



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

Specific Aim 1: GENOMES

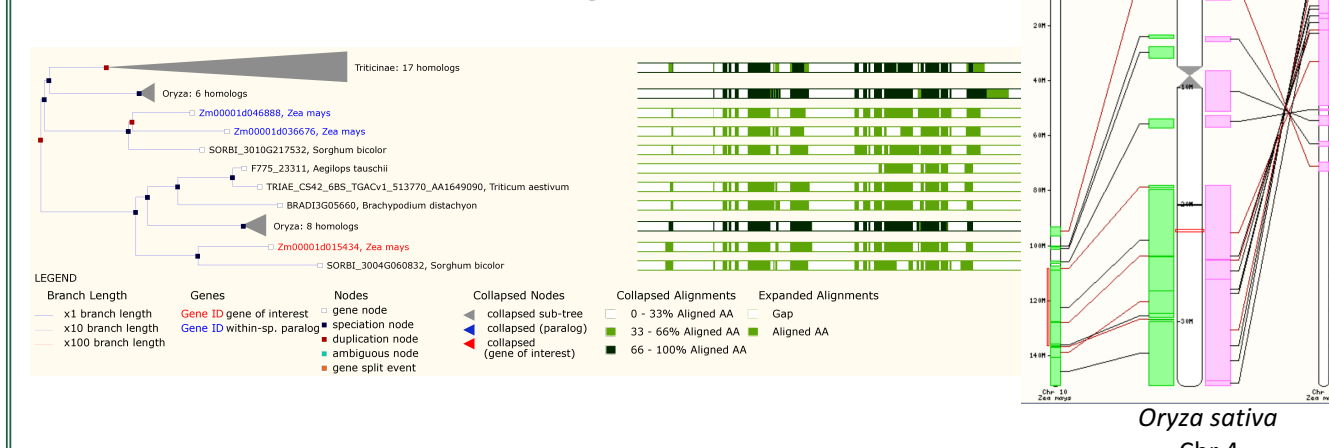
Year Highlights

- 5 database releases: build 54 (July 2017); build 55 (Sept 2017); build 56 (Jan 2018); build 56b (Feb 2018); build 57 (May 2018)
- Ensembl software updates V89-92
- 53 plant reference assemblies including:
 - 9 new genomes:
 - Cucumis sativus* (cucumber)
 - Dioscorea rotundata* (white Guinea yam)
 - Gossypium raimondii* (cotton)
 - Helianthus annuus* (common sunflower)
 - Lupinus anqustifolius* (blue lupin)
 - Manihot esculenta* (cassava)
 - Nicotiana attenuata* (coyote tobacco)
 - Phaseolus vulgaris* (common bean)
 - Corchorus capsularis* (Jute)
 - 4 updated genomes:
 - Sorghum bicolor* (sorghum [V3])
 - Glycine max* (soybean [V3])
 - Prunus persica* (peach [V2])
 - Hordeum vulgare* (barley [V2])
 - Updated gene models:
 - Zea mays* (corn [V4])
 - Oryza sativa japonica* (rice [IRGSP1])
- New polyploid views for wheat
- New gene structural annotations: maize, barley & rice
- New functional annotations (e.g., InterPro domains)
- Updated protein gene trees
- New genetic variation to a total of 230.5 M variants:
 - 13M SNPs *Arabidopsis thaliana* (1001 Genomes Project)
 - 20,483 rice QTLs (Gramene archives & Q-TARO database)
 - 1,278 rice SSR/RFLPs (Gramene archives)
 - 7.4 M EMS-induced wheat point mutations (Ksenia *et al.*, 2017)
- Over 1,600 public RNA-Seq studies from Track Hub
- New gene neighborhood views for local synteny
- New whole-genome alignments (WGs) for maize vs sorghum, and barley vs rice and Brachypodium
- New ncRNA feature alignments across all plants
- New and updated functional genomics databases (*i.e.*, gene expression arrays probes)
- New maize transposon annotation (Jiao *et al.*, 2017)

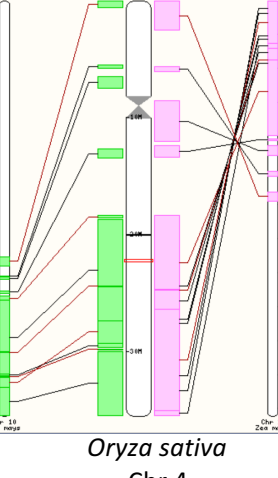
RNA-Seq Data from Public Track Hub Registry



