Gramene: Comparative Plant Genome Resource

(www.gramene.org)

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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

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

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

Alignment Overview

Multiple Sequence Alignment


Neighborhood Conservation (+/- 10 genes)

Plant Pan Genomes
Gramene-powered sites focused on specific crops

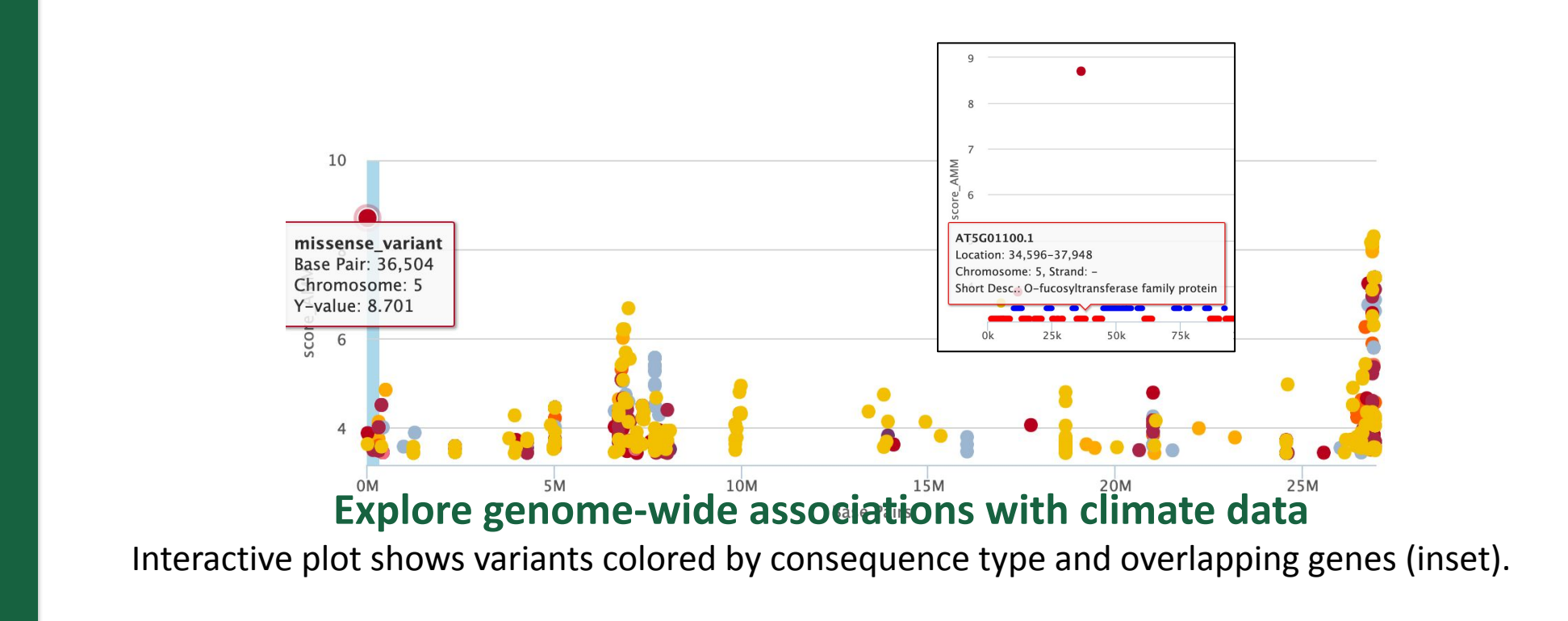| Crop	Current release (date)	Genomes	Gene Families
sorghum	R5 (Dec 2022)	28	44K
maize	R3 (Mar 2023)	35	31K
rice	R6 (Jan 2023)	28	38K
grapevine	R3 (May 2022)	18	28K

