



Mining Maize Data in the Gramene Database

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May 22nd, 2018



Transnational collaboration



Doreen Ware



Irene Papatheodorou
Robert Petryszak

Paul Kersey

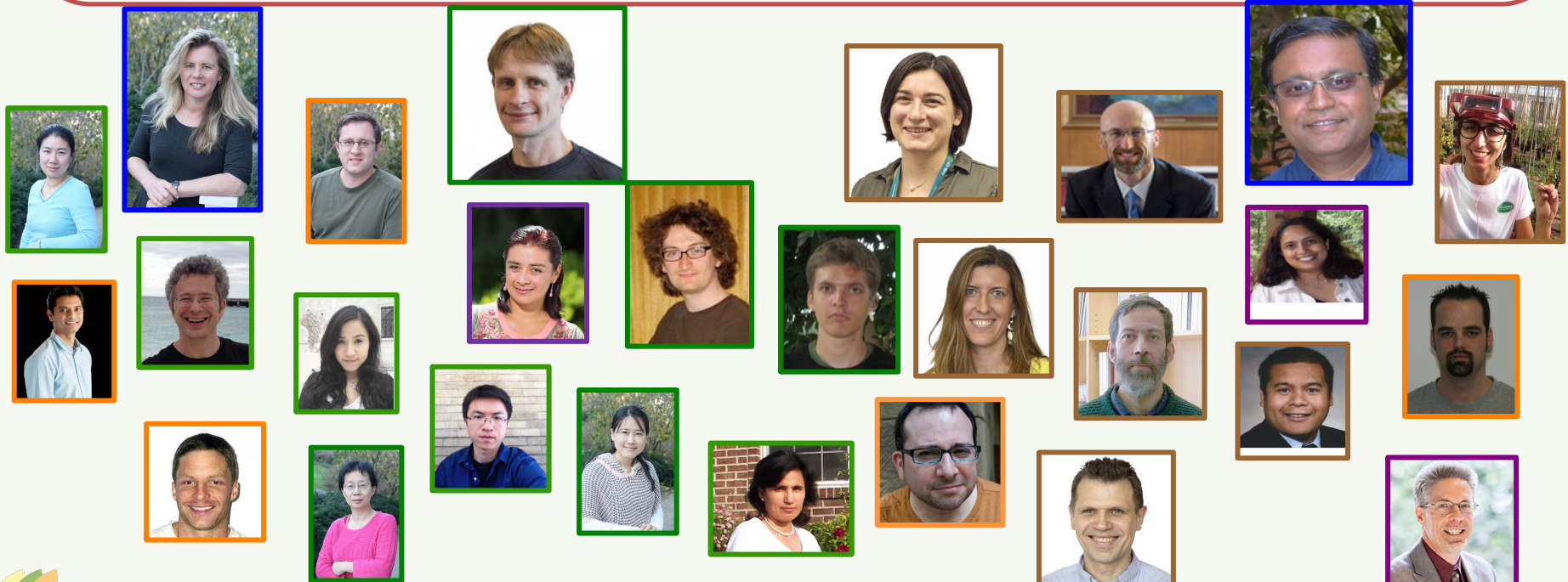
EMBL-EBI



Crispin Taylor



Pankaj Jaiswal



Outline

- Overview & *e*-learning
- Gramene Search
- Genome Browser
- Maize Pan-Genome
- Pathways

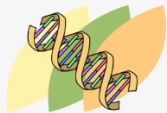


Search for genes, species, pathways, ontology terms, domains...



2076020 genes in 53 genomes ▾

Gramene Portals



Genome Browser

Browse genomes with annotations, variation and comparative tools



Plant Reactome

Browse and analyze metabolic and regulatory pathways



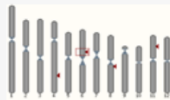
Tools

Tools for processing both our data and yours



Plant Expression ATLAS [↗](#)

Browse plant expression results at EBI ATLAS



BLAST

Query our genomes with a DNA or protein sequence



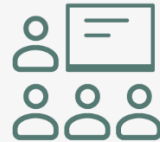
Gramene Mart

An advanced query interface powered by BioMart



Track Hub Registry [↗](#)

A global centralised collection of publicly accessible track hubs



Outreach and Training

Educational resources and webinars



Bulk Downloads

FTP download of our data



Archive

Legacy tools and data (markers, Cyc pathways, etc)

Latest News

Mining Maize with Gramene - Free Webinar May 22, 2018 @ 2 pm EDT
Wed, 16 May 2018

The Gramene Database build 57 is out with a new polyploid genomes view!
Thu, 03 May 2018

Gramene Workshop at the 2018 Maize Genetics Meeting in Saint-Malo, France
Tue, 06 Mar 2018

Gramene webinar Feb 27, 2018: Plant Reactome pathway updates and new features
Mon, 19 Feb 2018

Gramene release # 56b: updates to Plant Reactome
Thu, 01 Feb 2018

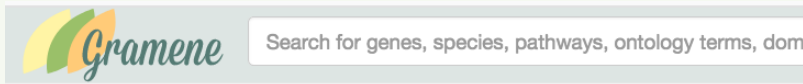
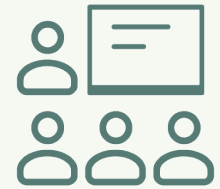
The Gramene Database build 56 is out with 8 new plant genomes!
Mon, 15 Jan 2018

Gramene will be at the PAG Conference 2018 — See you in San Diego!
Mon, 08 Jan 2018

The Gramene and MaizeCode Projects launched the first Maize Annotation Jamboree
Tue, 12 Dec 2017

Outreach

gramene.org/outreach



Welcome to the Gramene Outreach Site!

- [Gramene News](#)
- [Gramene Collaborators](#)
- [Contact Form](#)
- [Mailing List](#)
- [Facebook](#)
- [Twitter](#)

- [Gramene's YouTube channel](#) - Look here for recorded webinars
- [Gramene's FTP](#) - Look here for past webinar slides, brochures, posters, and exercises
- [Gramene's Outreach Wiki](#)

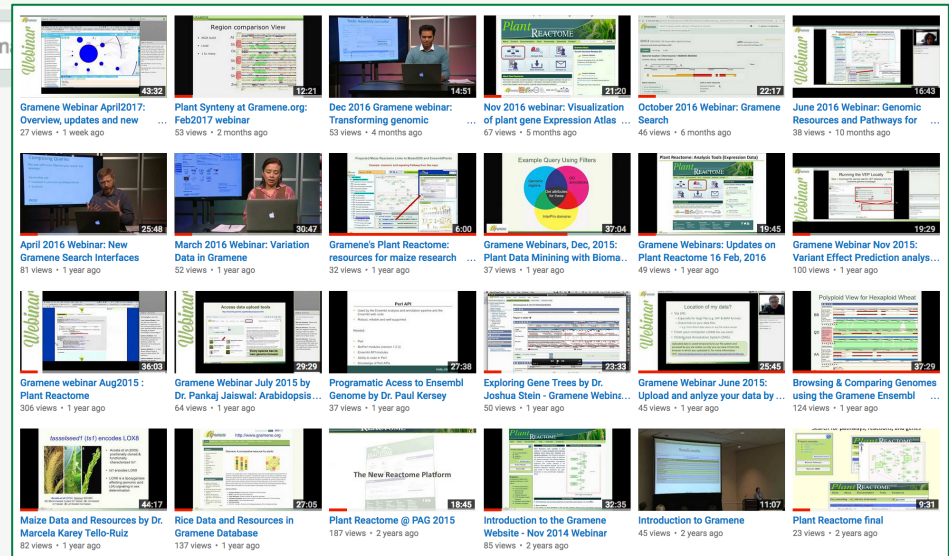
<ftp://ftp.gramene.org/pub/gramene/outreach/webinars>

Upcoming Conferences

- [American Society for Horticultural Science 2018](#)
- [Plant Biology 2018](#)

Past Conferences

- [The Biology of Genomes 2018](#)
- [Maize Genetics Conference 2018](#)

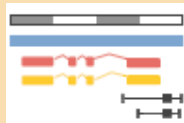


53 reference
Genomes



 EnsemblPlants

2.1M gene
annotations



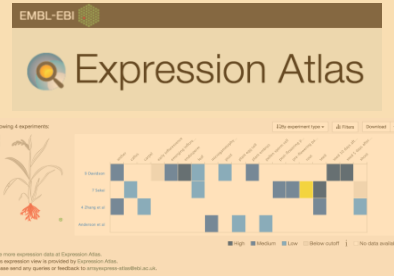
67K gene
trees



318 whole-
genome
alignments

ATCGAGCT
ATCCAGCT
ATCGAGAT

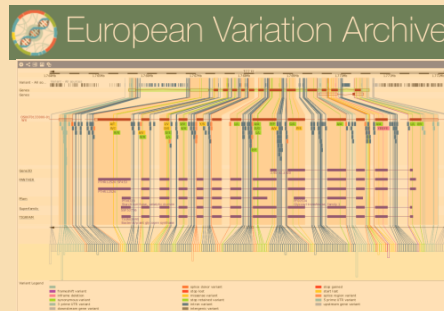
Expression



780 experiments in
18 species

***Integrated search
and visualization***

Variation



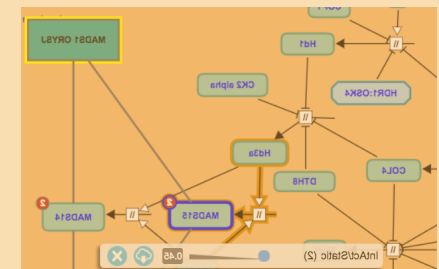
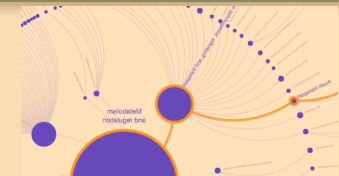
~231M SNPs in
9 genomes