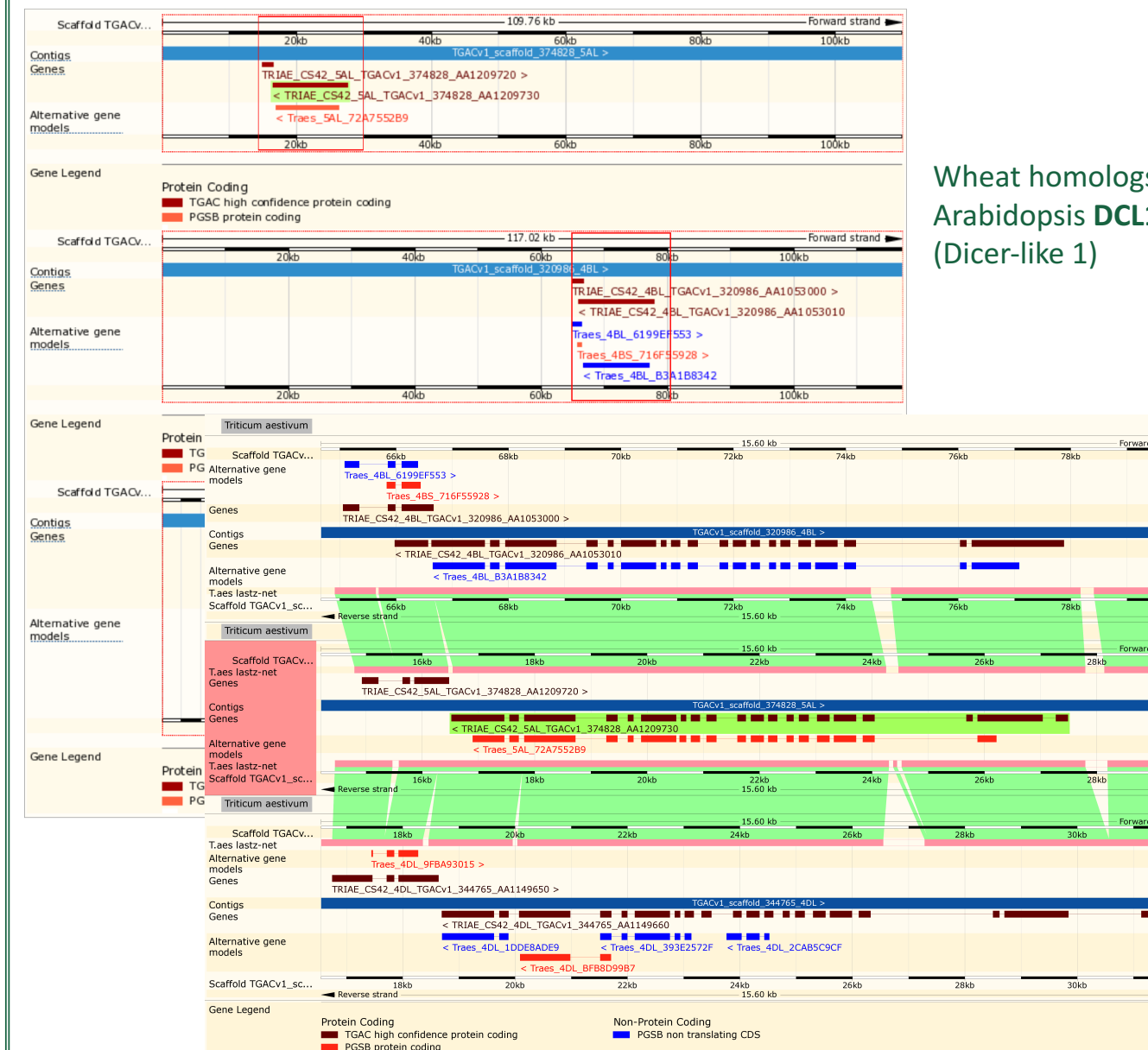
Gene Family Trees



Synteny



Polyploid Views & Whole-Genome Alignments



Wheat homologs of Arabidopsis DCL1 (Dicer-like 1)