CLIMTOOLS

Arabidopsis CLIMtools v2.0

https://gramene.org/CLIMtools

CLIMtools is a set of interactive web-based databases of the environment × genome associations and correlations between the local environment and a pool of curated phenotypes.
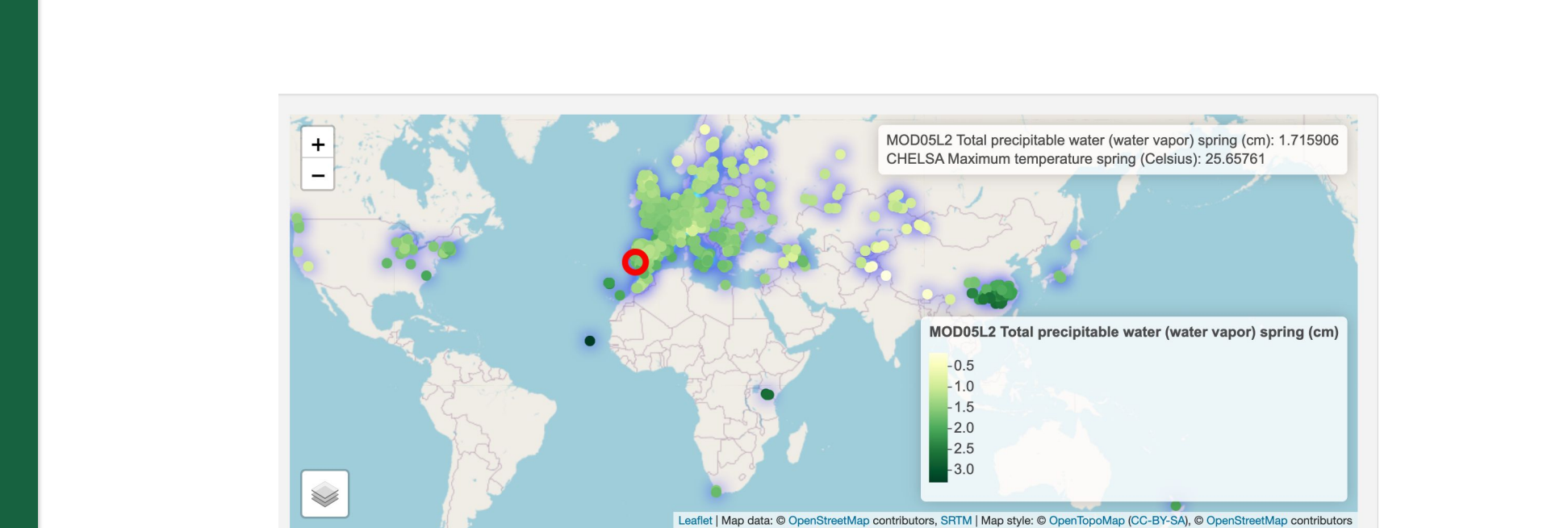
Global distribution of germplasm climate data
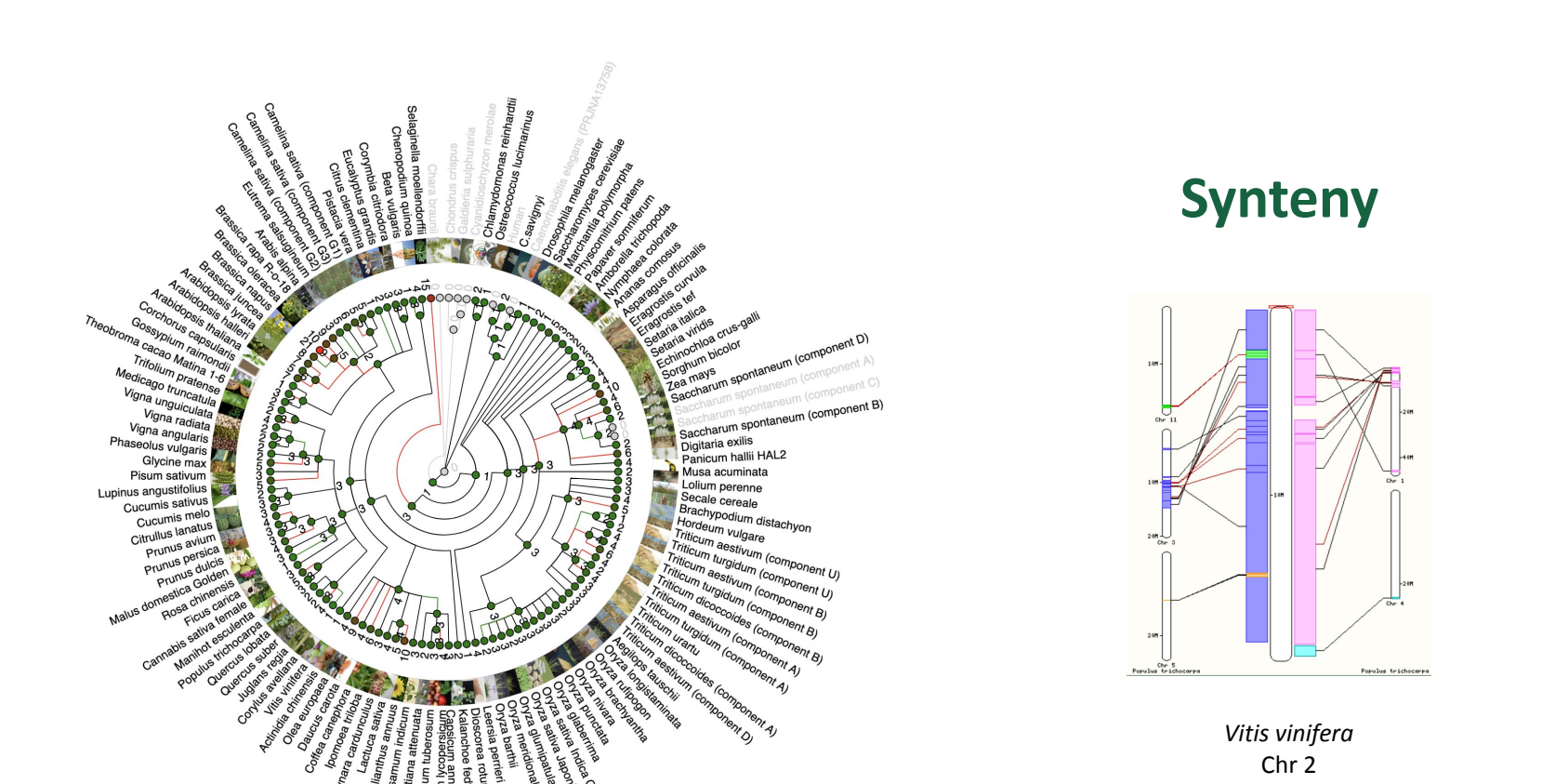Map view shows locations where specific germplasm were collected, color coded by climate variables.