Pathways

264 curated rice
projected to
74 species



Plant REACTOME



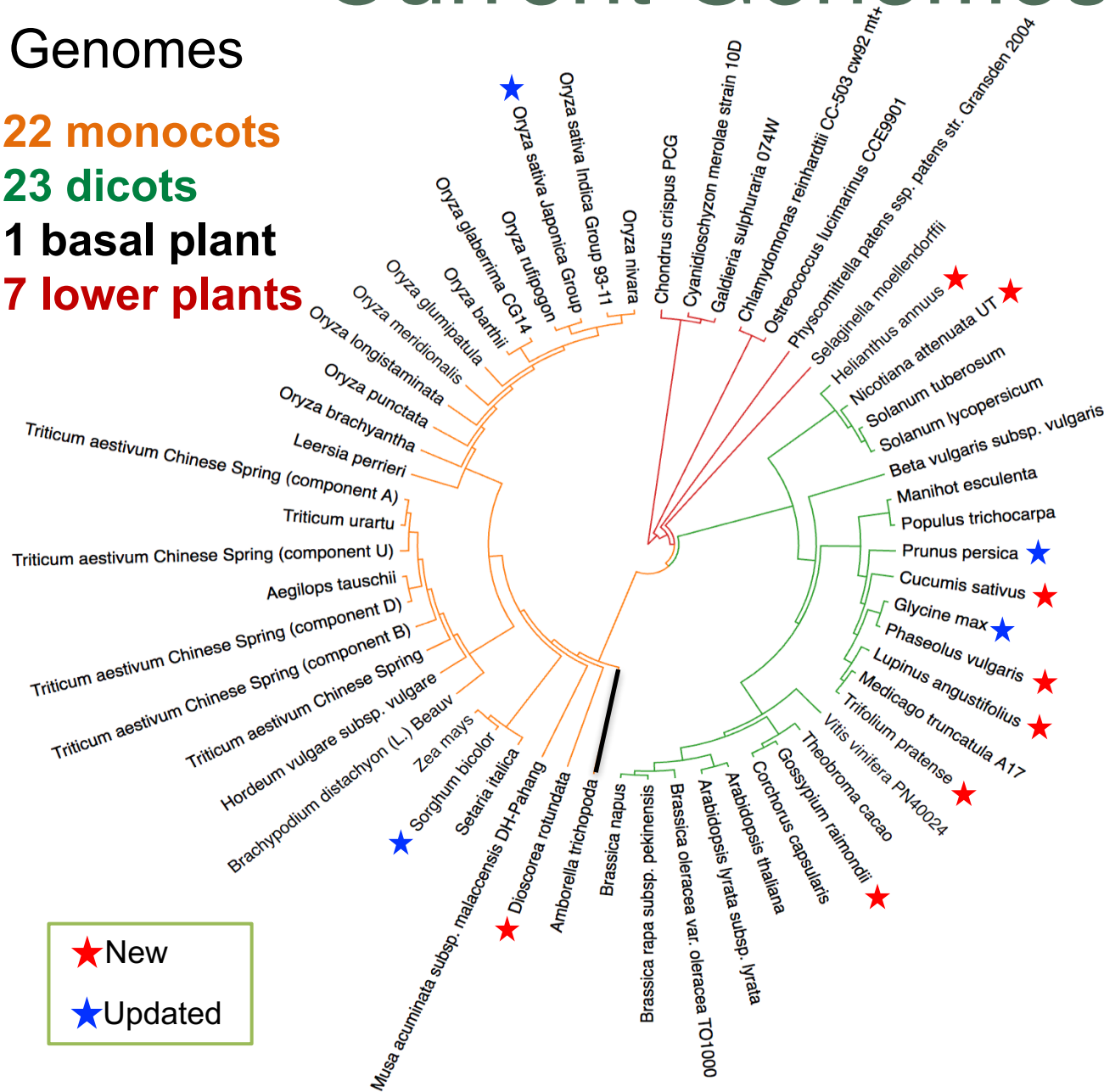
Homepage & Search (Video)

The screenshot shows the Gramene.org homepage. At the top, there is a navigation bar with the Gramene logo on the left, a search bar in the center with the placeholder text "Search for genes, species, pathways, ontology terms, domains...", and a status indicator on the right showing "2075935 genes in 53 genomes". Below the navigation bar, the page is organized into several sections. On the left, under the heading "Gramene Portals", there are seven items: "Genome Browser" (Browse genomes with annotations, variation and comparative tools), "Tools" (Tools for processing both our data and yours), "BLAST" (Query our genomes with a DNA or protein sequence), "Track Hub Registry" (A global centralised collection of publicly accessible track hubs), and "Bulk Downloads" (FTP download of our data). On the right, under the heading "Latest News", there is a list of recent updates and events, including the Gramene Workshop at the 2018 Maize Genetics Meeting, a webinar on Plant Reactome pathway updates, a release of updates to Plant Reactome, the release of Database build 56 with 8 new plant genomes, the PAG Conference 2018, the launch of the first Maize Annotation Jamboree, the Plant Genome Evolution 2017 Conference, an award for plant scientists, the release of Database build 55 with a new Jute genome, and a gene annotation and Reactome pathway update.

Current Genomes

53 Genomes

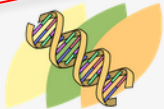
- 22 monocots
- 23 dicots
- 1 basal plant
- 7 lower plants



- NEW**
- Cucumber
 - Cotton
 - Sunflower
 - Blue lupin
 - Cassava
 - Coyote tobacco
 - Common bean
 - White Guinea yam
- UPDATED**
- Sorghum V3
 - Soybean V3
 - Peach V2
 - Japonica rice (models)

Genomes

Gramene Portals



Genome Browser

Browse genomes with annotations, variation and comparative tools



Plant Reactome

Browse and analyze metabolic and regulatory pathways



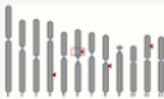
Tools

Tools for processing both our data and yours



Plant Expression ATLAS [↗](#)

Browse plant expression results at EBI ATLAS



BLAST

Query our genomes with a DNA or protein sequence



Gramene Mart

An advanced query interface powered by BioMart



Track Hub Registry [↗](#)

A global centralised collection of publicly accessible track hubs



Outreach and Training

Educational resources and webinars



Bulk Downloads

FTP download of our data



Archive

Legacy tools and data (markers, Cyc pathways, etc)

Search: for

e.g. [Carboxy*](#) or [chx28](#)

All genomes

-- Select a species --

- [View full list of all Gramene-Ensembl Plants species](#)
- [Edit your favourites](#)

Favourite genomes

Arabidopsis thaliana
TAIR10

Oryza sativa Japonica
IRGSP-1.0

Triticum aestivum
TGACv1

Hordeum vulgare
Hv_IBSC_PGSA_v2

Zea mays
AGPv4

Physcomitrella patens
ASM242v1

Polyploid View Enabled

Polyploid view for [wheat](#) has been enabled, allowing users to view alignments between all 3 wheat components [simultaneously](#).

Functional Genomics

26 new and updated functional genomic databases ([example](#) for Arabidopsis).

Arabidopsis variation data from the 1001 Genomes Project

The representation of genetic variation of [Arabidopsis thaliana](#) incorporates the full data set from the [1001 Genomes Project](#), covering more than 10 million variant loci across 1,135 samples ([Cell 2016](#)).

Ensembl Plants Archive Site

Alongside release 32, Ensembl Plants launched a new [archive site](#), where selected previous releases of Ensembl Plants are being kept publicly available. The first release available on the archive site is release 31, and includes the previous assemblies for wheat and maize.

This work is a joint project between [EnsemblGenomes](#) at the [European Bioinformatics Institute](#) and the group of [Doreen Ware](#) at the [Cold Spring Harbor Laboratory](#), who have developed the [Gramene](#) database, a resource for plant comparative genomics based on Ensembl technology. A common set of databases are available through EnsemblGenomes and Gramene, and the two groups are collaborating on the integration of content, quality control and the development of new features.

Organelle Annotation

For annotations relating to Organelles, see the [organelles page](#)

What's New in Release 57

- New features:
 - Polyploid view for wheat has been enabled, allowing users to view alignments between all 3 wheat components [simultaneously](#).
 - SIFT scores are now displayed on the Genes and regulation view of a gene variant. Here is a [sorghum SNP](#).
- Updated data:
 - Added gene name synonyms for [Oryza sativa](#) using from database sources such as [CGSNL](#), [Oryzabase](#) and [Rap-DB](#).
 - Updated protein features for all (nearly 2 million) plant proteins using [InterProScan](#) with version 67 of [InterPro](#).

Did you know...?

You can search the [Track Hub Registry](#) to find more than 1,400 public RNA-Seq studies aligned to plants ([read more](#))!

Wheat
Polyploid
Views, rice
gene synonyms,
SIFT scores

In collaboration with



53 Species

Show All entries		Show/hide columns				Filter				
Name	Classification	Taxon ID	Assembly	Accession	Variation database	Regulation database	Whole genome alignments	Other alignments	In peptide compara	In pan-taxonomic compara
Aegilops tauschii	Liliopsida	37682	ASM34733v1	GCA_000347335.1	-	-	✓	✓	✓	-
Amborella trichopoda	Amborellales	13333	AMTR1.0	GCA_000471905.1	-	-	✓	✓	✓	✓
Arabidopsis lyrata	eudicotyledons	81972	v.1.0	GCA_000004255.1	-	-	✓	✓	✓	-
Arabidopsis thaliana	eudicotyledons	3702	TAIR10	GCA_000001735.1	✓	✓	✓	✓	✓	✓
Beta vulgaris subsp. vulgaris	eudicotyledons	3555	RefBeet-1.2.2	GCA_000511025.2	-	-	-	✓	✓	-
Brachypodium distachyon	Liliopsida	15368	v1.0	GCA_000005505.1	✓	-	✓	✓	✓	-
Brassica napus	eudicotyledons	3708	AST_PRJEB5043_v1	GCA_000751015.1	-	-	-	✓	✓	-
Brassica oleracea	eudicotyledons	109376	v2.1	GCA_000695525.1	-	-	✓	✓	✓	-
Brassica rapa	eudicotyledons	51351	IVFCAASv1	GCA_000309985.1	-	-	✓	✓	✓	-
Setaria italica	Liliopsida	4555	JGIV2	GCA_000000000.1	-	-	-	-	-	-
Solanum lycopersicum	eudicotyledons	4081	SL2.50	GCA_000188115.2	✓	-	✓	✓	✓	✓
Solanum tuberosum	eudicotyledons	4113	SoITub_3.0	GCA_000226075.1	-	-	✓	✓	✓	-
Sorghum bicolor	Liliopsida	4558	Sorghum_bicolor_NCBIv3	GCA_000003195.3	✓	-	✓	✓	✓	-
Theobroma cacao	eudicotyledons	3641	Theobroma_cacao_20110822	GCA_000403535.1	-	-	✓	✓	✓	-
Trifolium pratense	eudicotyledons	57577	Trpr	GCA_900079335.1	-	-	-	✓	✓	-
Triticum aestivum	Liliopsida	4565	TGACv1	GCA_900067645.1	✓	-	✓	✓	✓	-
Triticum urartu	Liliopsida	4572	ASM34745v1	GCA_000347455.1	-	-	✓	✓	✓	-
Vitis vinifera	eudicotyledons	29760	IGGP_12x	GCA_000003745.2	✓	✓	✓	✓	✓	✓
Zea mays	Liliopsida	4577	AGPv4	GCA_000005005.6	✓	✓	✓	✓	✓	-





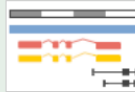
<http://ensembl.gramene.org/species.html>

ensemblPlants




Searche.g. [Zm00001d048577](#) or [1:109000-145001](#) or [Carboxypeptidase](#)**About *Zea mays***



Zea mays (maize) has the highest world-wide production of all grain crops, yielding 875 million tonnes in 2012 (<http://faostat.fao.org/>). Although a food staple in many regions of the world, most is used for animal feed and ethanol fuel. Maize was domesticated from wild teosinte in Central America and its cultivation spread throughout the Americas by Pre-Columbian civilizations. In addition to its economic value, maize is an important model organism for studies in plant genetics, physiology, and development. It has a large genome of about 2.4 gigabases with a haploid chromosome number of 10 (Schnable *et al.*, 2009; Zhang *et al.*, 2009). Maize is distinguished from other grasses in that its genome arose from an ancient tetraploidy event unique to its lineage.