Specific Aim 2: PATHWAYS & EXPRESSION

Year Highlights

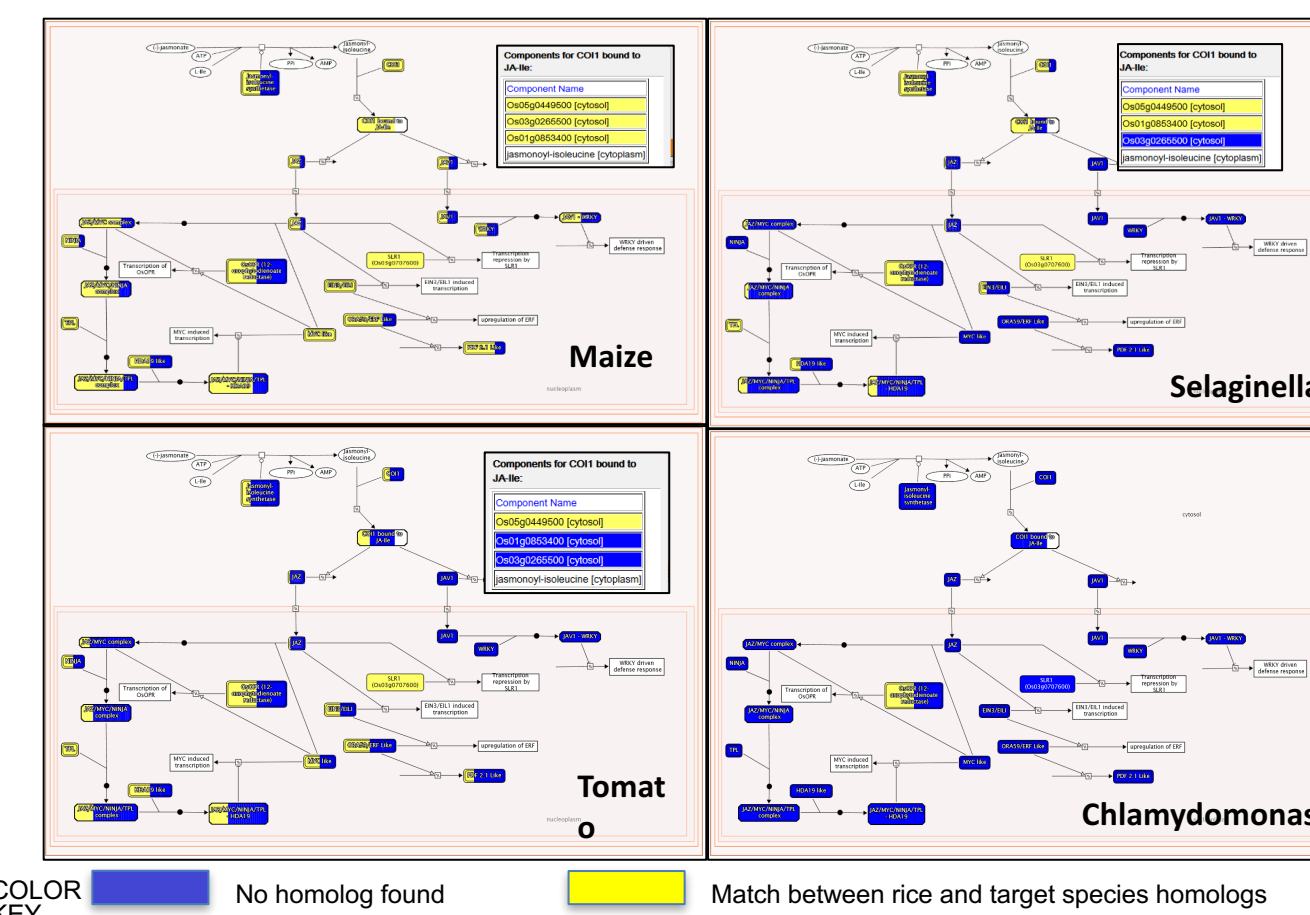
- 22 newly curated rice pathways to a total of 264 reference rice pathways
- Orthology-based projections to 74 plant species including maize allows pathway enrichment and inter-species comparison
- Baseline and differential expression data sets from 780 experiments and >20 reference plant species (Expression Atlas)

Newly curated pathways

- Reproductive structure development
- Anther and pollen development
- Vegetative structure development
- Primary root development
- Response to submergence
- Underwater shoot and internode elongation
- Response to phosphate deficiency
- Photorespiration
- Ureide biosynthesis
- Beta-alanine betaine biosynthesis
- Proline biosynthesis V from arginine
- Phospholipid biosynthesis I
- Sphingolipid metabolism
- Response to iron deficiency
- Mugineic acid biosynthesis
- Iron uptake and transport in root vascular system
- Proline degradation
- Glutamate degradation
- Phenylalanine degradation III
- Lysine degradation II
- Threonine degradation

