



Mining Maize Data in the PanMaize Gramene Database



March 16th, 2023

Workshop Resources

http://ftp.gramene.org/outreach/maize_2023/Gramene_Workshop/

Slide URLs

http://ftp.gramene.org/outreach/maize_2023/Gramene_Workshop/maize_meeting_urls_for_workshop.txt

Trans-national collaboration

Doreen Ware



Irene Papatheodorou

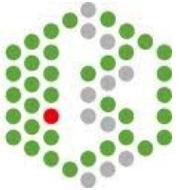
Pankaj Jaiswal

Sarah Dyer



Crispin
Taylor

EMBL-EBI



Track Us Down If You Have Questions!



Doreen Ware



Janeen Braynen



Zhenyuan Lu



Nick Gladman

Workshop Slideshow Access Information

Slides and other info are located here:

http://ftp.gramene.org/pub/gramene/outreach/maize_2023/



Gramene Protocol Book Chapters:

https://link.springer.com/protocol/10.1007/978-1-4939-3167-5_7



YouTube:

<https://www.youtube.com/@gramenedatabase3929>





Genomes

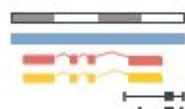
43 Genomes

26 NAM

8 New Genomes

- 4 European Flint, Mo17,
W22, PH207, & A118

6.5M gene
annotations



36K gene
trees

109 B73 v4
curated
genes

ATCGAGCT
ATCCAGCT
ATCGAGAT

Expression



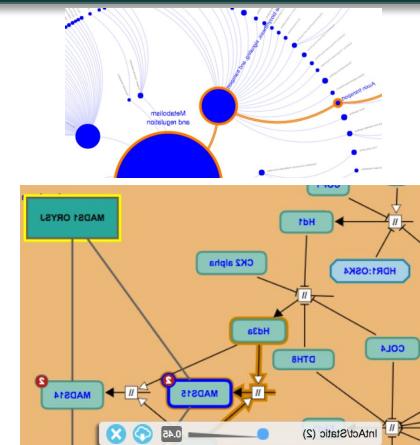
982 experiments in
23 species

Pathways

320 curated
Projected to 120
species



Plant REACTOME



Variation

>700K SNPs in >16K maize
and teosinte lines
Panzea 2.7



 European Variation Archive

>55M SNPs in 103
genomes
HapMap2

Maize PanGenome Release 3.0

Released: March 2023

Summary

[Gramene's Maize PanGenome](#), a web portal for comparative plant genomics focused on Maize crop varieties, has now released a new version featuring eight new maize genomes that include four **European flint maize genomes**: **DK105**, **EP1**, **F7** and **PE0075** (Haberer et al, 2020), **Mo17** (Yang et al, 2017), **W22** (Springer et al, 2018), **PH207** (Hirsch et al, 2016), **A188** (Lin et al, 2021). The site now hosts a total of 43 genomes including three assembly versions of the B73 *Zea mays* reference (RefGen_v3, RefGen_v4, and RefGen_v5), 25 NAM maize founder genomes, and seven outgroups (*Arabidopsis thaliana*, *Oryza sativa* Japonica, *Sorghum bicolor*, *Vitis vinifera* ssp. *vinifera* PN40024, *Selaginella moellendorffii*, *Chlamydomonas reinhardtii*, and *Drosophila melanogaster*).

The maize gene models, together with the seven outgroups were used to build 36,021 protein-coding gene family trees. Data from 25 baseline gene expression studies from the EBI Expression Atlas, and 267 orthology-based pathway projections from the Plant Reactome are provided for B73 (v5).

The outgroup genome databases were built in direct collaboration with the [Ensembl Plants](#) project. Other data sets were facilitated via collaborations with the [Expression Atlas](#), and the [Plant Reactome](#) databases.

Release Information

- [Overall Highlights](#)
- [Comparative Genomics](#)
- [Gene Expression](#)
- [Pathways](#)
- [Publications](#)
- [Funding](#)

Overall Highlights

- Eight new maize reference genomes: DK105, EP1, F7, PE0075, Mo17, W22, PH207, and A188
- 36,021 protein-coding gene family trees from 1,668,034 protein sequences
- Gene expression and orthology-based pathway projections for the reference genome *Zea mays* B73 v4 and v5
- Genetic variation from Gramene/Ensembl Plants (HapMap2 and Panzea 2.7 GBS SNPs)
- Structural variation tracks for the NAM genomes
- Manually curated gene models track [Example: incw3](#). Complete [list of curated genes \(B73 v4\) in Gramene](#).

41 Genomes at Maize Gramene

Gramene MAIZE BLAST Tools Help Feedback Gramene Search

Search Zea mays B73 v5...

Login/Register

Zea mays B73 v5 (Zm-B73-REFERENCE-NAM-5.0) ▾

Zea mays B73 v5
Zea mays B73 v5
Data Source nam | Taxonomy ID [4577](#)

Search Zea mays B73 v5...

e.g. [Zm00001eb000010](#) or [1:109000-145001](#)

Genome assembly: Zm-B73-REFERENCE-NAM-5.0

More information and statistics
 Download DNA sequence (FASTA)
 Display your data in Maize PanGenome

View karyotype
 Example region

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

Carboxy* CAB Rubisco F-box ADH PSII
Example gene
 Example transcript

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)

Example gene tree

Variation

What can I find? Short sequence variants.