Taxonomy ID [4577](#)Data source [wareLab](#) [More information and statistics](#)**Genome assembly: [AGPv4](#)** [More information and statistics](#) [Download DNA sequence \(FASTA\)](#) [Convert your data to AGPv4 coordinates](#) [Display your data in Gramene](#)[View karyotype](#)[Example region](#)**Comparative genomics**





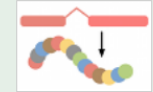
What can I find? Homologues, gene trees, and whole genome alignments across multiple species.

 [More about comparative analyses](#) [Phylogenetic overview of gene families](#) [Download alignments \(EMF\)](#) [Genomic alignments \[7\] \[\\[Show\\]\]\(#\)](#)[Example gene tree](#)**Regulation**


What can I find? Microarray annotations.

 [More about regulation in *Zea mays*](#) [More about the Gramene microarray annotation strategy](#)**Gene annotation**

What can I find? Protein-coding and non-coding genes, splice variants, cDNA and protein sequences, non-coding RNAs.

 [More about this genebuild](#) [Download genes, cDNAs, ncRNA, proteins - FASTA - GFF3](#) [Update your old Ensembl IDs](#) [Gene function summary](#) [Transposon annotation download](#)[Example gene](#)[Example transcript](#)**Variation**

What can I find? Short sequence variants.

 [More about variation in *Zea mays*](#) [More about variation in Gramene](#) [Download all variants - VGF - VCF - VEP](#)

Variant Effect Predictor

[Example variant](#)**Links**

- [Maize B73 RefGen v4 related data at NCBI \(raw data included\)](#)
- [MaizeSequence.org FTP site](#)
- [Legacy Gramene Maize RefGen V4 genome browser](#) (includes RefGen_V3)
- [MaizeGDB - Look here for RefGen V3 on the generic genome browser](#)
- Description of the B73 *Zea mays* RefGen_V4 assembly in [MaizeGDB](#)

Navigating Browsers

Zea mays (AGPv4) ▼

Location: 6:85,061,295-85,065,182 Gene: yellow endosperm1 Trans: Zm00001d036345_T001 Variant: PZE0680878460 Jobs ▼

Location-based displays

- Whole genome
- Chromosome summary
- Region overview
- Region in detail**
- Comparative Genomics
 - Synteny
 - Alignments (image)
 - Alignments (text)
 - Region Comparison
- Genetic Variation
 - Resequencing
 - Linkage Data
 - Markers
- Other genome browsers
 - maizeGDB
 - Phytozome

Configure this page
Custom tracks
Export data
Share this page
Bookmark this page

[Gramene is produced in collaboration with Ensembl Plants](#)

Chromosome 6: 85,061,295-85,065,182

chromosome 6

Region in detail

Scroll: Track height: Drag/Select:

2.00 Mb Forward strand

Genes

Gene Legend: protein coding (red), RNA gene (purple)

Location: 6:85061295-85065182 Go Gene: Go

3.89 kb Forward strand

85.062Mb 85.063Mb 85.064Mb 85.065Mb

Zm00001d036345_T002 > protein coding
Zm00001d036345_T001 > protein coding

Setaria italica
B. distachyon
O. s. Japonica
GrmZmAGPv3_mapped.

Variant - HapMap2

0.65 B73_CpG.bw
0.00
0.17 MO17_CHH.bw

Navigating Browsers

Zea mays (AGPv4) ▼

Location: 6:85,061,295-85,065,182 **Gene: yellow endosperm1** Trans: Zm00001d036345_T001 Variant: PZE0680878460 Jobs ▼

Gene-based displays

- Summary
 - Splice variants
 - Transcript comparison
 - Gene alleles
- Sequence
 - Secondary Structure
 - Gene families
 - Literature
- Plant Compara
 - Genomic alignments
 - Gene tree
 - Gene gain/loss tree
 - Orthologues
 - Paralogues
- Pan-taxonomic Compara
 - Gene Tree
 - Orthologues
- Ontologies
- Phenotypes
- Genetic Variation
 - Variant table
 - Variant image**
 - Structural variants
- Gene expression
- Pathway
- Regulation
- External references
- Supporting evidence
- ID History
 - Gene history

Gene: yellow endosperm1 Zm00001d036345

Description yellow endosperm1

Synonyms GRMZM2G300348, pb1, Psy1, rs130328408, rs131175743, y1, y4

Location [Chromosome 6: 85,061,295-85,065,182](#) forward strand.

About this gene This gene has 2 transcripts ([splice variants](#)), [75 orthologues](#) and [7 paralogues](#).

Transcripts [Show transcript table](#)

Variant image ⓘ

Navigating Browsers

 **Zea mays** (AGPv4) ▼

Location: 6:85,061,295-85,065,182

Gene: yellow endosperm1


Trans: **Zm00001d036345_T001**

Variant: PZE0680878460

Jobs ▼

Transcript-based displays

- Summary
- Sequence
 - Exons
 - cDNA
 - Protein
- Protein Information
 - Protein summary**
 - Domains & features
 - Variants
- Genetic Variation
 - Variant table
 - Variant image
 - Population comparison
 - Comparison image
- External References
 - General identifiers
 - Oligo probes
- Supporting evidence
- ID History
 - Transcript history
 - Protein history

 Configure this page

 Custom tracks

 Export data

 Share this page

 Bookmark this page

[Gramene is produced in collaboration with Ensembl Plants](#)

Transcript: Zm00001d036345_T001

Description yellow endosperm1

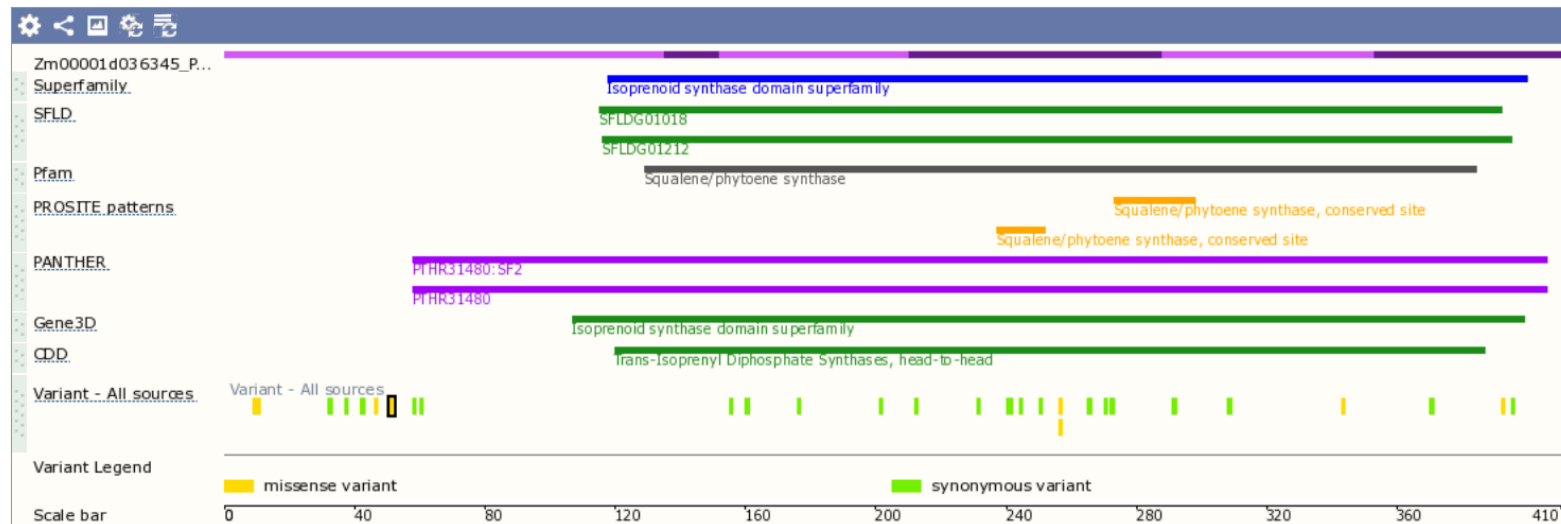
Location [Chromosome 6: 85,061,295-85,064,797](#) forward strand.

About this transcript This transcript has [6 exons](#), is annotated with [24 domains and features](#), is associated with [29 variations](#) and maps to [22 oligo probes](#).

Gene This transcript is a product of gene [Zm00001d036345](#) [Show transcript table](#)

Protein summary

Protein domains for Zm00001d036345_P001.



Statistics

Ave. residue weight: 113.274 g/mol
Charge: 7.0
Isoelectric point: 8.6840
Molecular weight: 46,442.40 g/mol
Number of residues: 410 aa

Navigating Browsers

Zea mays (AGPv4)

Location: 6:85,061,295-85,064,797 Gene: yellow endosperm1 Trans: Zm00001d036345_T001 Variant: **PZE0680878460** Jobs ▾

Variant displays

- Explore this variant
- Genomic context
 - Genes and regulation
 - Flanking sequence**
 - Genotype frequency
 - Phenotype data
 - Sample genotypes
 - Linkage disequilibrium
 - Phylogenetic context
 - Citations

Configure this page Custom tracks Export data Share this page Bookmark this page

Gramene is produced in collaboration with Ensembl Plants

PZE0680878460 SNP

Most severe consequence | [See all predicted consequences](#)
missense variant

Alleles **G/C** | Highest population MAF: **0.09**

Location [Chromosome 6:85061564](#) (forward strand) | VCF: 6 85061564 PZE0680878460 G C

HGVS names This variant has 5 HGVS names - [Hide](#) ▾

- 6:g.85061564G>C
- [Zm00001d036345_T001.c.155G>C](#)
- [Zm00001d036345_P001.p.Trp52Ser](#)
- [Zm00001d036345_T002.c.155G>C](#)
- [Zm00001d036345_P002.p.Trp52Ser](#)

Original source This variant overlaps [2 transcripts](#).

