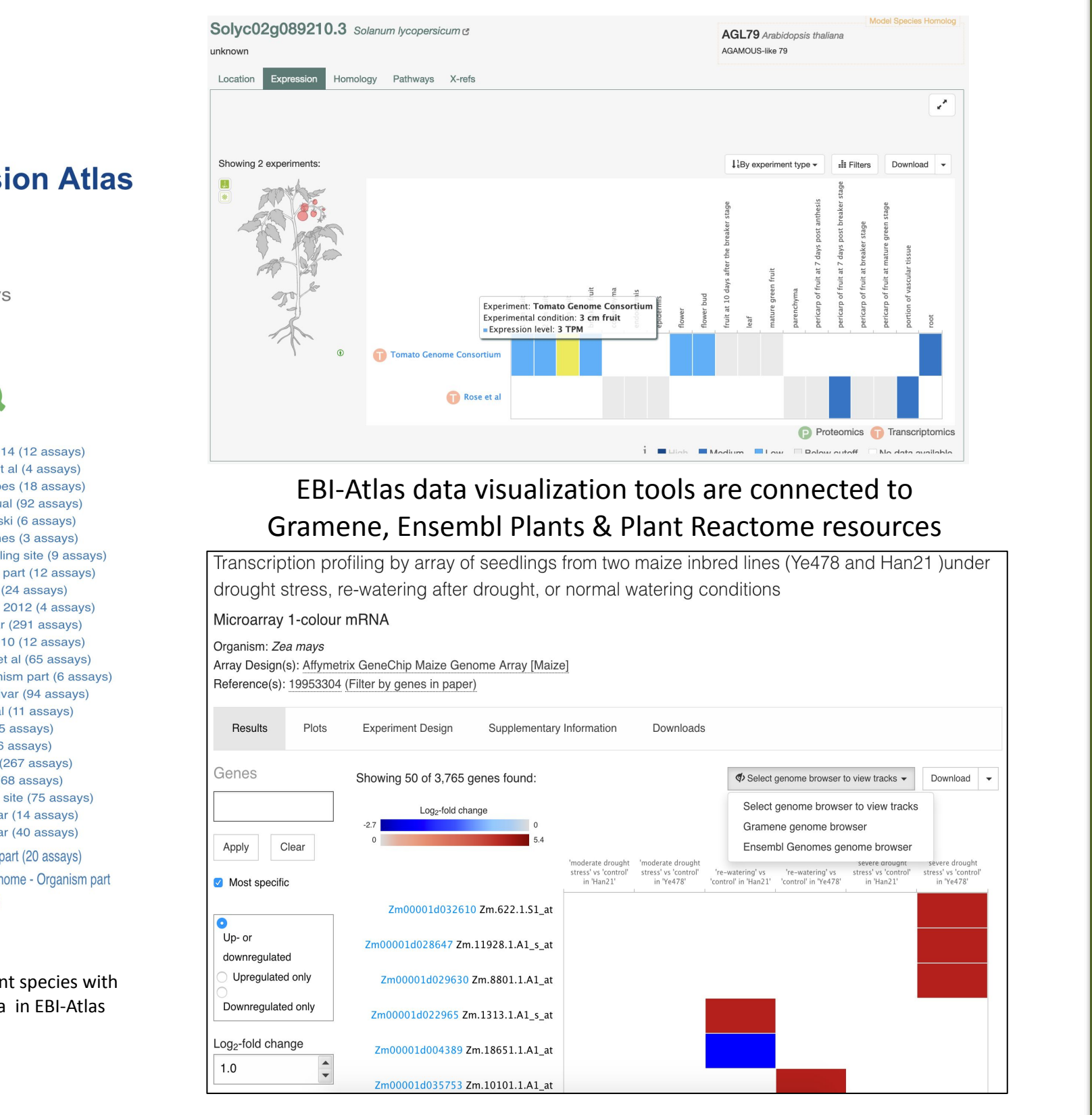
Example: JA signaling in rice vs 4 species