More about variation in Maize PanGenome
 Download all variants - GVF - VCF - VEP

Variant Effect Predictor

ATCGAGCT ATCCAGCT ATCGAGAT
Example variant

Contact Us | Help



Arabidopsis thaliana

eud



Zea mays B73 v5 Assembly and Gene Annotation



Chlamydomonas reinhardtii

Chl



Oryza sativa (Geng/Japonica-temp var. Nipponbare)

Lili



Selaginella moellendorffii

Lyc



Sorghum BTx623

Lili



Vitis vinifera ssp. vinifera PN40024 v3

eud



Zea mays B73 v3

Lili



Zea mays B73 v4

Lili



Zea mays B73 v5

Lili



Zea mays b73_Ab10

Lili



Zea mays b97

Lili



Zea mays cml103

Lili



Zea mays cml228

Lili



Zea mays cml247

Lili



Zea mays cml277

Lili



Zea mays cml322

Lili



Zea mays cml333

Lili



Zea mays cml52

Lili



Zea mays cml69

Lili

About Zea mays

Maize or *Zea mays* had the highest world-wide production of all grain crops in 2019. 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 civilisations. 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 ($2n=2x=20$) [2-4]. Maize is distinguished from other grasses in that its genome arose from an ancient tetraploid event unique to its lineage. This sequence corresponds to inbred line B73.

Assembly

The B73 genome was sequenced to high depth using PacBio long-read technology together with 25 founder inbred lines strategically selected to represent the breadth of maize diversity including lines from temperate, tropical, sweet corn, and popcorn germplasm. All lines were assembled into contigs using a hybrid approach, corrected with long-read and Illumina short-read data, scaffolded using Bionano optical maps and ordered into pseudomolecules using linkage data from the NAM recombinant inbred lines and maize pan-genome anchor markers. The 26 lines were also annotated with a common pipeline.

The current assembly is named Zm-B73-REFERENCE-NAM-5.0 and was aligned to the previous B73_RefGen_v4 version with software ATAC/A2Amapper [5], obtaining 96.76% mapped positions. Those mappings can be used to translate coordinates across with the [Assembly Converter](#).

Annotation

The gene annotations were produced with the CSHL gene pipeline developed under the [NAM project](#). In summary, it is an automated, evidence-based method combining third-party software including Mikado, BRAKER and PASA. Gene models were filtered by conservation and Maker Annotation Edit Distance (AED) score, and then classified into protein_coding and misc_non-coding sets.

Gene models from version B73_RefGen_v4 have been mapped to the current Zm-B73-REFERENCE-NAM-5.0 and can be retrieved with the [ID History Converter](#).

Evidence-based predictions were directly inferred from assembled transcripts, which were generated using five different genome-guided transcript assembly programs and processed using Mikado to pick the optimal set of transcripts for each locus. To generate assembled transcripts, quality inspected RNA-seq reads were mapped to the genome. In order to pick the final transcripts, Mikado uses assembled transcripts combined with high-confidence splice junctions with the mapped reads as input, predicted ORFs for the assembled transcripts generated and homology results of transcripts to SwissProt (Viridiplantae) sequences.

Ab initio predictions were performed using BRAKER with both evidence-based predicted proteins and mapped RNA-seq reads as input.

A working set (WS) of models was generated to capture the complete gene space by combining evidence based and non-overlapping BRAKER gene models using BEDtools. Additional structural improvements on the WS models were completed using the software PASA. Transposable element related genes were filtered from the evidence and non-overlapping BRAKER sets using the TEsorter tool, which uses the REXdb database of TEs.

The TE filtered WS models were given AED scores using MAKER-P (v.3.0). Only models with AED < 0.75 passed to the high-confidence set (HCS). The HCS gene models were further classified based on homology to related species, and assigned coding and non-coding biotypes. The HCS gene models were checked for missing start and stop codons. The CDS boundaries of the transcripts were modified based on conserved start codon positions or extended to a start or stop codon whenever possible. All conserved genes in addition to lineage-specific genes that had a complete CDS were marked as protein-coding. The remaining lineage-specific genes were marked as non-coding. HCS gene models were checked and potentially split or merged using the GFF3toolkit. Gene ID assignment was made as per [MaizeGDB nomenclature schema](#).

Repeats

Repeat features were annotated with the RepeatMasker pipeline with RepBase and wessler-bennetzen-2015/TE_12-Feb-2015_15-35 libraries.

Regulation

Gene expression probes

Oligo probes from the [GeneChip Maize Genome Array](#) have been aligned using the standard Ensembl 2-step [mapping procedure](#).