About this variant

Flanking sequence ⓘ

[Download sequence](#) [BLAST this sequence](#)

Flanking sequence

The sequence below is from the **reference genome** flanking the variant location. The variant is shown in **red** text. Neighbouring variants are shown with highlighted letters and ambiguity codes.

To change the display of the flanking sequence (e.g. hide the other variants, change the length of the flanking sequence), use the "**Configure this page**" link on the left.

Variants **5 prime UTR** **Focus variant** **Intronic** **Missense** **Synonymous** **Upstream**

Markup loaded

```

TCCTGTCCAAGCCCGCCGCTTATTCTACCGTGCCGGGCTCGGACCGGGCCCCAAAAGCG
GGCTTCGTGCCGGGCTCACGGGCTCGTGCTTTTTCGCCATCTAYSAGCCGCACACTTAG
CATACRTACGCAAGAAGAGGAGAGGGCCGGAGGTGCCGCTGCTCCTTGTCTGTTCTGCTGAC
TGGTCTCATCATCTCATCCCACCACCACCACCATCACCATCTTTAGGATAAGATAGC
AAATATATGGCCATCATACTCGTACGAGCAGCGTSGCTGGGCTCTCCGCCCGCACAGC
ATCAGCCACCAGGGGACTCTCCAGTGTCCACCCCTGCTCAAGACXAAGAGCCGGCGGCT
CGCCGGTGGATGCCGFGCTCGCTCMTTGGCCTCAACCCGTSGGAGGTGGCCGTCCCTCC
CCGCCGTTTACTCCAGCCTCGCCGTCAACCCGGCGGAGGGCCGTCTGCTCGTCCGAG
CAGAAGGTCTACGACGTCGTGCTCAAGCAGGCGCATTGCTCAAACGCCAGCTGCGCACG
CCGTCTCGACGCCAGGCCCCAGGACATGGACATGCCACGCAACGGGCTCAAGGAAGCC
TAGCACCGCTGCGCGGAGATCTGTGAGGAGTATGCCAAGACGTTTTACCTCGGTACGTAC
KRREATATATATGGATCCATCTTTCTCCAATCCACATTCTATCGTTTCAGTCTGCT
GCGAAGTCTCGGTCATGCTCGGCGCCCGTCGATCGTCAATCCAGCCGCGGCGGCGGCGG

```


Configuring Browser Views

The screenshot displays the Gramene browser interface with several tracks and configuration options. A red circle highlights the 'Configure this page' button in the left sidebar. A red arrow points from this button to a gear icon in the top toolbar of the first track. Another red arrow points from the gear icon to a context menu that appears over the 'B73_CpG_ratio' track. This menu includes options for 'Change track style' (Off, Wiggle plot, Gradient, P-value) and a gear icon for further configuration. A blue text box with a white background and a red arrow points to the gear icon in the context menu, containing the text 'Mouse over track name & configure symbol'. A white text box with a black border and a red arrow points to the 'Configure this page' button, containing the text 'Click on "Configure this page" image" symbol'. The browser tracks include 'Chromosome bands', 'Contigs', 'Gramene gene', 'B73_CpG_ratio', 'B73_CpG_coverage', 'cDNA', 'EST.Cluster (Maize)', 'MAKER-P.genes', 'Gramene.gene', 'mRNA alignments', 'HapMap2', 'Panzea_2.7GBS', and '%GC'. The top toolbar shows 'Scroll:', 'Track height:', and 'Drag/Select:' controls. The main display area shows a genomic region from 45.00 Mb to 46.50 Mb, with various gene models and tracks overlaid.

Mouse over track name & configure symbol

Click on "Configure this page" image" symbol

Variation

SNPs

ENSVATH00125659 SNP

Most severe consequence | **Stop gained** | [See all predicted consequences](#)

Alleles **A/T** | Highest population MAF: **0.22**

Location Chromosome 1:24628699 (forward strand) | [View in location tab](#)

HGVS names This variant has 3 HGVS names - [Show](#)

Synonyms **Perlegen** PERL0223135

Original source Variation features from Affy_250k, Perlegen_1M, WTCBG and 1001 Genomes, with Ensembl identifiers

About this variant This variant overlaps [2 transcripts](#), has [200 sample genotypes](#) and is associated with [2 phenotypes](#).

Explore this variant

- Genomic context
- Genes and regulation ²
- Flanking sequence **ATTCATT
CGGSGTG
TCATGCT**
- Genotype frequency ⁷
- Phenotype data ²
- Sample genotypes ²⁰⁰
- Linkage disequilibrium
- Phylogenetic context
- Citations

Structural variants (Arabidopsis & sorghum)

Structural variant: ENSSVATH00000001

Variation class deletion ([SO:0000159](#))

Source Ensembl - Variation features from Affy_250k, Perlegen_1M, WTCBG and 1001 Genomes, with Ensembl identifiers

Study [Structural variation](#) - unknown

Location Chromosome 1:10019676-10020065 (forward strand) | [View in location tab](#)

Genomic size 390 bp

About this structural variant This structural variant overlaps [1 transcript](#).

Explore this SV

- Genomic context
- Genes and regulation ¹
- Supporting evidence
- Phenotype data

EMS-induced (sorghum & wheat)

tmp_3_55893324_G_A SNP

Most severe consequence | **Stop gained** | [See all predicted consequences](#)

Alleles **G/A** | Highest population MAF: **< 0.01**

Location Chromosome 3:55905987 (forward strand) | [View in location tab](#)

HGVS names This variant has 3 HGVS names - [Show](#)

Original source [A Sorghum Mutant Resource as an Efficient Platform for Gene Discovery in Grasses](#). Contact [Dr. Zhanguo Xin](#) for seeds

About this variant This variant overlaps [1 transcript](#) and has [251 sample genotypes](#).

Explore this variant

- Genomic context
- Genes and regulation ¹
- Flanking sequence **ATTCATT
CGGSGTG
TCATGCT**
- Genotype frequency ¹
- Phenotype data
- Sample genotypes ²⁵¹
- Linkage disequilibrium
- Phylogenetic context
- Citations

Variation Data Summary

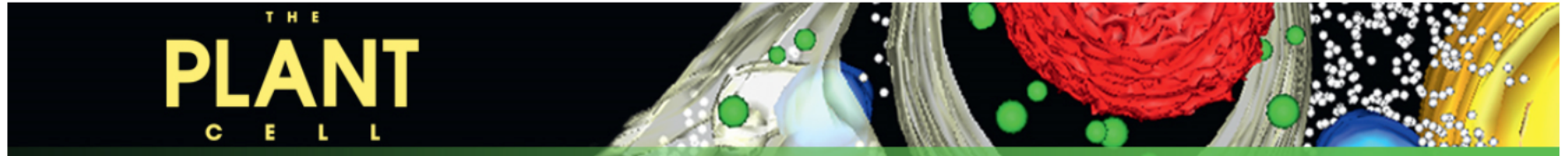


~230 M plant SNPs in 9 species

- **Arabidopsis** –1001 Genomes (3 studies; includes **structural**), Horton *et al* , BBSRC-funded collaboration, Atwell *et al* [**phenotypes**]
- **Barley** – Barley Consortium, Mascher *et al*, Comadran *et al*
- **Brachypodium** – *B. sylvaticum* (Fox *et al*)
- **Grapevine** – USDA germplasm collection (Myles *et al*)
- **Maize** – HapMap 1 & 2 (Gore *et al*, Chia *et al*), Panzea 27, HapMap 3 (coming soon)
- **Rice** [*Oryza sativa* Japonica & Indica, *O. glumaepatula*, *O. glaberrima*, *O. barthii*] – dbSNP (Yu *et al*), McNally *et al*, Zhao *et al*, Duitman *et al* (CGI), 3000 Genomes IRRI (coming soon)
- **Sorghum** – Morris *et al*, Mace *et al*, Xin *et al* [**EMS**]; DGVa (**structural**)
- **Tomato** – 100 Tomato Genome Sequencing Consortium
- **Wheat** – HapMap (Jordan *et al*), CerealsDB, Krasileva *et al* [**EMS**]

Sorghum as a functional genomics platform for the maize community!

Sorghum EMS-mutant collection



256 mutant lines sequenced

Other | Large-Scale Biology Article

A Sorghum Mutant Resource as an Efficient Platform for Gene Discovery in Grasses

Yinping Jiao, John J. Burke, Ratan Chopra, Gloria Burow, Junping Chen, Bo Wang, Chad Hayes, Yves Emendack, Doreen Ware, Zhanguo Xin

Published June 2016. DOI: <https://doi.org/10.1105/tpc.16.00373>



Order seeds from USDA
or contact Dr. Xin

Variation Use Case

Find “stop_gained” alleles in transcription factors

Step 1: Use Gramene BioMart
Search genes with GO:0003700 (transcription factor activity) with predicted stop-gain variants

Step 2: Use Genome Browser to explore structure, expression, conservation, and other features in gene of interest

bio::mart Login/Register

Search all species...