Explore genome-wide associations with climate data
Interactive plot shows variants colored by consequence type and overlapping genes (inset).

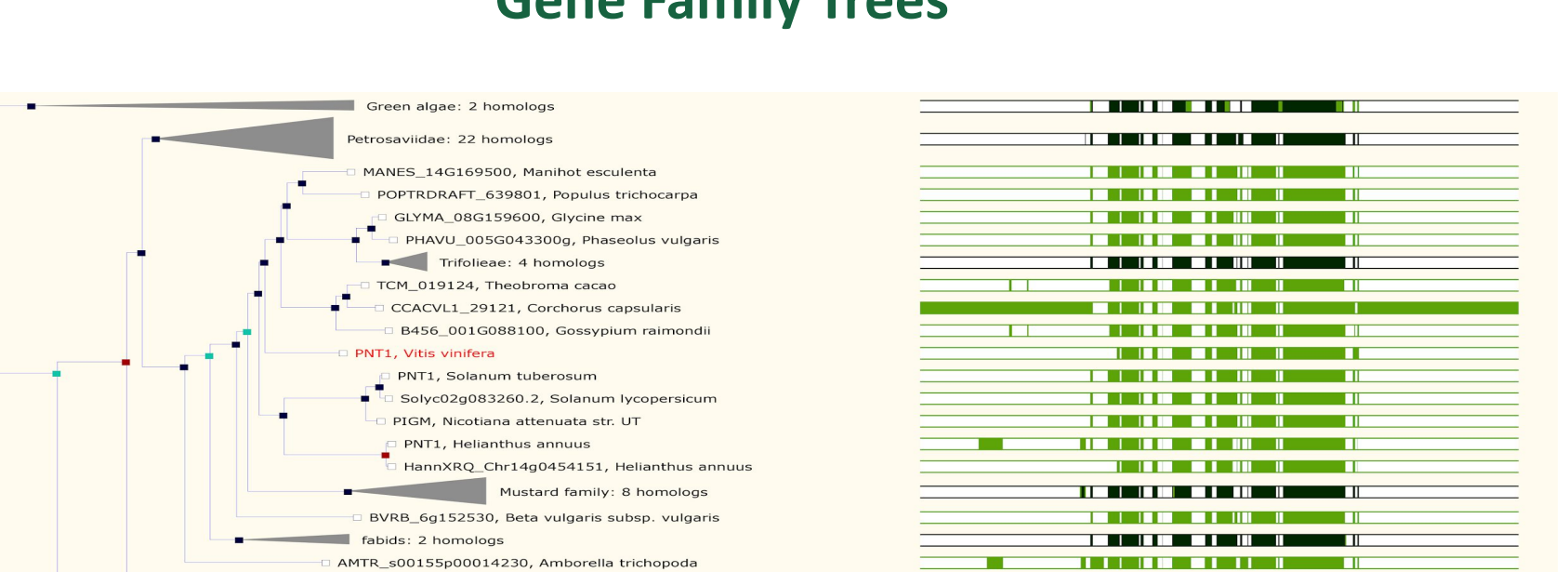## GENOMES, PATHWAYS & EXPRESSION – BUILD 66