Variation

The following variation datasets were remapped from assembly B73_RefGen_v4 to Zm-B73-REFERENCE-NAM-5.0

Summary

Assembly: Zm-B73-REFERENCE-NAM-5.0,

Database version: 87.1

Base Pairs: 2,182,074,994

Golden Path Length: 2,182,075,994

Genebuild method: Mikado

Genebuild started: blank 2019

Genebuild version: 2019-cshl

Gene counts

Coding genes: 41,577

Gene transcripts: 77,341

Coordinate Systems

chromosome 10 sequences ▾

Sequence	Length (bp)	Filter
1	308452471	
2	243675191	
3	238017767	
4	250330460	
5	226353449	
6	181357234	
7	185808916	
8	182411202	
9	163004744	
10	152435371	

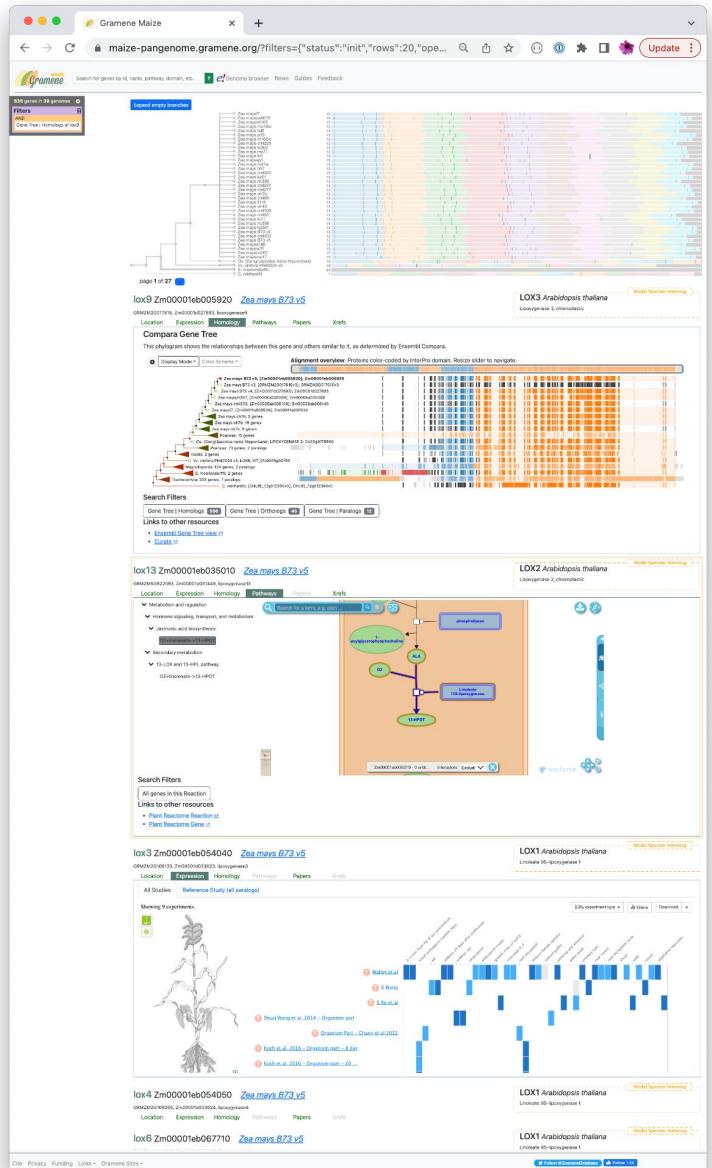
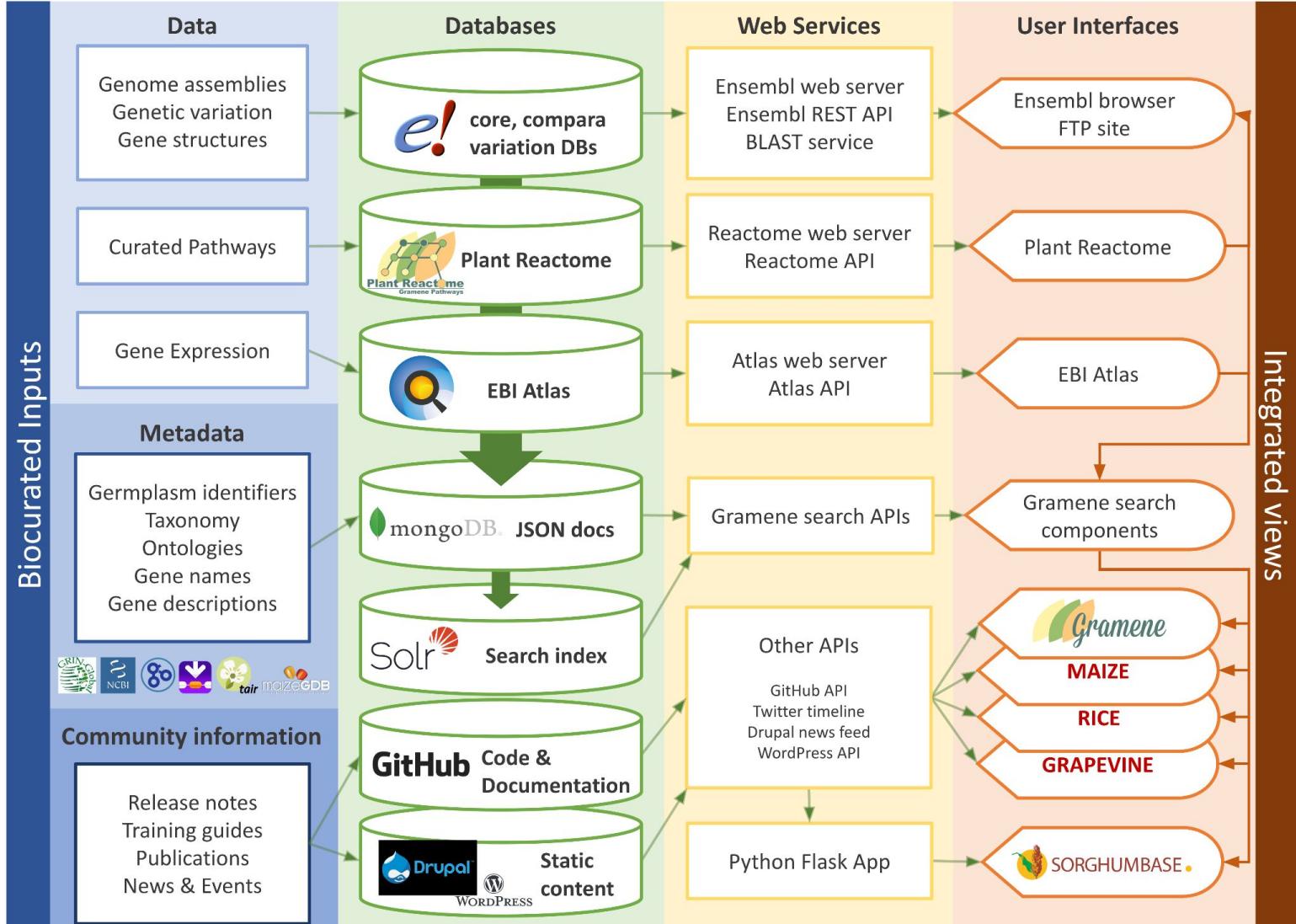
scaffold 695 sequences ▾