Export all results to File tsv Unique results only Go

View 200 rows as HTML Unique results only

Gene stable ID	InterPro ID	InterPro short description	Variation ID	Consequence to transcript	Variation source	Variant allele
Sb04g000300	IPR004827	TF_bZIP	tmp_4_112236_G_A	stop_gained	Mace_2013	G/A
Sb08g004360	IPR000679	Znf_GATA	tmp_8_5166294_C_G	stop_gained	Mace_2013	C/G
Sb08g004360	IPR013088	Znf_NHR/GATA	tmp_8_5166294_C_G	stop_gained	Mace_2013	C/G
Sb08g003700	IPR007125	Histone_core_D	tmp_8_4256587_G_A	stop_gained	Mace_2013	G/A
Sb08g003700	IPR007125	Histone_core_D	tmp_8_4256587_G_A	stop_gained	Mace_2013	G/A
Sb08g003700	IPR009072	Histone-fold	tmp_8_4256587_G_A	stop_gained	Mace_2013	G/A
Sb08g003700	IPR009072	Histone-fold	tmp_8_4256587_G_A	stop_gained	Mace_2013	G/A
Sb07g004580	IPR001471	TF_ERF_DNA-bd	tmp_7_5865063_G_A	stop_gained	Mace_2013	G/A
Sb07g004580	IPR016177	DNA-bd_integrase-tyr	tmp_7_5865063_G_A	stop_gained	Mace_2013	G/A
Sb07g004580	IPR031112	AP2-like_transcript_factor	tmp_7_5865063_G_A	stop_gained	Mace_2013	G/A
Sb08g005635	IPR004827	TF_bZIP	tmp_8_7821495_C_T	stop_gained	Mace_2013	C/T
Sb01g038370	IPR002589	A1pp	tmp_1_61895020_G_A	stop_gained	Sorghum_EMS_mutants	G/A
Sb01g038370	IPR011146	His_triad-like_motif	tmp_1_61895020_G_A	stop_gained	Sorghum_EMS_mutants	G/A
Sb01g038370	IPR019808	Histidine_triad_CS	tmp_1_61895020_G_A	stop_gained	Sorghum_EMS_mutants	G/A
Sb01g038370	IPR026963	Apratxin	tmp_1_61895020_G_A	stop_gained	Sorghum_EMS_mutants	G/A
Sb01g038370	IPR032566	zf-C2HE	tmp_1_61895020_G_A	stop_gained	Sorghum_EMS_mutants	G/A
Sb01g030770	IPR004827	TF_bZIP	tmp_1_53392629_C_T	stop_gained	Sorghum_EMS_mutants	C/T
Sb01g039810	IPR000943	RNA_pol_sigma70	tmp_1_63256928_G_A	stop_gained	Sorghum_EMS_mutants	G/A
Sb01g039810	IPR000943	RNA_pol_sigma70	tmp_1_63256928_G_A	stop_gained	Sorghum_EMS_mutants	G/A
Sb01g039810	IPR007624	RNA_pol_sigma70_r3	tmp_1_63256928_G_A	stop_gained	Sorghum_EMS_mutants	G/A
Sb01g039810	IPR007624	RNA_pol_sigma70_r3	tmp_1_63256928_G_A	stop_gained	Sorghum_EMS_mutants	G/A
Sb01g039810	IPR007627	RNA_pol_sigma70_r2	tmp_1_63256928_G_A	stop_gained	Sorghum_EMS_mutants	G/A

biomart version 0.7



Step 3: Identify germplasm containing genotype of interest:

tmp_1_53392629_C_T SNP

Original source: A Sorghum Mutant Resource as an Efficient Platform for Gene Discovery in Grasses. Contact Dr. Zhanguo Xin for seeds

Alleles: C/T | Ambiguity code: Y

Location: Chromosome 1:53392629 (forward strand) | View in location tab

Most severe consequence: Stop gained | See all predicted consequences (Genes and regulation)

HGVS names: This variant has 3 HGVS names - Hide

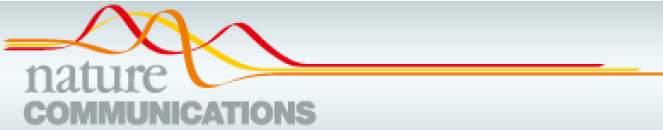
- 1.g.53392629C>T
- Sb01g030770.1:c.943C>T
- Sb01g030770.1:p.Gln315Ter

Genotypes for Sorghum_EMS_mutant_population

Sample	Genotype (forward strand)
ARS230	CIT
ARS1	CIC
ARS10	CIC
ARS100	CIC
ARS101	CIC



Sorghum *msd1*



ARTICLE

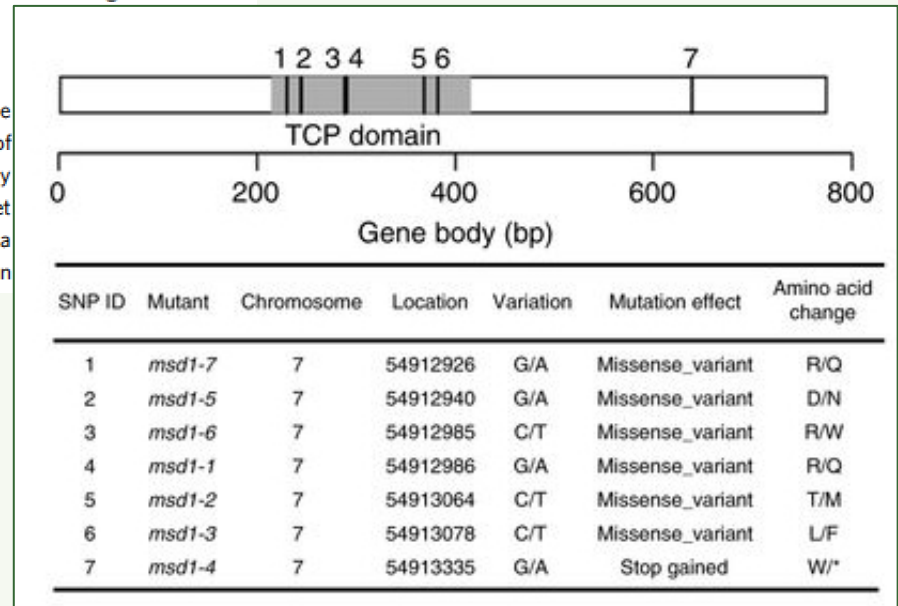
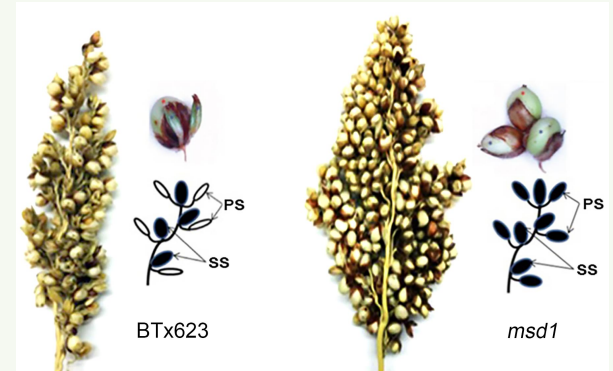
DOI: 10.1038/s41467-018-03238-4

OPEN

MSD1 regulates pedicellate spikelet fertility in sorghum through the jasmonic acid pathway

Yinping Jiao^{1,2}, Young Koung Lee^{2,3}, Nicholas Gladman^{1,2}, Ratan Chopra¹, Shawn A. Christensen⁴, Michael Regulski², Gloria Burow¹, Chad Hayes¹, John Burke¹, Doreen Ware^{1,2,5} & Zhanguo Xin¹

Grain number per panicle (GNP) is a major determinant of grain yield in cereals. However, the mechanisms that regulate GNP remain unclear. To address this issue, we isolate a series of sorghum [*Sorghum bicolor* (L.) Moench] *multiseeded* (*msd*) mutants that can double GNP by increasing panicle size and altering floral development so that all spikelets are fertile and set grain. Through bulk segregant analysis by next-generation sequencing, we identify *MSD1* as a TCP (Teosinte branched/Cycloidea/PCF) transcription factor. Whole-genome expression



Tools

<http://ensembl.gramene.org/tools.html>



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Tools





We provide a number of ready-made tools for processing both our data and yours. We routinely delete results from our servers after 10 days, but if you have an [gramene genome account](#) you will be able to save the results for about 2-3 months until next release.

Processing your data

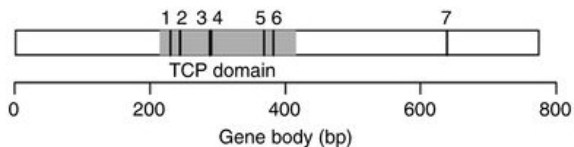
Name	Description	Online tool	Upload limit	Download script	Documentation
Variant Effect Predictor 	Analyse your own variants and predict the functional consequences of known and unknown variants via our Variant Effect Predictor (VEP) tool.		50MB*		
HMMER	Quickly search our genomes for your protein sequence.				
BLAST/BLAT	Search our genomes for your DNA or protein sequence.		50MB		
Assembly Converter	Map (liftover) your data's coordinates to the current assembly.		50MB		

* For larger datasets we provide an API script that can be downloaded (you will also need to install our Perl API, below, to run the script).

Accessing Gramene data

Name	Description	Get it from:	Documentation
BioMart	Use this data-mining tool to export custom datasets from Gramene.	Gramene BioMart	
Ensembl Perl API	Programmatic access to all Ensembl data using simple Perl scripts	GitHub or FTP download (current release only)	
Ensembl Genomes Virtual Machine	Pre-configured VirtualBox virtual machine (VM) running the latest Ensembl Genomes browser.		
Ensembl Genomes REST server	Access Ensembl data using your favourite programming language		



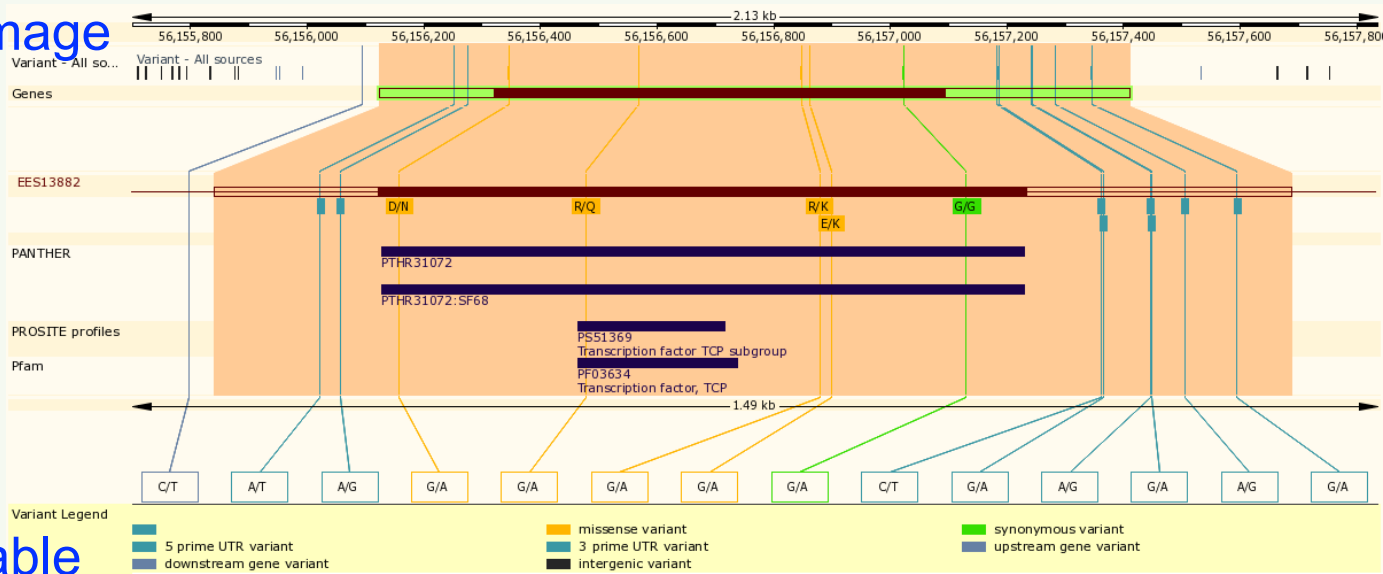


msd1 [SORBI_3007G135700]

The *msd1* mutants are not in the sequenced population. But... Is the amino acid sequence conserved in other species like maize?