Comparative pathway analysis

Example: JA signaling in rice vs 3 species

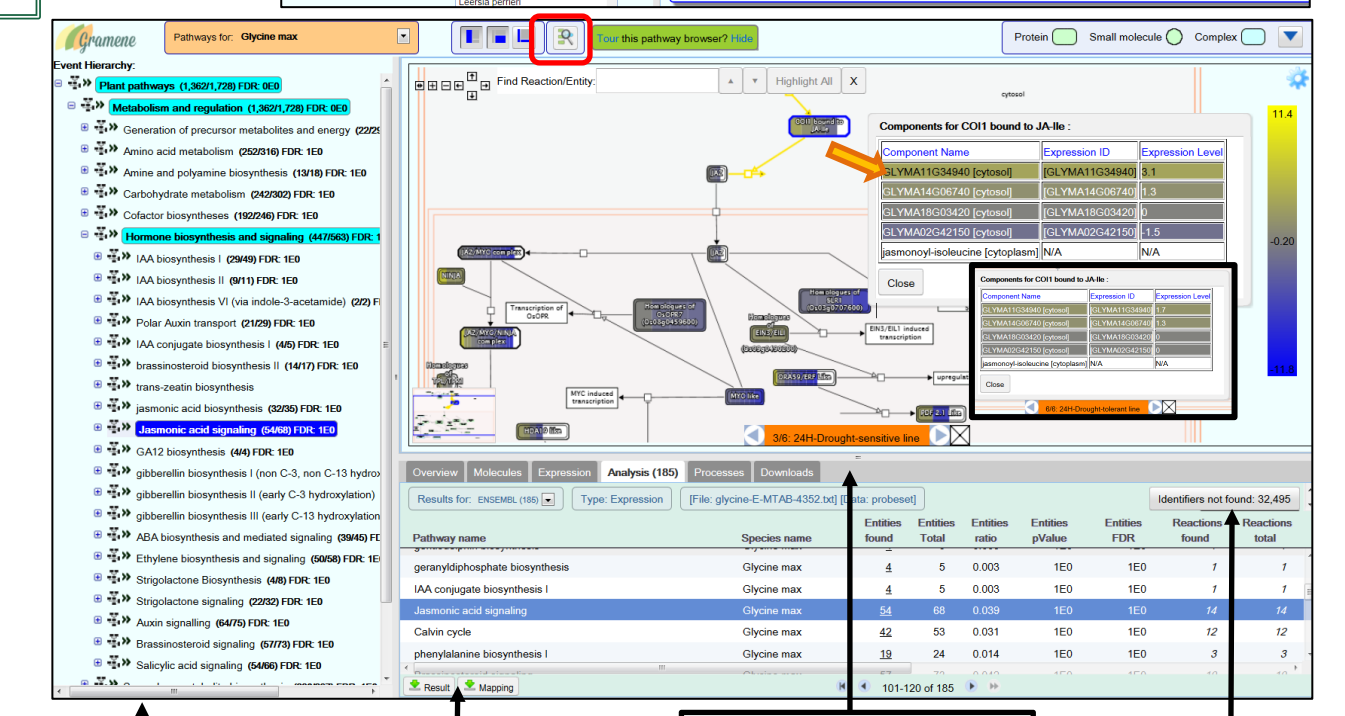
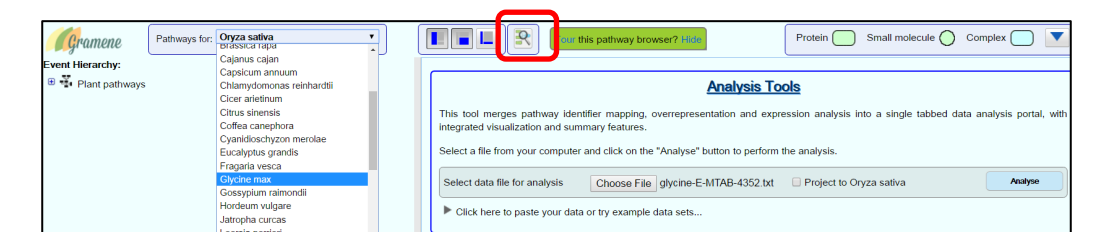


COLOR KEY: No homolog found (blue), Match between rice and target species homologs (yellow), If more than one gene (e.g. paralogs) is associated to a reaction, then only some (yellow) had orthology match (orange)