Sequence	Length (bp)	Filter
scaf_1	242938814	
scaf_2	238017767	
scaf_3	232638519	
scaf_4	20058289	
scaf_5	163004744	
scaf_6	160853524	
scaf_7	152435371	
scaf_8	137725724	
scaf_9	122593601	
scaf_10	112909852	

Showing 1 to 10 of 695 entries

<< < > >>

Integrating Data for Search



<https://maize-pangenome.gramene.org/>

Gramene MAIZE

Search for genes by id, name, pathway, domain, etc.

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e! Genome browser News Guides Feedback

Welcome to Gramene Maize release 3

Comparative plant genomics focused on maize varieties

Hide Slideshow

NAM founder inbreds

This site includes full genome sequences of the NAM founder lines and comparative genomic analyses of protein-coding gene families.

McMullen et al. Science (2009)

Gramene Database Retweeted

Sorghumbase @sorghumbase · Mar 8

On International Women's Day, @sorghumbase recognizes the achievements of 9 early career female scientists #8March2023 #plantscience #sorghum #genderequity sorghumbase.org/post/sorghumba...

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Gramene Database Retweeted

EVA @evarchive · Feb 7

Adama Science And Technology University buff.ly/3HXzeEC

Single nucleotide polymorphism (SNP) markers for genetic diversity and population structure study in Ethiopian barley (*Hordeum vulgare* L.) germplasm. Variation data now available to download buff.ly/3HE4eby

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Genome Browser

Genome annotations, variation and comparative tools

BLAST

Query our genomes with a DNA or protein sequence

Plant Pan Genomes

Gramene-powered sites focused on specific crops

Curated Gene Function

Genes described in the literature

Bulk Downloads

FTP download of our data

Genes

NAC 1 NAC4 1 NAC8 1 nac5 1 nac1 1 nac 1 NAC104 2 NAC13 2 NAC60 2 OsNAC1 3

InterPro: Domain

NAC-dom 6377 NAC-like_UBA 82 GPI-GlcNAc_Trfase_PIG-H_dom 77 Semialdehyde_DH_NAD-bd 90 Chitin-bd_1 431 Nas_poly-pep-assoc_cplx_dom 372
Fe_hydrogenase_ssu 82 Calx_beta 2 Fe_hydrogenase_Isu_C 93 Cellulose/chitin-bd_N 8

InterPro: Family

GlcNAc_MurG 4 GlcNAc_Gpi1 44 GlcNAc_II 46 Chond_GalNAc 3 GlcNAc_6-P_deAcase 1 Plno_GlcNAc_GPI2 48 GlcNAc_6-SO4ase 2
UDP_GlcNAc_COvinyl_MurA 3 GlcNAc_PI_deacetylase-related 81 UDP-acyl_GlcNac_deAcase 44

InterPro: Homologous_superfamily

NAC_dom_sf 2058 NAC_A/B_dom_sf 2 UDP-acyl_GlcNac_deAcase_C 6 ENTH_VHS 938 Fe_hydrogenase 49 Trimer_LpxA-like_sf 439
Metal-dep_hydrolase_composite 148 UDP-acyl_N-AcGlcN_deAcase_N 6 Acyl_CoA_acyltransferase 1277 2Fe-2S_ferredoxin-like_sf 524

Gene Ontology: molecular function

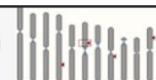
dolichyl-P-Man:Man(7)GlcNAc(2)-PP-dolichol alpha-1,6-mannosyltransferase 5 dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase activity 61
dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransferase activity 1 dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glucosyltransferase activity 17
GDP-Man:Man1GlcNAc2-PP-Dol alpha-1,3-mannosyltransferase activity 19 GDP-Man:Man3GlcNAc2-PP-Dol alpha-1,2-mannosyltransferase activity 20
Glc3Man9GlcNAc2 oligosaccharide glucosidase activity 25 acetylglucosaminyltransferase activity 302 acetylgalactosaminyltransferase activity 21
beta-1,4-N-acetylgalactosaminyltransferase activity 2

Plant Reactome: BlackBoxEvent

Expression of OsNAC10 1



Genome annotations, variation and comparative tools



Query our genomes with a DNA or protein sequence

On International Women's Day,
@sorghumbase recognizes the achievements of 9 early career female scientists #8March2023
#plantscience #sorghum
#genderequity
sorghumbase.org/post/sorghumba...