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).
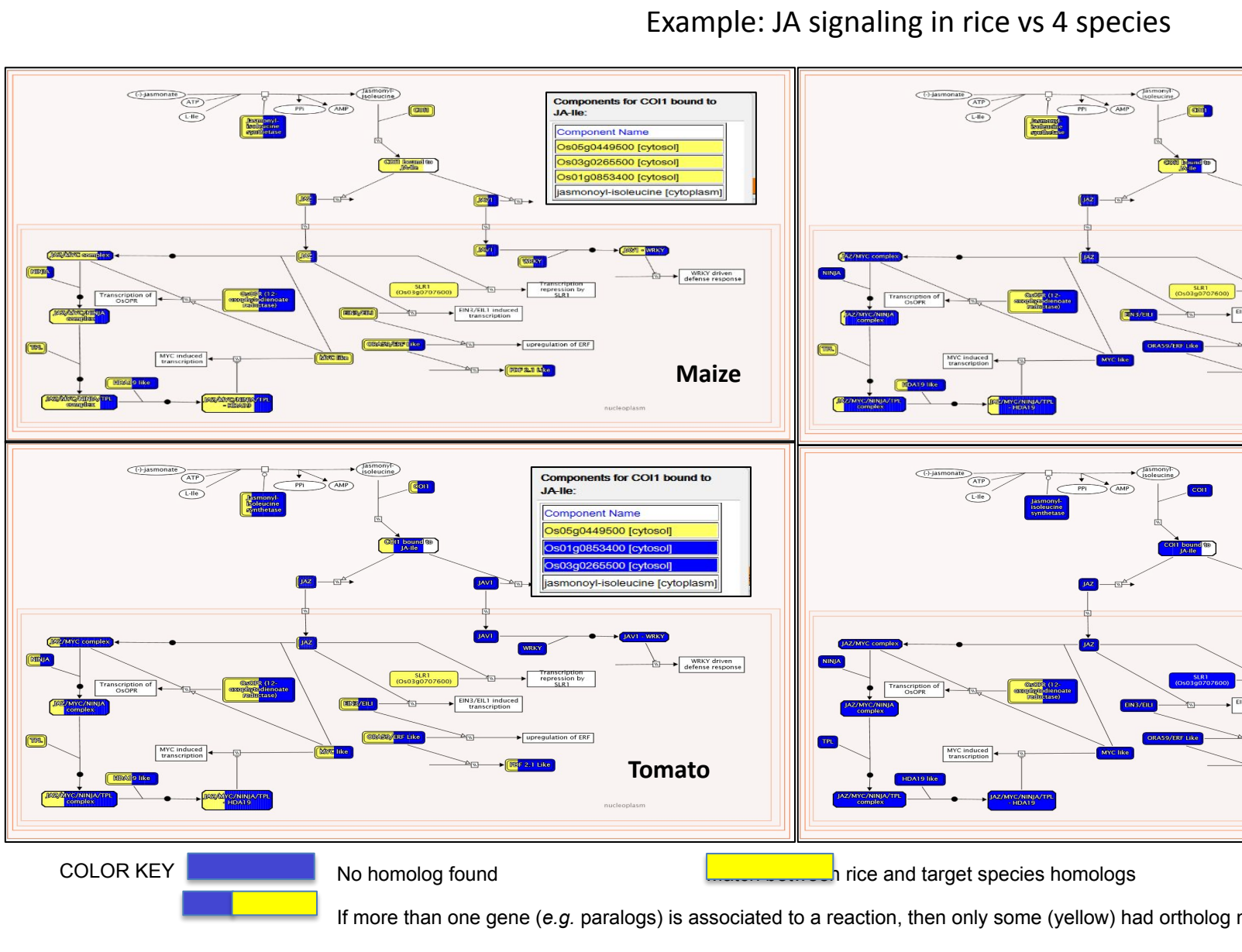- Read more: https://www.gramene.org/news