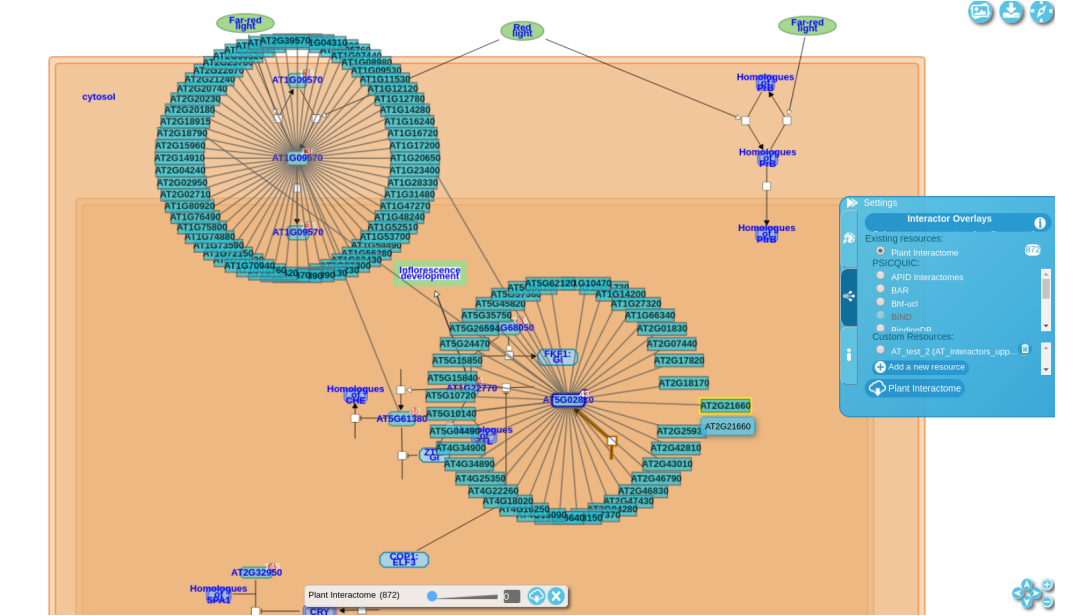
<http://plantreactome.gramene.org>



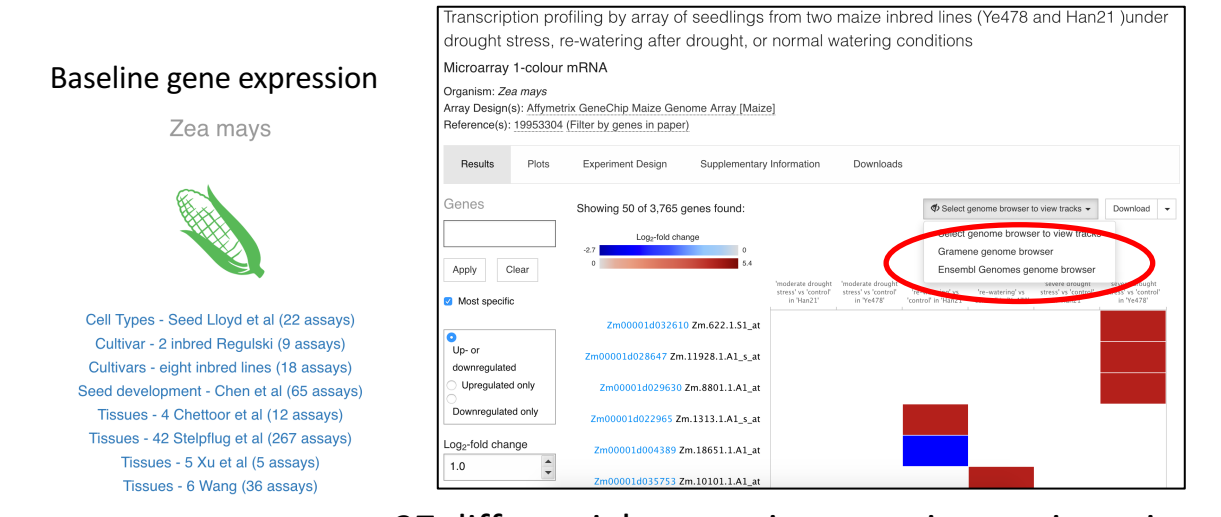
OMICS data analysis tool



Interactor Overlay



ATLAS data visualization tools are connected to Gramene, Ensembl Plants and Plant Reactome resources



27 differential expression experiments in maize

Specific Aim 3: INFRASTRUCTURE

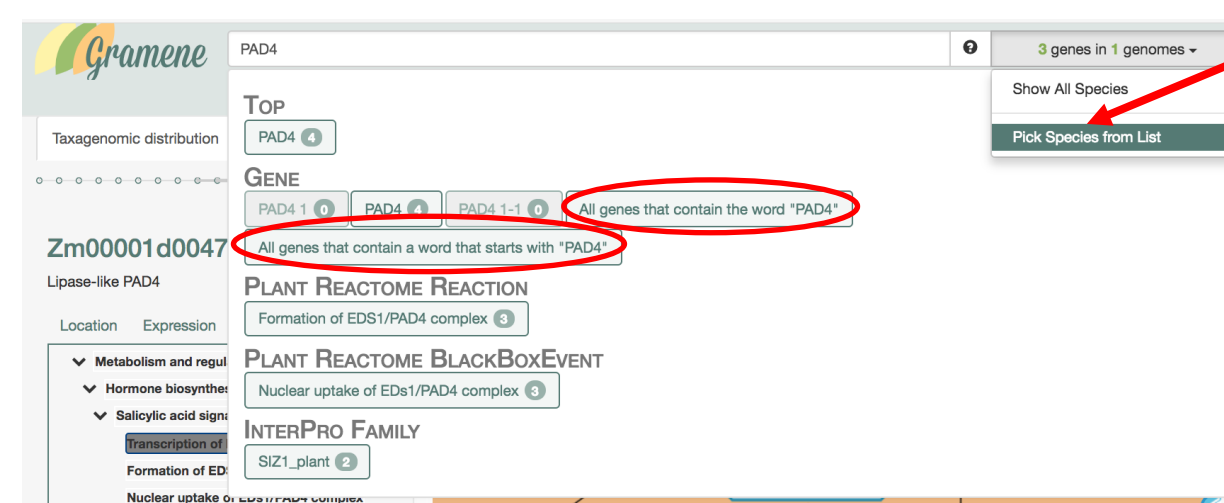
Year Highlights

- The Gramene Search Interface became Gramene's new front page <http://www.gramene.org>
- New pathways view in Gramene Search
- New neighborhood conservation mode in the Homology tab of the results of a query