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Plant Pan Genomes

Gramene-powered sites focused on specific crops



Curated Gene Function

Genes described in the literature

Gene Search By ID, Domain, GO, Reactome, and Trait

Gramene MAIZE

Search for genes by id, name, pathway, domain, etc.

?

e! Genome browser News Guides Feedback

5752 genes in 36 genomes

Filters AND InterPro: Domain | NAC-dom

Expand empty branches

page 1 of 288 >

nactf78 Zm00001eb001460 [Zea mays B73 v5](#)

GRMZM2G406204, Zm00001d027395
NAC-transcription factor 78

Location Expression Homology Pathways Papers Xrefs

nactf33 Zm00001eb001990 [Zea mays B73 v5](#)

GRMZM2G025642, Zm00001d027459
NAC-transcription factor 33

Location Expression Homology Pathways Papers Xrefs

148 158 160 168 155 159 168 166 159 156 149 159 161 165 157 166 153 168 158 158 164 166 148 164 166 164 161 167 170 175 149 152 140 146 163

Model Species Homolog

NAC045 *Arabidopsis thaliana*

NAC domain-containing protein 45

Model Species Homolog

NAC037 *Arabidopsis thaliana*

NAC domain-containing protein 37

Gene Trees

Zm00001eb038920 [Zea mays B73 v5](#)

Zm00001d031898

Model Species Homolog

NAC078 *Arabidopsis thaliana*

NAC domain-containing protein 78

Location Expression Homology Pathways Papers Xrefs

Compara Gene Tree

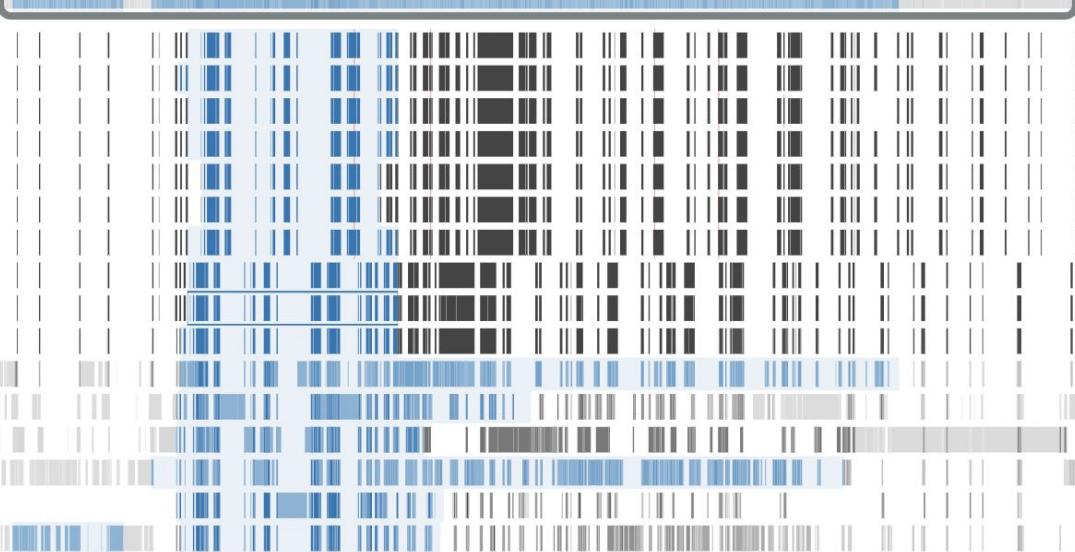
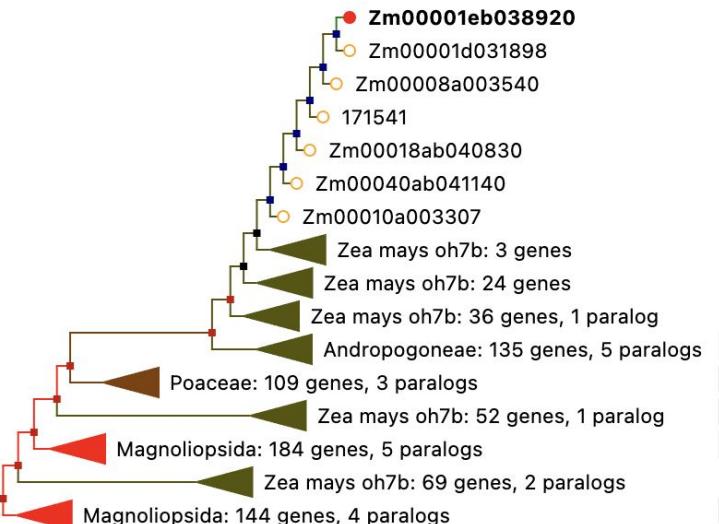
This phylogram shows the relationships between this gene and others similar to it, as determined by Ensembl Compara.