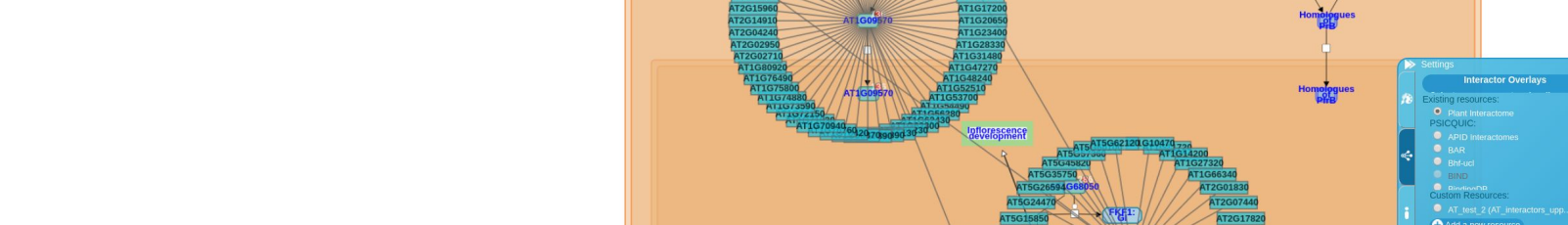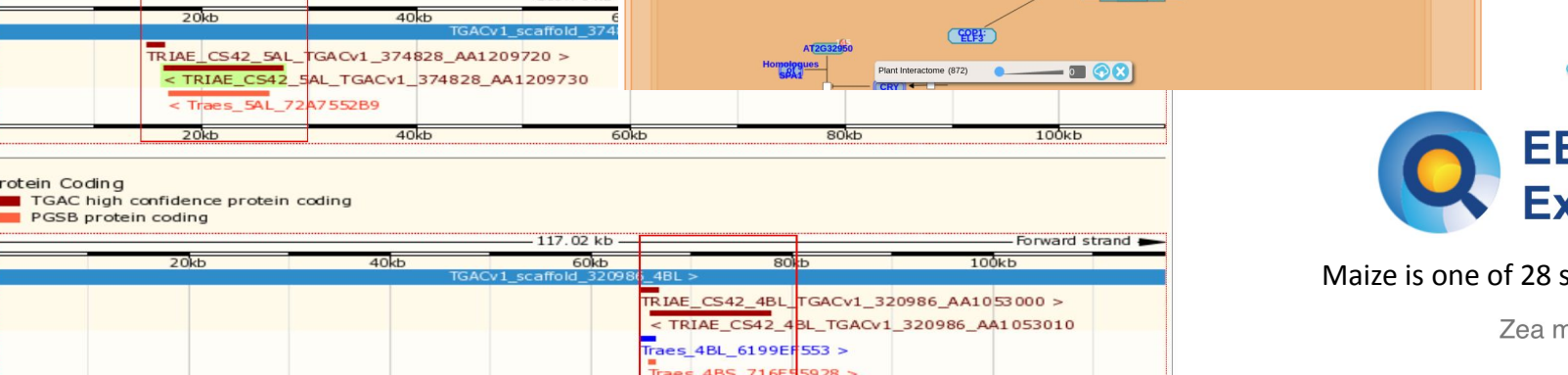
Contact us! gramene.org/feedback