SNP ID	Mutant	Chromosome	Location	Variation	Mutation effect	Amino acid change
1	<i>msd1-7</i>	7	54912926	G/A	Missense_variant	R/Q
2	<i>msd1-5</i>	7	54912940	G/A	Missense_variant	D/N
3	<i>msd1-6</i>	7	54912985	C/T	Missense_variant	R/W
4	<i>msd1-1</i>	7	54912986	G/A	Missense_variant	R/Q
5	<i>msd1-2</i>	7	54913064	C/T	Missense_variant	T/M
6	<i>msd1-3</i>	7	54913078	C/T	Missense_variant	L/F
7	<i>msd1-4</i>	7	54913335	G/A	Stop gained	W/*

Variant image



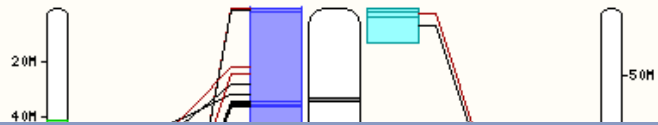
Variant table

Variant ID	Chr: bp	Alleles	Source	Conseq. Type	AA	AA coord	SIFT
tmp_7_54912721_G_A	7:56156345	G/A	Sorghum_EMS_mutants	missense variant	D/N	9	0.03
tmp_7_54912944_G_A	7:56156568	G/A	Sorghum_EMS_mutants	missense variant	R/Q	83	0
tmp_7_54913223_G_A	7:56156847	G/A	Sorghum_EMS_mutants	missense variant	R/K	176	0.25
tmp_7_54913237_G_A	7:56156861	G/A	Sorghum_EMS_mutants	missense variant	E/K	181	0.25
tmp_7_54913398_G_A	7:56157022	G/A	Sorghum_EMS_mutants	synonymous variant	G	234	-

Most deleterious

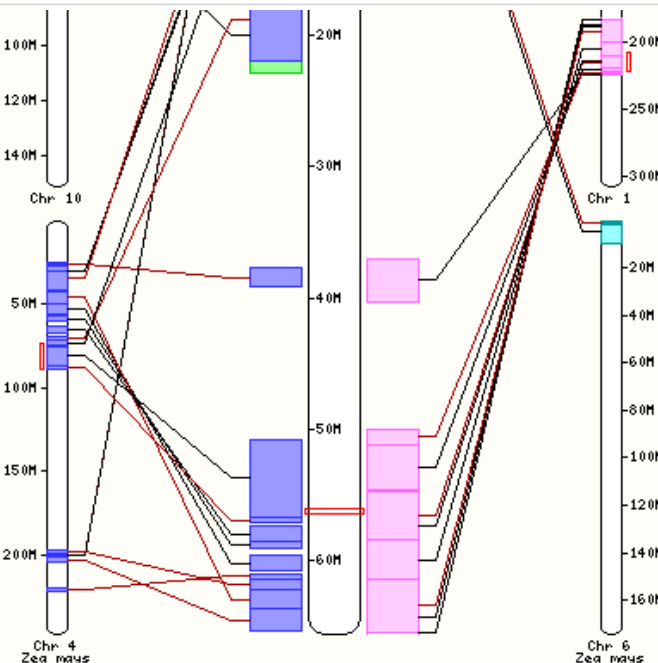
vs tolerated

Are the sorghum *msd1* variant sites conserved in maize?



Sorghum bicolor genes **Location** **Zea mays homologues** **Location**

SORBI_3007G135700 **7:56156125-56157410** **TCP-transcription factor 11** **1:217455034-217455756**
 (SORBI_3007G135700) (Zm00001d032217)



Sorghum chr7

- Alignments (text)
- Region Comparison
- Genetic Variation
- Resequencing
- Linkage Data
- Markers
- Other genome browsers
- Phytozome

Alignments (text)

Alignment: Zea mays - lastz

Location: 7:56156218-56157410 Gene: Go

Download alignment

Species Tree

No tree is drawn when there is more than one block displayed because each block is represented by a separate tree

Sorghum bicolor > chromosome:Sorghum_bicolor_NCBIV3.7:56156218:56157410.1
Zea mays > chromosome:AGPV4.4:85370657:85371903.1

Alignment

Currently showing full alignment. Please click the button below to show the alignment for first 120 columns.

Hide full alignment

Species	Coordinate	Sequence	Variant	Class	SNP	Location	Alleles	Consequences	missense variant
Sorghum bicolor	7:56156218	TCATTAACCCCTAACACAGCCGGGCTCTCATCACCTTCATGATCATTCGGCTTACCAGCAGAGAGCAGTCA	---	TTTACCGAACCCCTACTGCAGCTGTTT	GTTTTCTTATGCCCTCAGCC	7:56156332	G/A		
Zea mays	4:85370657	TCATTAACCCCTAACACAGCCGGGCTCTCATCACCTTCATGATCATTCGGCTTACCAGCAGAGAGCAGTCA	---	TTTACCGAACCCCTACTGCAGCTGTTT	GTTTTCTTATGCCCTCAGCC	4:85370168	G/A		
Sorghum bicolor	7:56156333	GC-----GATGCTTGGACGGGTACGGCGGCGAGATCTCCGGCCGACATCGTCTGCTCCACC	---	ACCAGGACACCCCTGGAGCCGCTGTCGG	---	7:56156434	G/A		
Zea mays	4:85370769	GC-----GATGCTTGGACGGGTACGGCGGCGAGATCTCCGGCCGACATCGTCTGCTCCACC	---	ACCAGGACACCCCTGGAGCCGCTGTCGG	---	4:85370888	G/A		
Sorghum bicolor	7:56156435	ACGGCCGCTCTCCAGCCGCGCCG	---	CTCTGAGGACGGGTCTCCGCTACCCGGTGGGATCCGGGGTTCATGCCCGCCGCGCAGCGGGAAGCGGGCC	---	7:56156554	G/A		
Zea mays	4:85370889	ACGGCCGCTCTCCAGCCGCGCCG	---	CTCTGAGGACGGGTCTCCGCTACCCGGTGGGATCCGGGGTTCATGCCCGCCGCGCAGCGGGAAGCGGGCC	---	4:85370975	G/A		
Sorghum bicolor	7:56156555	TTTCAGCAGGATTCACACAGCA	---	AGCCCGCCGATCGCGCTCGCTGGTGGGGTCCGGCCGAGGTTCTTCGGCTCAGGACCCGCTGGGTTGAC	---	7:56156674	G/A		
Zea mays	4:85370976	TTTCAGCAGGATTCACACAGCA	---	AGCCCGCCGATCGCGCTCGCTGGTGGGGTCCGGCCGAGGTTCTTCGGCTCAGGACCCGCTGGGTTGAC	---	4:85371095	G/A		
Sorghum bicolor	7:56156675	AAGCCAGCAAGACG	---	AAGCCCGCCATCGACCCCTCGTGCAGCCGCGCC	---	7:56156779	G/A		
Zea mays	4:85371096	AAGCCAGCAAGACG	---	AAGCCCGCCATCGACCCCTCGTGCAGCCGCGCC	---	4:85371215	G/A		
Sorghum bicolor	7:56156780	CCGACGGTGGTGAAG	---	AGCACTTGCTGTTGACGCTGACTGAGG	---	7:56156890	G/A		
Zea mays	4:85371216	CCGACGGTGGTGAAG	---	AGCACTTGCTGTTGACGCTGACTGAGG	---	4:85371335	G/A		
Sorghum bicolor	7:56156891	GGCGTACCGGTGTCCTGATGGCCACCG	---	GGGTCATGGGAAGCA	---	7:56156998	G/A		
Zea mays	4:85371336	GGCGTACCGGTGTCCTGATGGCCACCG	---	GGGTCATGGGAAGCA	---	4:85371437	G/A		
Sorghum bicolor	7:56156999	GCGCAGCCGACGAGTGGACGG	---	CTGGGATCTACTACCAAGTATGCCTGCAGCTCGAGGAGATGA	---	7:56157106	G/A		
Zea mays	4:85371438	ACGACCCGACGAGTGGACGG	---	CTGGGATCTACTACCAAGTATGCCTGCAGCTCGAGGAGATGA	---	4:85371556	G/A		
Sorghum bicolor	7:56157107	TATGCAAGATTATATAGGCTATAAAGCTCC	---	AACCGCGCTGAGGA	---	7:56157199	G/A		
Zea mays	4:85371557	TATGCAAGATTATATAGGCTATAAAGCTCC	---	AACCGCGCTGAGGA	---	4:85371673	G/A		
Sorghum bicolor	7:56157200	TAGTACATATAAATCCCAACTGGGCTTCTCTATCAAT	---	AAAGCCCATAGCCGGTGGTG	---	7:56157304	G/A		
Zea mays	4:85371674	TAGTACATATAAATCCCAACTGGGCTTCTCTATCAAT	---	AAAGCCCATAGCCGGTGGTG	---	4:85371793	G/A		
Sorghum bicolor	7:56157305	GGTATGCGTGTGCAATTAATTC	---	ATCAATGTGGCAATAGATATCGTATCTTTAT	---	7:56157410	G/A		
Zea mays	4:85371794	GGTATGCGTGTGCAATTAATTC	---	ATCAATGTGGCAATAGATATCGTATCTTTAT	---	4:85371903	G/A		



Track Hubs in Gramene

EBI Atlas team: RNAseq-er API aligns all ENA short reads for genomes in Ensembl updated daily

Gramene Search for genes, species, pathways, ontology terms, domains... **1759450** genes in **44** genomes ▾

Gramene Portals

- Genome Browser**
Browse genomes with annotations, variation and comparative tools
- Plant Reactome**
Browse and analyze metabolic and regulatory pathways
- Tools**
Tools for processing both our data and yours
- Plant Expression ATLAS**
Browse plant expression results at EBI ATLAS
- BLAST**
Query our genomes with a DNA or protein sequence
- Gramene Mart**
An advanced query interface powered by BioMart
- Track Hub Registry**
A global centralised collection of publicly accessible track hubs
- Outreach and Training**
Educational resources and webinars
- Bulk Downloads**
FTP download of our data
- Archive**
Legacy tools and data (markers, Cyc pathways, etc)