Display Mode ▾

Color Scheme ▾

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



Search Filters

Gene Tree | Homologs 830

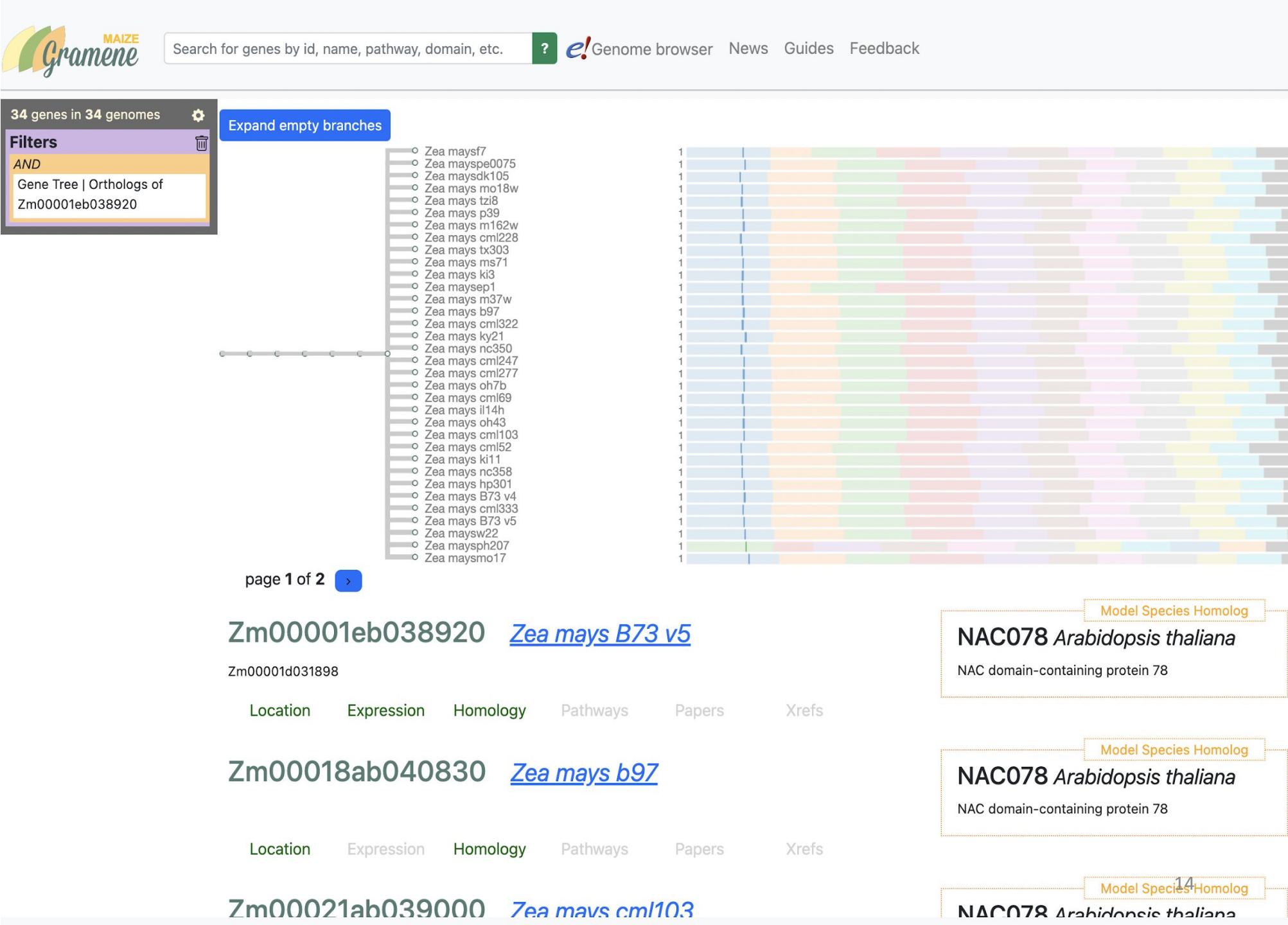
Gene Tree | Orthologs 45

Gene Tree | Paralogs 22

Links to other resources

- [Ensembl Gene Tree view](#)
- [Curate](#)

Gene Orthologs



Gene Trees

Zm00001eb038920 [Zea mays B73 v5](#)