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 to
- Follow Gramene in Social Media:

@GrameneDatabase

128 reference genomes

Synteny

Vitis vinifera Chr 2

Gene Family Trees

Whole-Genome Alignments

Whole-Genome Alignment region comparison view between Nipponbare, Sorghum and Maize

Comparative pathway analysis
Example: JA signaling in rice vs 4 species

Maize / Selaginella / Tomato / Chlamydomonas

COLOR KEY: No homolog found / If more than one gene (i.e. paralogs) is associated to a reaction, then only some (yellow) had ortholog match / rice and target species homologs

Interactor Overlay

Polyploid Views

http://plantreactome.gramene.org

Plant Reactome — Gramene Pathways

OMICs data analysis tool

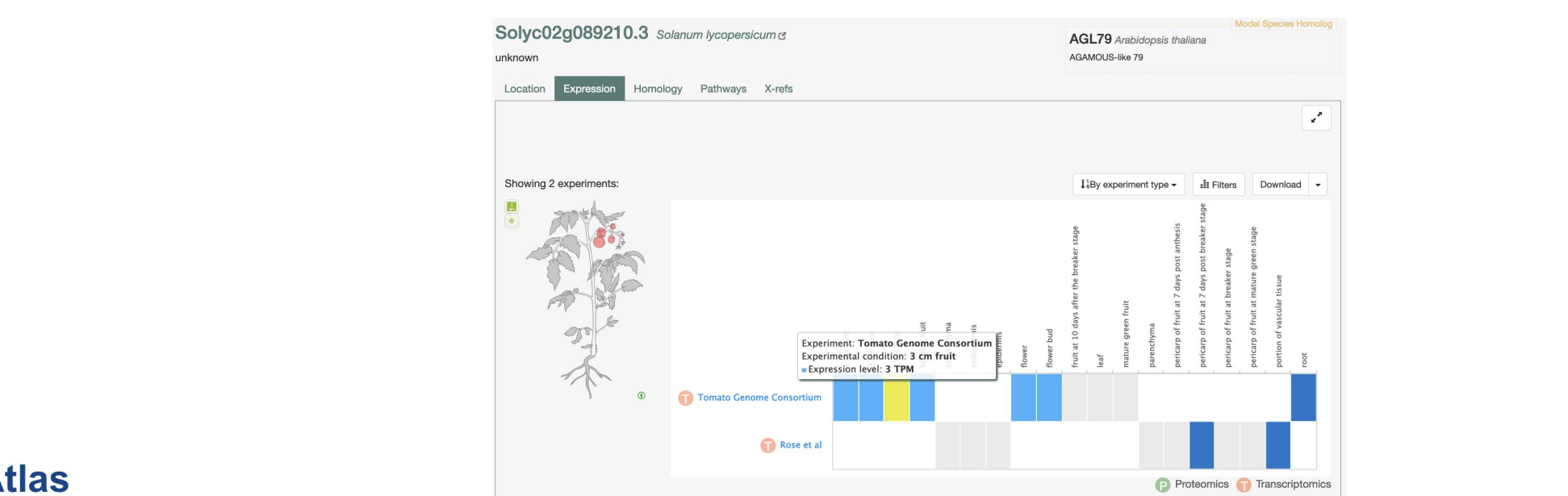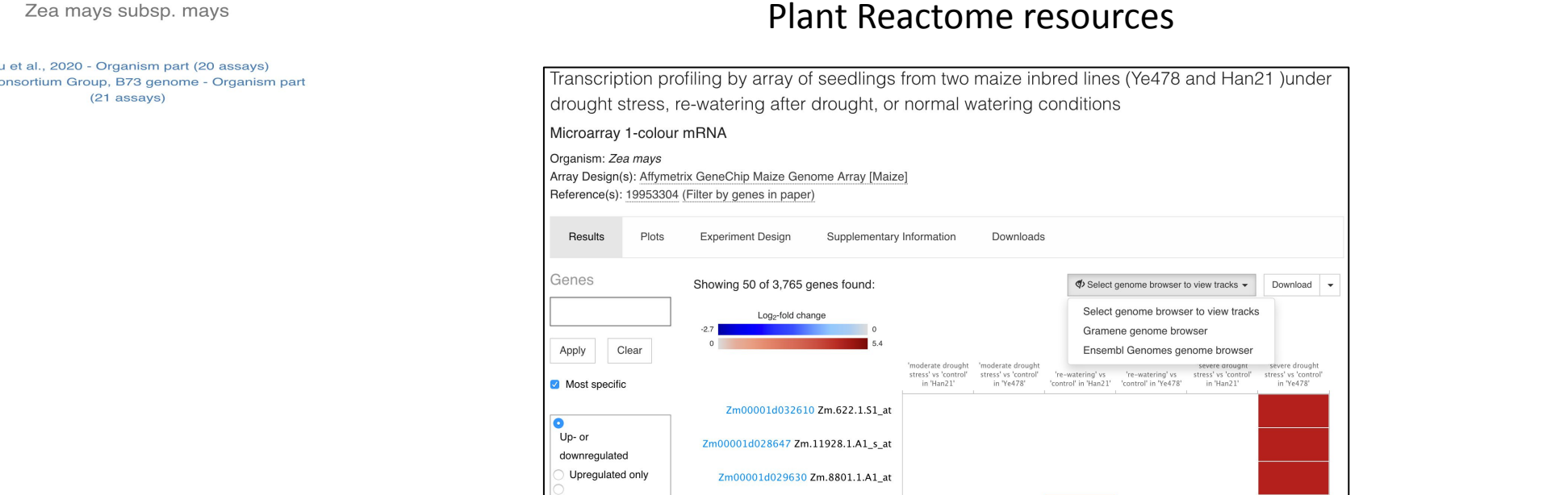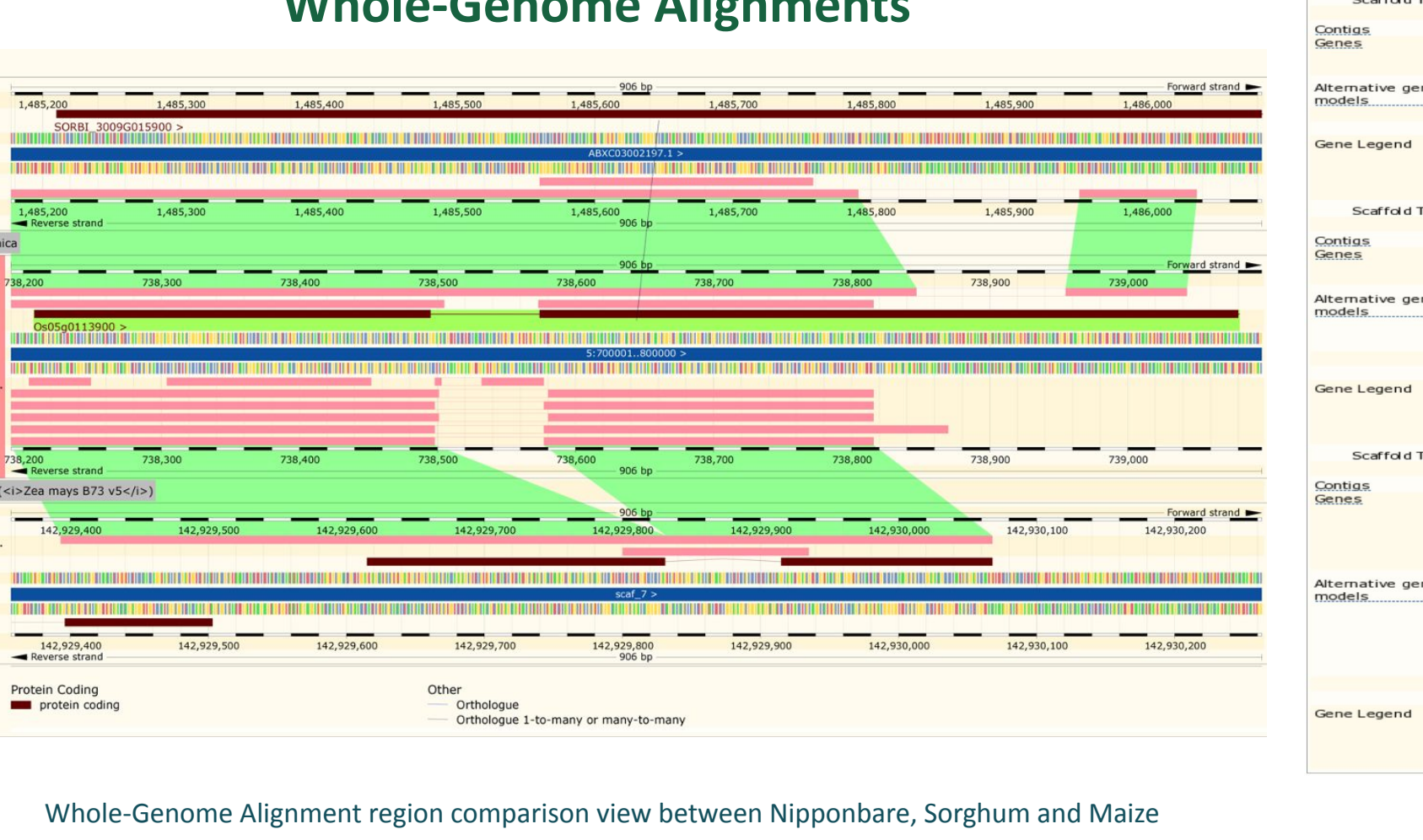|			
Events with Enrichment Statistics	Download pathway Enrichment data and mapped gene loci	Use arrows to view expression from different data points	Data for unmapped gene loci

EBI Expression Atlas

Maize is one of 28 species with gene expression in EBI-Atlas

Zea mays / Zea mays subsp. mays

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

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

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