Powerful search interface

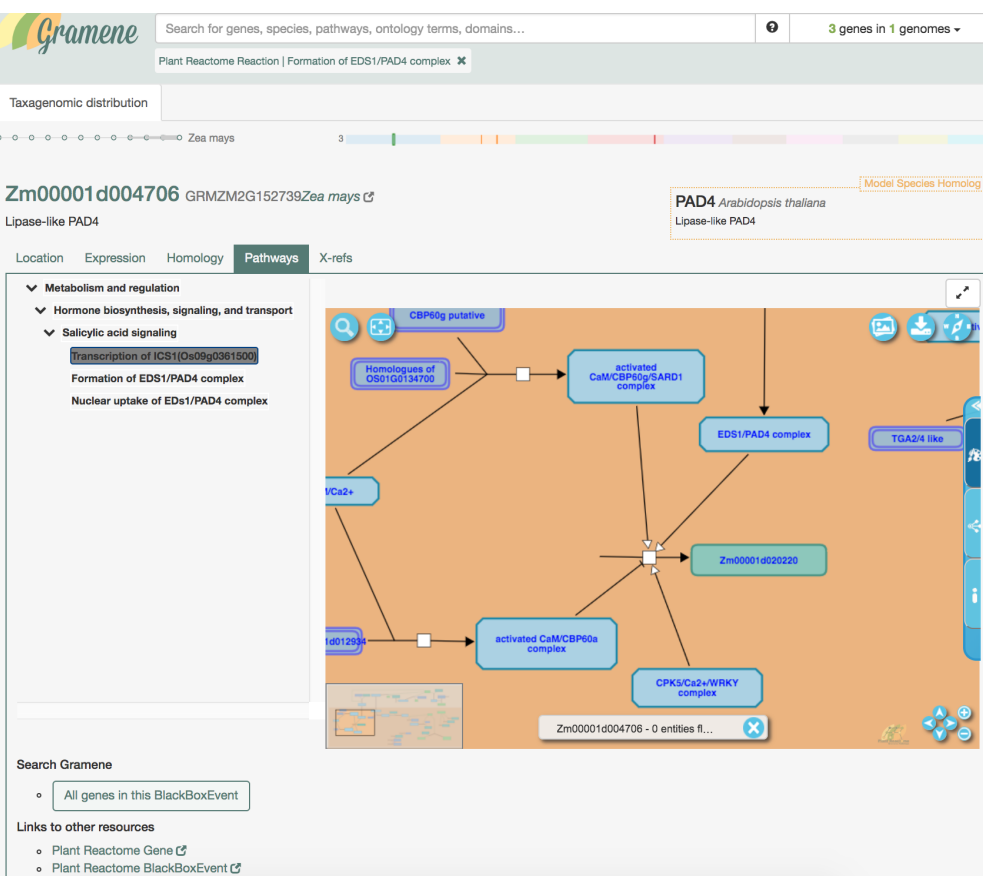
<http://www.gramene.org>

Summarize results by category, suggest text-based queries, filter by species



Pathways view

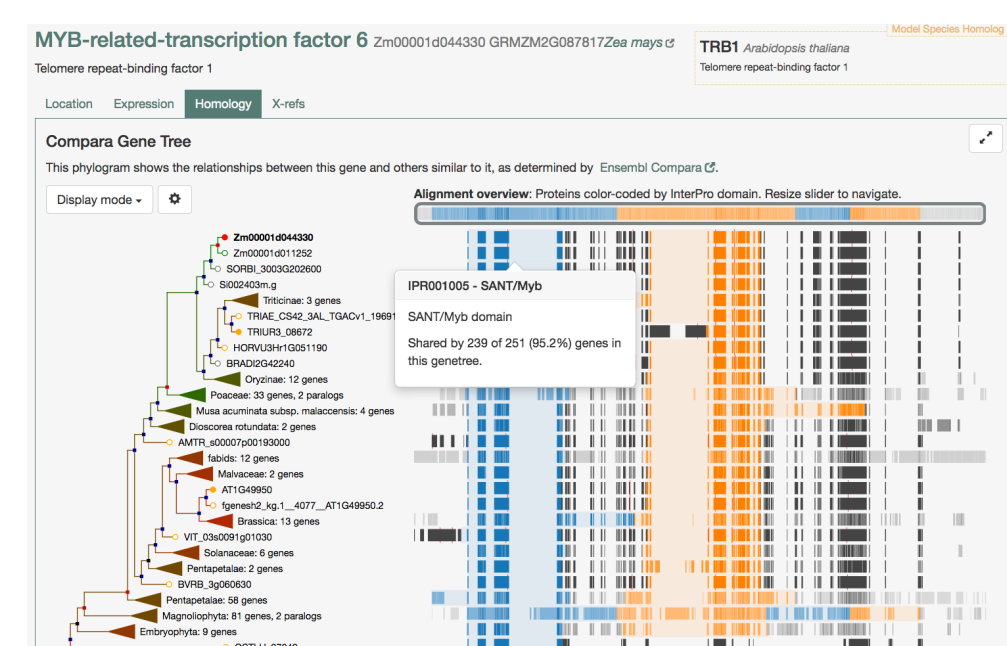
Shows the reactions and pathways that a gene takes part in with links to data downloads in Plant Reactome