Latest News

What's New with Gramene? An Overview - Webinar May 9, 2017 @ 2 pm EDT

Older news

- Plant Breeding for Drought Tolerance, Online course - Fall 2017
- Agricultural Data Curation Survey -- Your feedback matters!
- Notes from Biocuration 2017 conference
- Gramene webinar 11th April 2017: Overview, updates and new fireworks display in Plant Reactome
- Gramene at the 2017 Maize Genetics Pre-Conference Workshops
- Everything you wanted to know about plants syteny! -- Join our Gramene Webinar on February 7th
- Gramene is attending the PAG Conference 2017 -- See you in San Diego!
- GARNet newsletter available for download
- Illinois Corn Breeders' School, March 6-7, 2017

Release Notes (53) About Cite Feedback Like 489 Follow @GrameneDatabase 203 followers

Track Hubs in Gramene

EBI Atlas team: RNAseq-er API aligns all ENA short reads for genomes in Ensembl updated daily

Location view

The screenshot displays the Gramene web interface in 'Location view'. On the left, a sidebar contains navigation options: 'Other genome browsers', 'Phytosome', 'Configure this page' (highlighted with a red circle), 'Add your data', 'Export data', 'Bookmark this page', and 'Share this page'. Below these is a link: 'Gramene is produced in collaboration with Ensembl Plants'. The main view shows a genomic track for chromosome ctg78, with a zoomed-in section of 75.72 kb. The track includes 'Chromosome bands', 'B73_CpG_ratio', 'B73_CpG_coverage', 'cDNA', 'EST_Cluster (Maize)', 'MAKER-P.genes', 'Gramene.gene', 'Contigs', 'mRNA.alignments', 'MAKER-P.genes', 'EST_Cluster (Maize)', 'cDNA', 'HapMap2', 'Panzea_2.7.GBS', and '%GC'. A pop-up window titled 'Change track style:' is overlaid on the track, showing options for 'Off', 'Wiggle plot', 'Gradient', and 'P-value'. The track shows various gene models, including GRMZM2G104843, GRMZM2G105542, GRMZM2G105617_T01, GRMZM2G105608_T01, and AC210825.3-Contig45. The 'Gene Legend' indicates that red bars represent 'protein coding' regions.

Track Hubs in Gramene

EBI Atlas team: RNAseq-er API aligns all ENA short reads for genomes in Ensembl updated daily

Location view

The screenshot displays the Gramene Track Hubs interface. On the left, a sidebar contains navigation options: 'Other genome browsers', 'Phytozome', 'Configure this page' (circled in red), 'Add your data', 'Export data', 'Bookmark this page', and 'Share this page'. Below these is a link: 'Gramene is produced in collaboration with Ensembl'. The main content area is titled 'Personal Data' (circled in red) and includes a 'Your data' section with a search link for public track hubs. The 'Add a custom track' section contains a form with the following fields: 'Name for this data (optional):', 'Species: Zea mays', 'Assembly: AGPv4', 'Data:' (with a text area for pasting or a file upload button), and 'Data format:' (with a link to help on supported formats). An 'Add data' button is at the bottom of the form. The top of the interface shows a genomic track with a scale from 45.00 Mb to 46.50 Mb and a 'Forward strand' indicator. At the bottom, a track for 'cDNA' is visible, showing gene models and associated data.

Track Hubs in Gramene

EBI Atlas team: RNAseq-er API aligns all ENA short reads for genomes in Ensembl updated daily

Location view

The screenshot displays the Gramene Track Hubs interface. At the top, there is a navigation bar with options for 'Scroll', 'Track height', and 'Drag/Select'. Below this is a genomic track showing chromosome bands and a 'Personal Data' tab. A red arrow points to the 'Personal Data' tab, and another red circle highlights the 'Configure this page' button in the left sidebar. The main content area shows search results for 'Zea mays AGPv4', listing 169 track hubs. The first two results are highlighted:

- RNA-Seq alignment hub SRP063765**
Description: Zea mays Genome sequencing ; [SRP063765](#)
Data type: transcriptomics
Number of tracks: 2
[Attach this hub](#)
- RNA-Seq alignment hub SRP066138**
Description: Zea mays subsp. mays Genome sequencing ; [SRP066138](#)
Data type: transcriptomics
Number of tracks: 2
[Attach this hub](#)

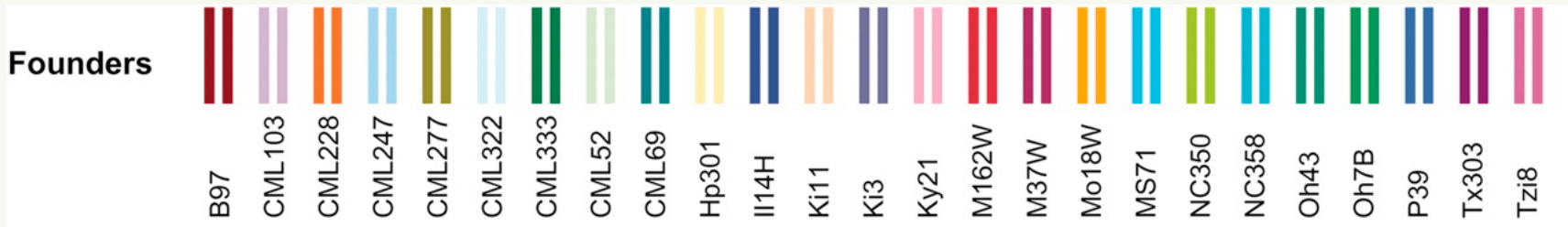
The interface also includes a 'Search Results' section with a 'Search for public track hubs' button and a 'Can't see the track hub you're interested in?' message. A pagination bar shows page 1 of 34 results.

Track Hubs in Gramene

EBI Atlas team: RNAseq-er API aligns all ENA short reads for genomes in Ensembl updated daily



24 Maize NAM Founder lines



Yu et al. (2008) Genetics 178:539-551; <https://doi.org/10.1534/genetics.107.074245>

- Chromosome-level assembly
- Uniform annotation protocol
- Compara gene trees—ortholog identification
- All pair-wise synteny maps
- Pan-genome analysis

NSF Award # 1744001

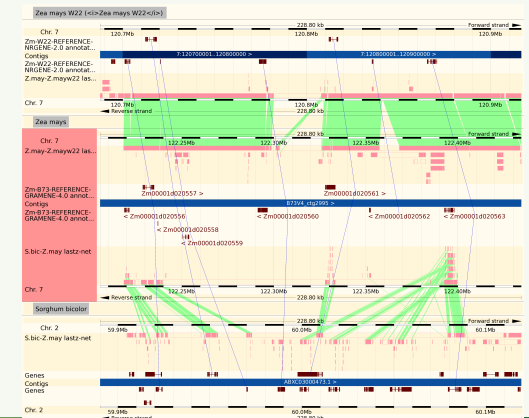
Preview at

maize-pangenome.gramene.org

Variation: copy-number presence/absence



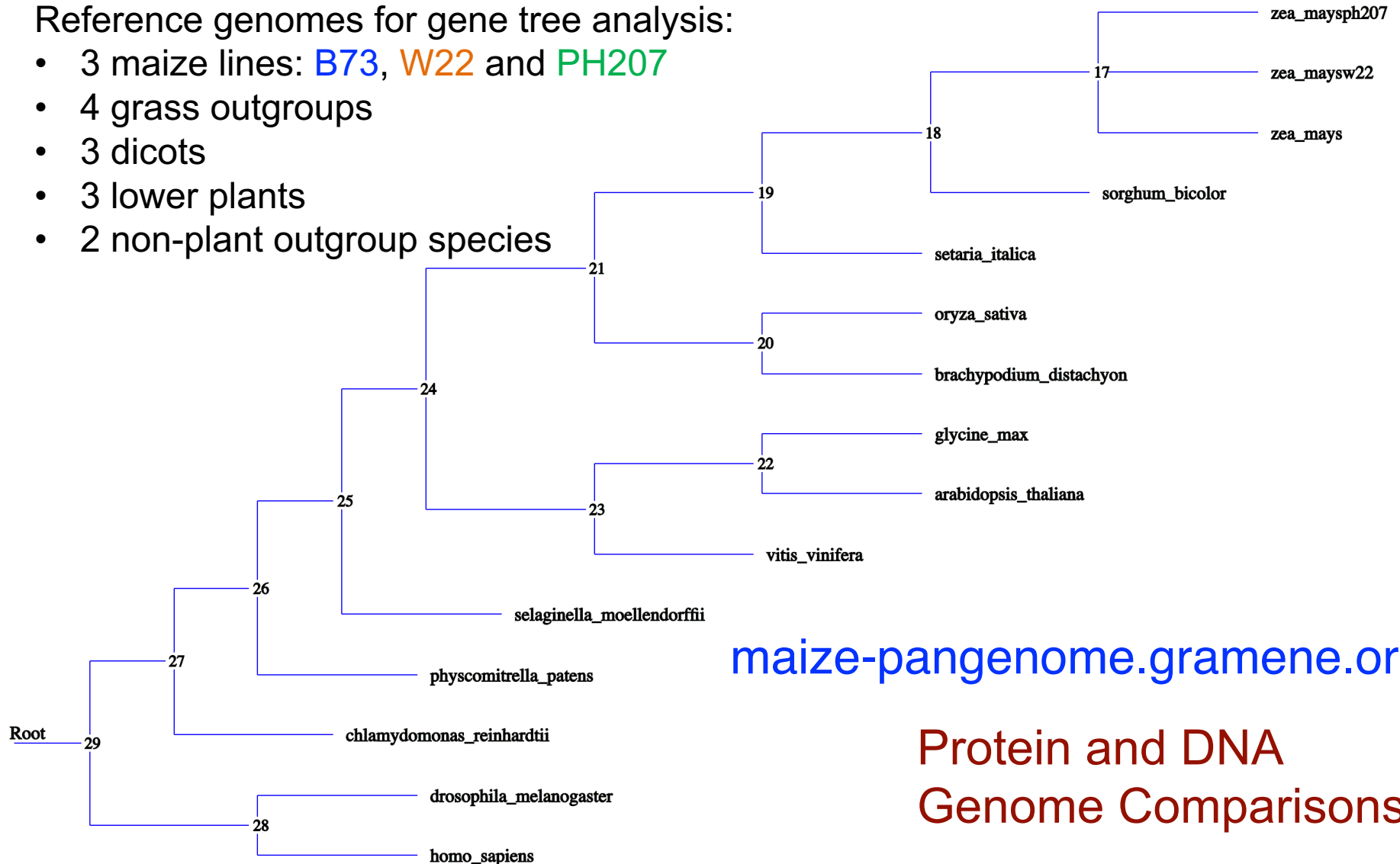
Pangenome site: B73, W22, PH207 maize + outgroups




Maize Genomes at PanMaize

Reference genomes for gene tree analysis:

- 3 maize lines: B73, W22 and PH207
- 4 grass outgroups
- 3 dicots
- 3 lower plants
- 2 non-plant outgroup species

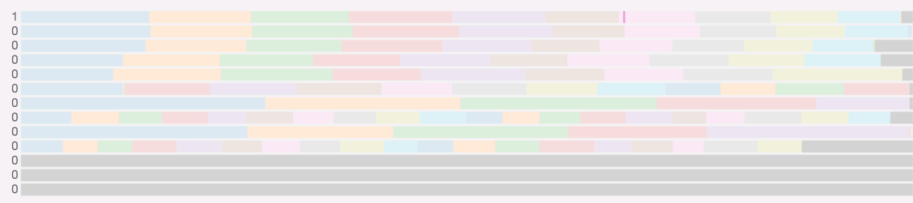
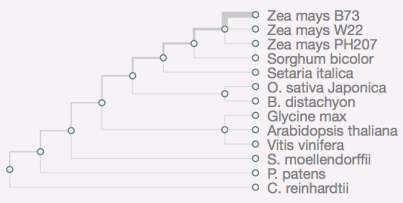


Maize Pan-Genome

 Search for genes, species, pathways, ontology terms, domains... 1 genes in 1 genomes ▾

Gene | Zm00001d018971 ✕

Taxagenomic distribution



opaque endosperm2 Zm00001d018971 GRMZM2G015534 *Zea mays B73* [↗](#)

Regulatory protein opaque-2

Location Expression **Homology** X-refs

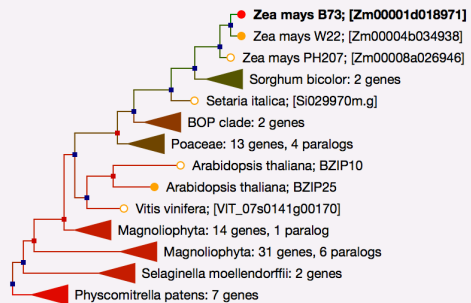
Model Species Homolog

BZIP25 *Arabidopsis thaliana*
Basic leucine zipper 25

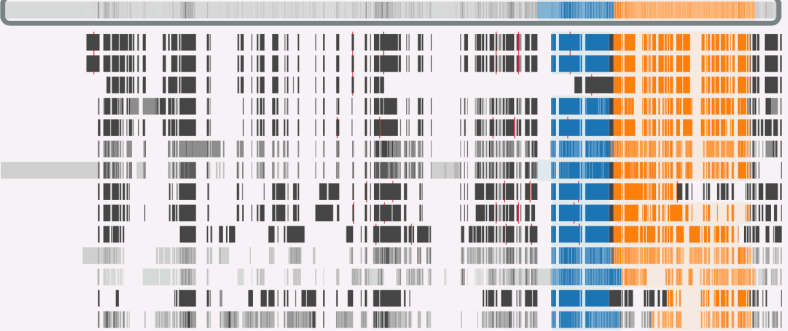
Compara Gene Tree

This phylogram shows the relationships between this gene and others similar to it, as determined by [Ensembl Compara](#).

Display mode ▾ ⚙



Alignment overview: Proteins color-coded by InterPro domain. Resize slider to navigate.



Search Gramene

Show All Homologs **78**

Show Orthologs **20**

Show Paralogs **12**

Links to other resources

[Ensembl Gene Tree view](#)

Gene tree alignment view

Maize Pan-Genome

opaque endosperm2 Zm00001d018971 *Zea mays* B73

Regulatory protein opaque-2

Compara Gene Tree

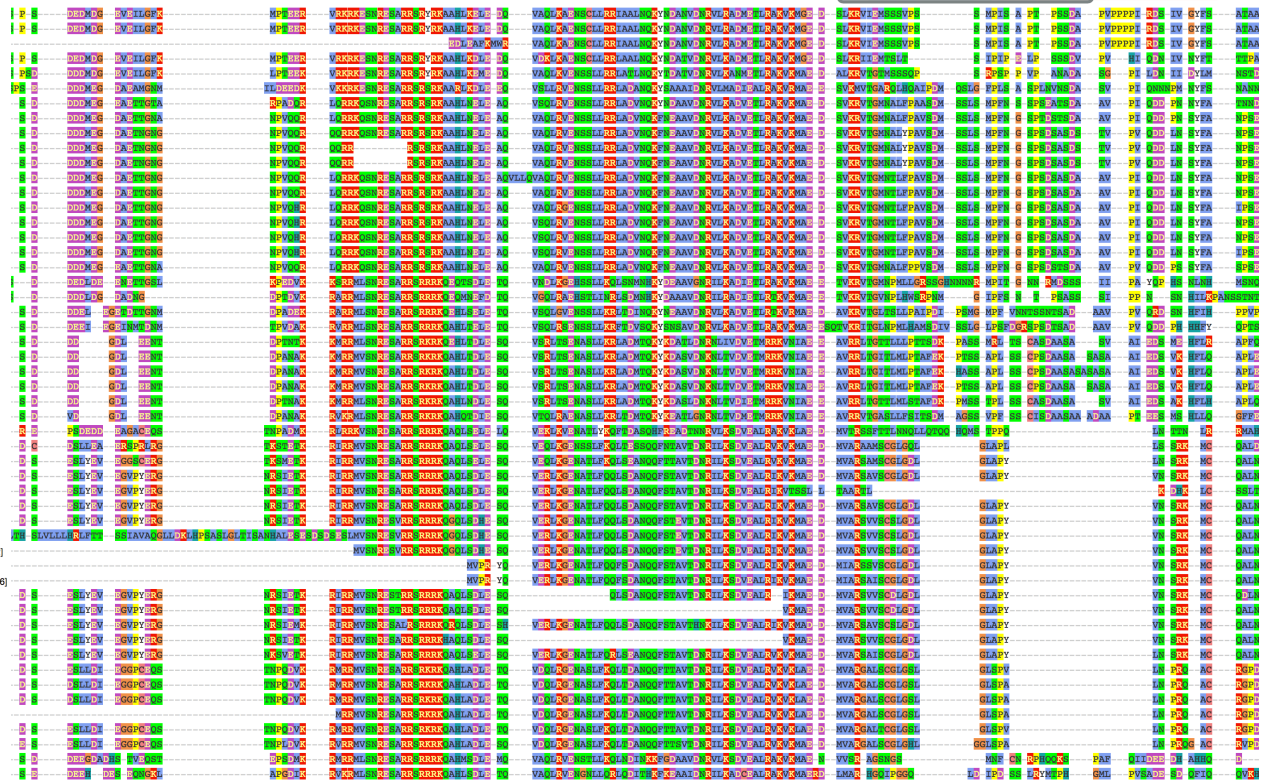
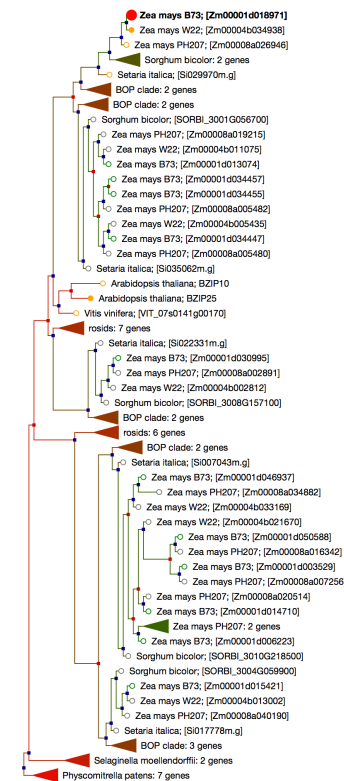
This phylogram shows the relationships between this gene and others similar to it, as determined by Ensembl Compara.

Display mode ▾

Color Scheme ▾



Multiple Sequence Alignment: Amino acid MSA. Drag slider to reposition.



Multiple-sequence alignment view



Maize Pan-Genome

opaque endosperm2 Zm00001d018971 GRMZM2G015534 *Zea mays* B73

Regulatory protein opaque-2

BZIP25 *Arabidopsis thaliana*

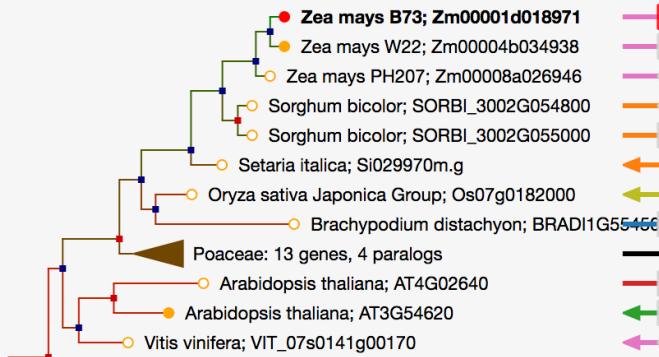
Basic leucine zipper 25

Location Expression Homology X-refs

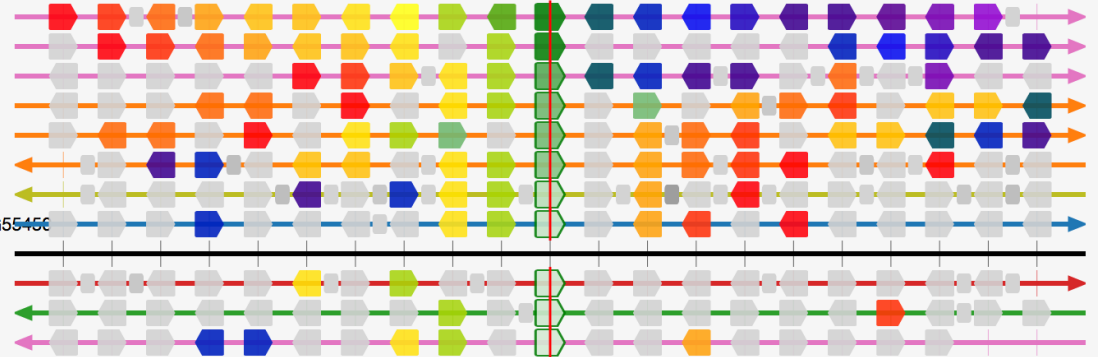
Compara Gene Tree

This phylogram shows the relationships between this gene and others similar to it, as determined by Ensembl Compara

Display mode ▾



Neighborhood conservation: +/- 10 flanking genes color-coded by gene family.



Gene neighborhood conservation view

Pathways (Video)



Plant Reactome: pathways, species, and analysis features

<http://plantreactome.gramene.org>

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2018 Maize Genetics Conference 22-25 March

Get in touch!

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Gramene - Exploring Function through Comparative Genomics and Network Analysis

NSF IOS 1127112 (2012- 2017)

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