Zm00001d031898

Model Species Homolog

NAC078 *Arabidopsis thaliana*

NAC domain-containing protein 78

Location Expression Homology Pathways Papers Xrefs

Compara Gene Tree

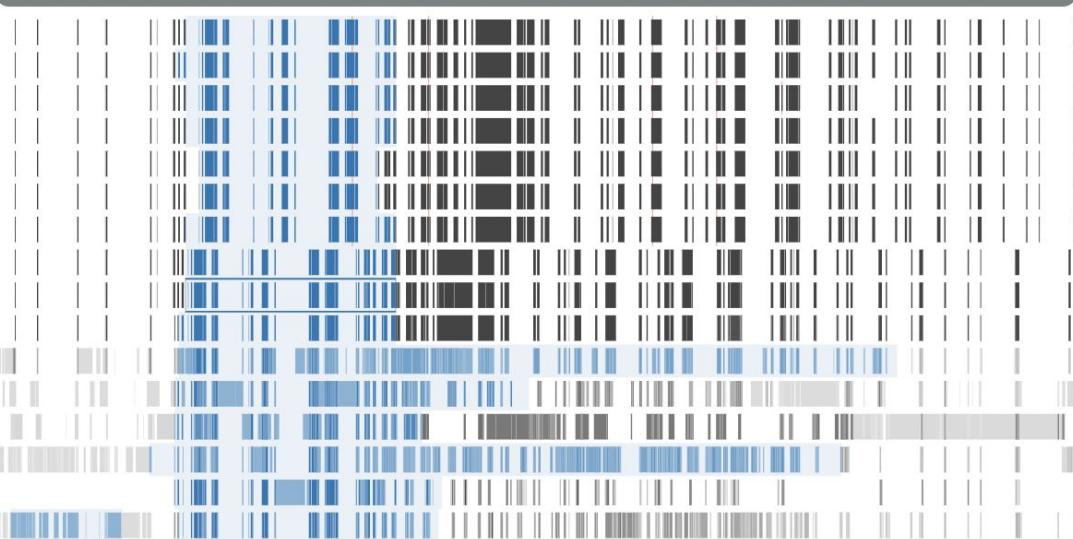
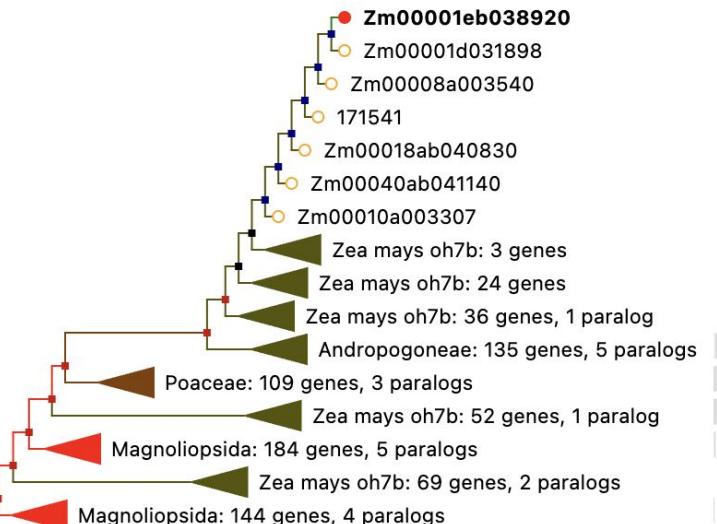
This phylogram shows the relationships between this gene and others similar to it, as determined by Ensembl Compara.



Display Mode ▾

Color Scheme ▾

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



Search Filters

Gene Tree | Homologs 830

Gene Tree | Orthologs 45

Gene Tree | Paralogs 22

Links to other resources

- [Ensembl Gene Tree view](#)
- [Curate](#)

Curation Flag

nrt2 Zm00001eb209670 [Zea mays B73 v5](#)

GRMZM2G010280, transport2
nitrate transport2

Location Expression Homology Pathways Papers Xrefs

Compara Gene Tree

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

This gene was flagged for potential gene structural annotation issues by 2 curators

Display Mode ▾ Color Scheme ▾

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

Zm00001eb209670

Zm00001d054057

Zm00018ab217820

Zm00028ab215690

Zea mays oh7b: 2 genes

Zm00033ab222150

Zea mays oh7b: 5 genes

Zm00016a022257

Zm00011a020893

Zea mays oh7b: 19 genes

Zm00017a022820

Zea mays oh7b: 24 genes, 1 paralog

Zea mays oh7b: 6 genes

Zea mays oh7b: 5 genes

Zea mays oh7b: 4 genes

Sb. bicolor BTx623: 2 genes

Andropogoneae: 37 genes, 1 paralog

Os. (Geng/Japonica-temp Nipponbare): 2 genes

Vv. vinifera PN40024 v3: 2 genes

AT5G60770

Arabidopsis thaliana: 2 genes

Arabidopsis thaliana: 2 genes

rosids: 2 genes

S. moellendorffii: 4 genes

Magnoliopsida: 189 genes, 7 paralogs

C. reinhardtii: 6 genes

17

Zm00001eb038920 Zea mays B73 v5

Zm00001d031898

NAC078 *Arabidopsis thaliana*

NAC domain-containing protein 78

Neighborhood View

[Location](#) [Expression](#) **Homology** [Pathways](#) [Papers](#) [Xrefs](#)