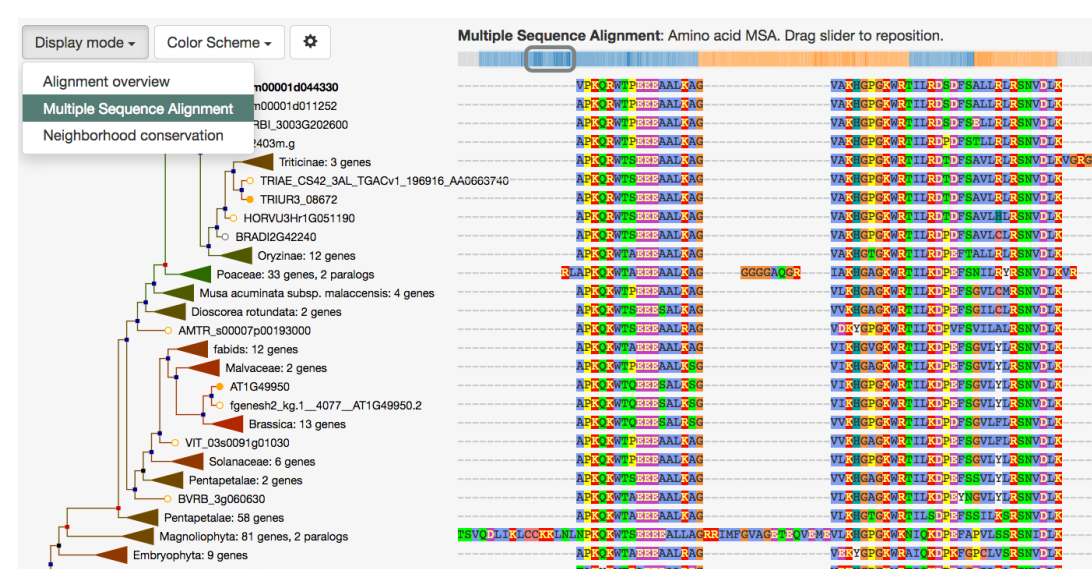
Homology view

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

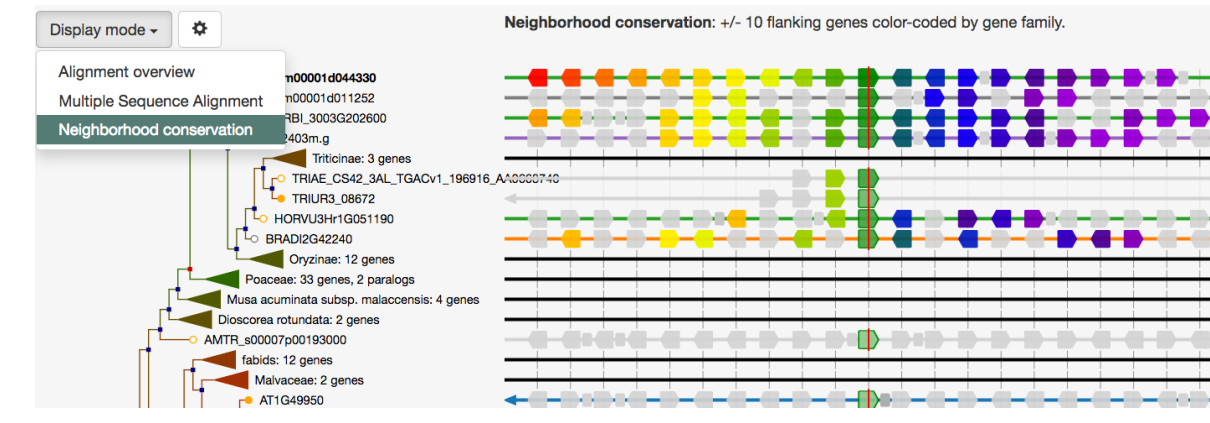
Overview



Multi-alignment view for viewing amino acid conservation



Neighborhood conservation mode +/-10 genes





Specific Aim 4: OUTREACH

Outreach and Training

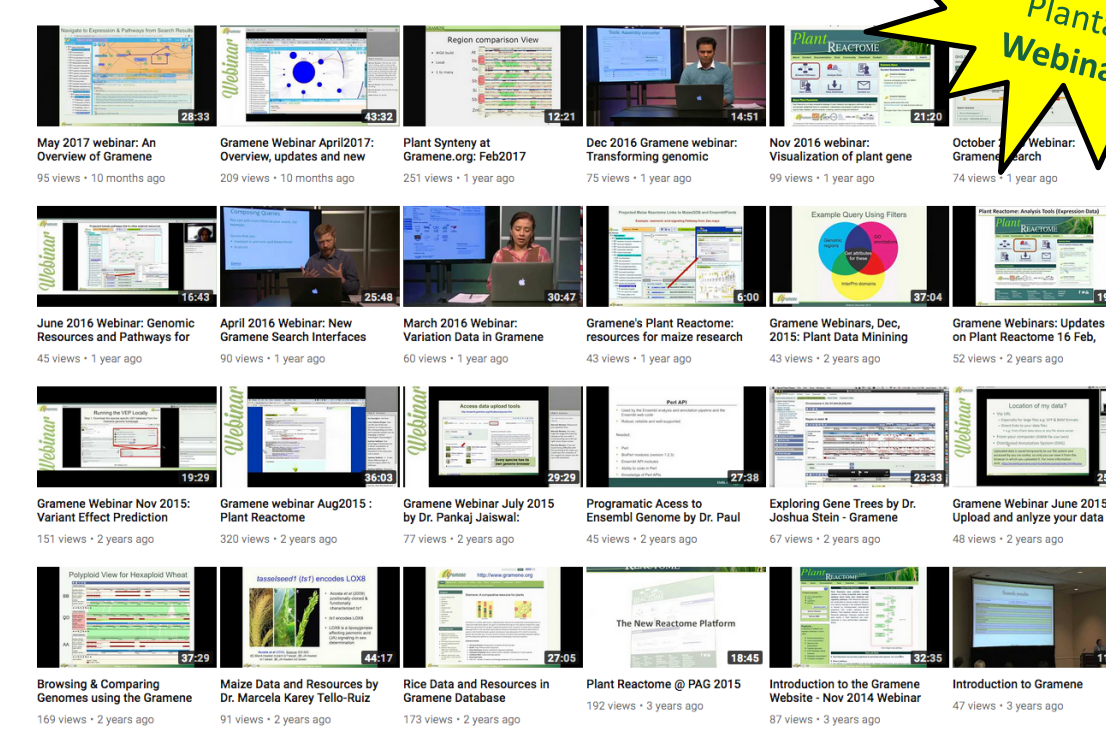
Educational resources and webinars

<http://www.gramene.org/outreach>

Find here links to:

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

Videotutorials in Gramene's YouTube



Selected outreach activities:

- Gene annotation jamboree in collaboration with the MaizeCODE project. Recruiting interested PUIs
- Coordination on data and metadata formats, standards and best practices with the AgBioData Consortium
- Bioinformatics resources outreach booths with AgBioData Consortium
- User workshops & developers hackathons
- DNA & bioinformatics summer camps



Maize Annotation Jamboree 2018

Are there targeted training needs for your project or university? Are you a scientist looking for short visit stays?

Contact us! feedback@gramene.org

Recent publications