Interactor Overlay

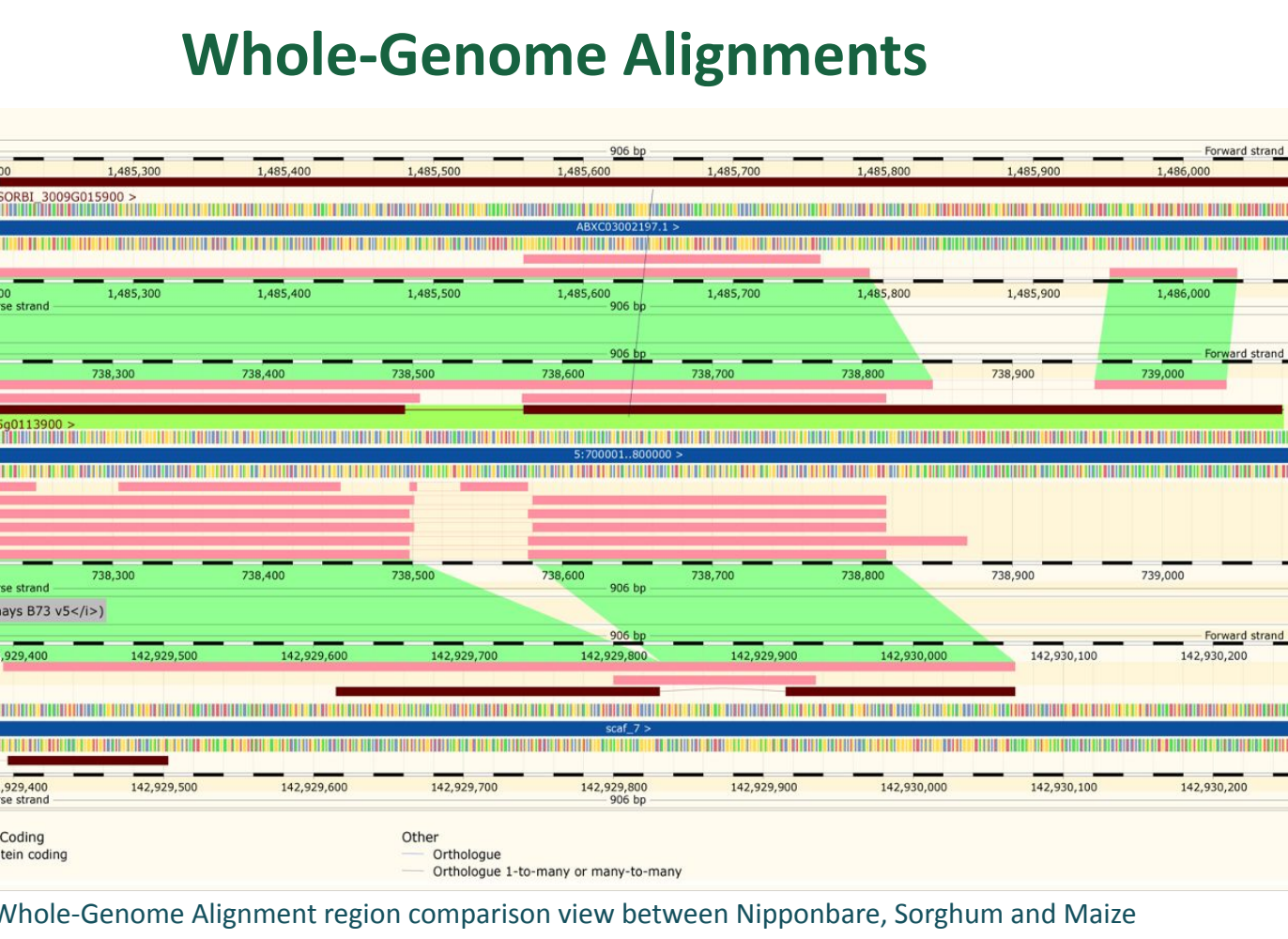


EBI Expression Atlas

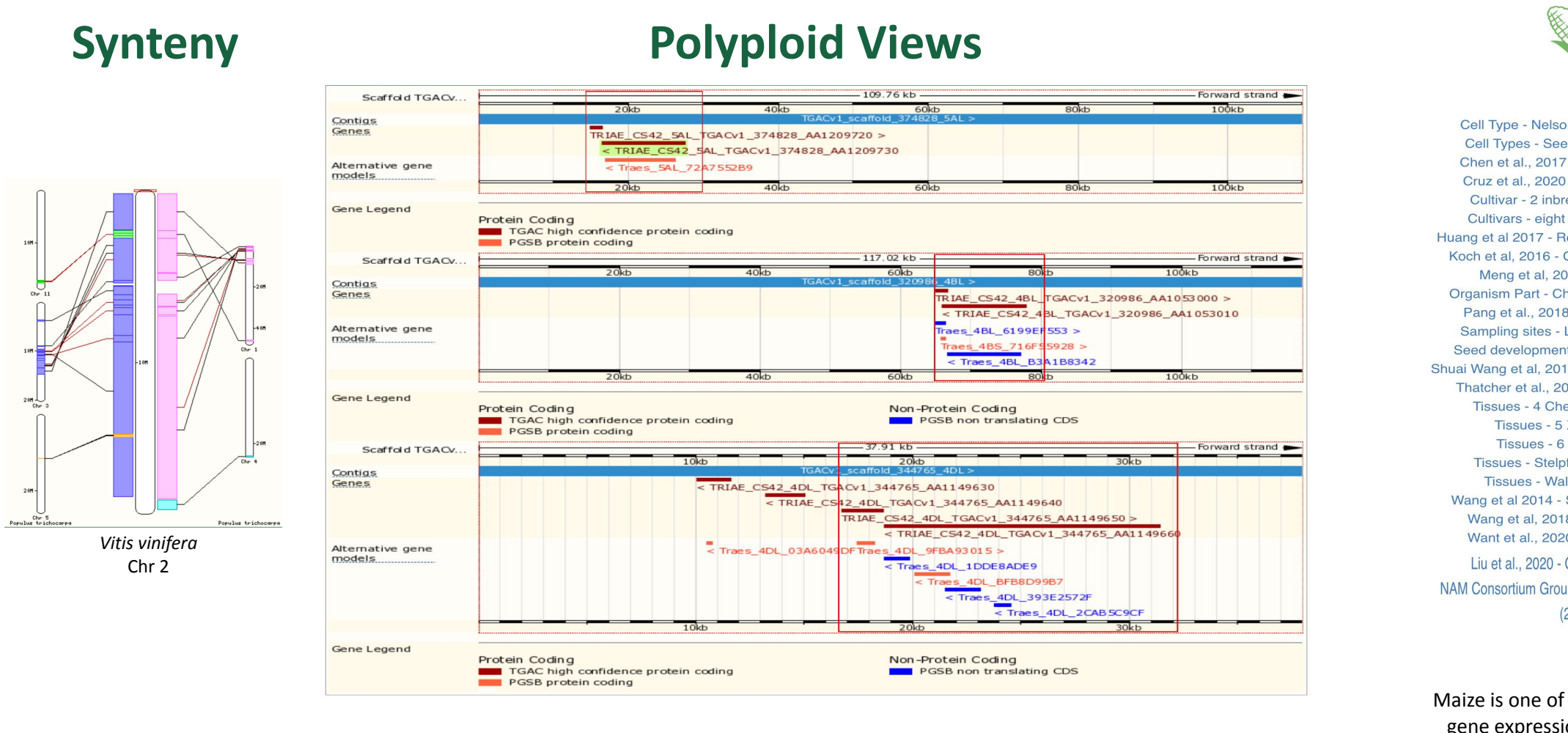


EBI-Atlas data visualization tools are connected to Gramene, Ensembl Plants & Plant Reactome resources


Whole-Genome Alignments



Synteny



Polyploid Views





BUILD 66 HIGHLIGHTS

- 128 plant reference assemblies including 14 new genomes added in the past year.
- Gene models with functional & structural annotations.
- Protein-based gene trees with 152K gene families (5.1M input proteins) provide access to orthologs and paralogs and the ability to transverse across species.
- 278 whole-genome alignments between each genome and a reference monocot (e.g., rice) and dicot (e.g., grape) genomes & 79 synteny maps.
- A new CLIMtools portal brings interactive web-based views of Environment x Genome associations, RiboSNitch prediction, and correlations between the local environment and a pool of curated phenotypes.
- Genetic variation amounts to >238 M markers including SNPs, QTLs, SSR/RFLPs and EMS-induced variants.
- 336 curated rice pathways and orthology-based projections for 120 species allow inter-species comparisons (Plant Reactome).
- Baseline and differential expression data sets from 982 experiments and 28 reference plant species (Expression Atlas).
- Read more: <https://www.gramene.org/news>

COMMUNITY ENGAGEMENT

Outreach and Training

Educational resources and webinars

- Download a quick start Gramene pamphlet and other e-learning materials: <http://www.gramene.org/outreach>
- Subscribe to Gramene's mailing list
- Gramene's YouTube channel
- Follow Gramene in Social Media:  

Gramene is developed in collaboration with Ensembl Plants, and leverages the Ensembl & Reactome platforms

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