- Tello-Ruiz *et al.* (2018). Gramene 2018: unifying comparative genomics and pathway resources for plant research. *Nucleic Acids Res.* 46(D1):D1181.
- Wang *et al.* (2018). A comparative transcriptional landscape of maize and sorghum obtained by single-molecule sequencing. *Genome Res.* 28(6):921.
- Jiao *et al.* (2018). Efficient Identification of Causal Mutations through Sequencing of Bulk F₂ from Two Allelic Bloomless Mutants of *Sorghum bicolor*. *Front Plant Sci.* 8:2267.
- Stein *et al.* (2018). Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus *Oryza*. *Nat Genet.* 50(2):285.
- Jiao *et al.* (2017). Improved maize reference genome with single-molecule technologies. *Nature* 546(7659):524.
- Bukowski *et al.* (2017). Construction of the third generation *Zea mays* haplotype map. *Gigascience*.
- Naithani *et al.* (2017). Plant Reactome: a resource for plant pathways and comparative analysis. *Nucleic Acids Res.* 45(D1): p. D1029.
- Kersey *et al.* (2018). Ensembl Genomes 2018: an integrated omics infrastructure for non-vertebrate species. *Nucleic Acids Res.* 46:D802.
- Papatheodorou *et al.* (2018). Expression Atlas: gene and protein expression across multiple studies and organisms. *Nucleic Acids Res.* 46(D1):D246.