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 ▾



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Multiple Sequence Alignment

Zm00001eb038920 Zea mays B73

Zm00001d031898, Zm00001e003884

NAC078 *Arabidopsis thaliana*

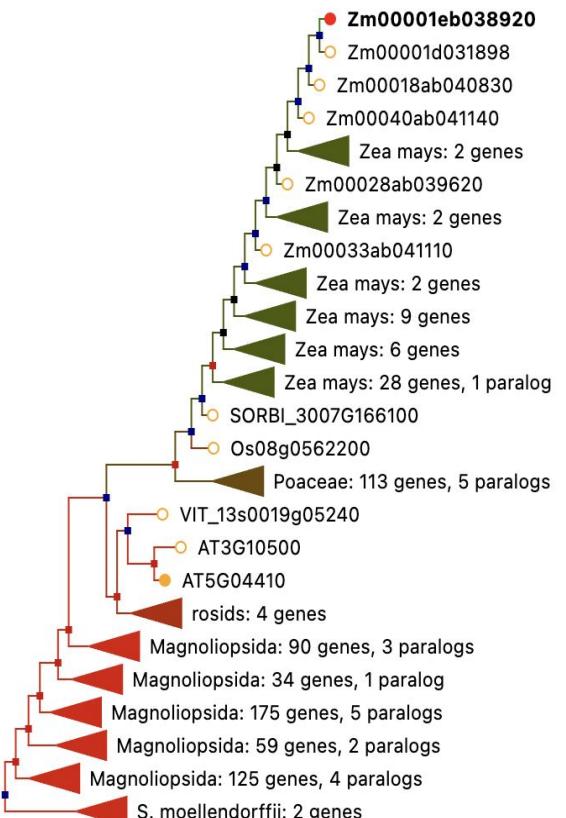
NAC domain-containing protein 78

Location Expression Homology Pathways Xrefs

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 ▾



Search Filters

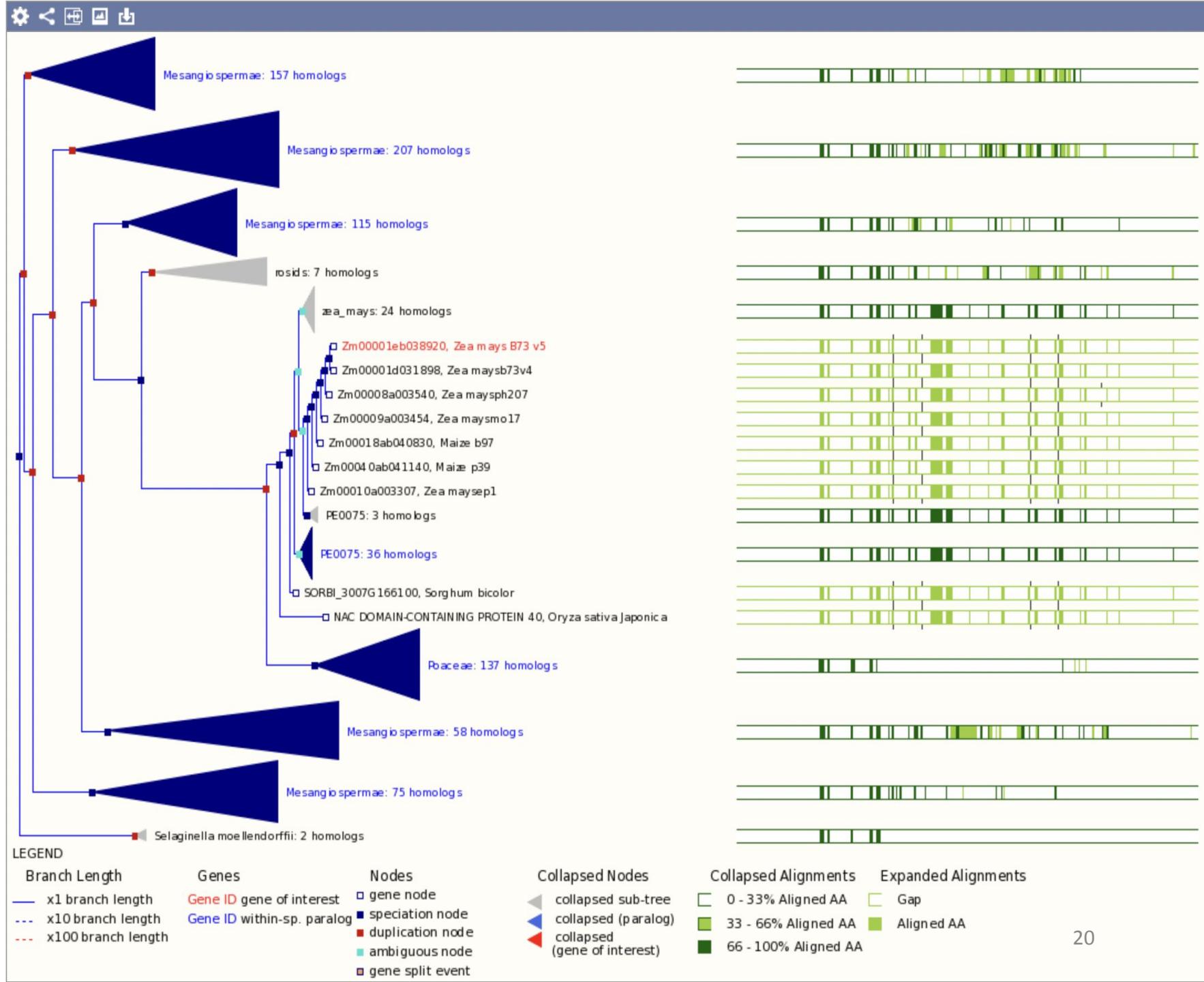
Gene Tree | Homologs

Gene Tree | Orthologs

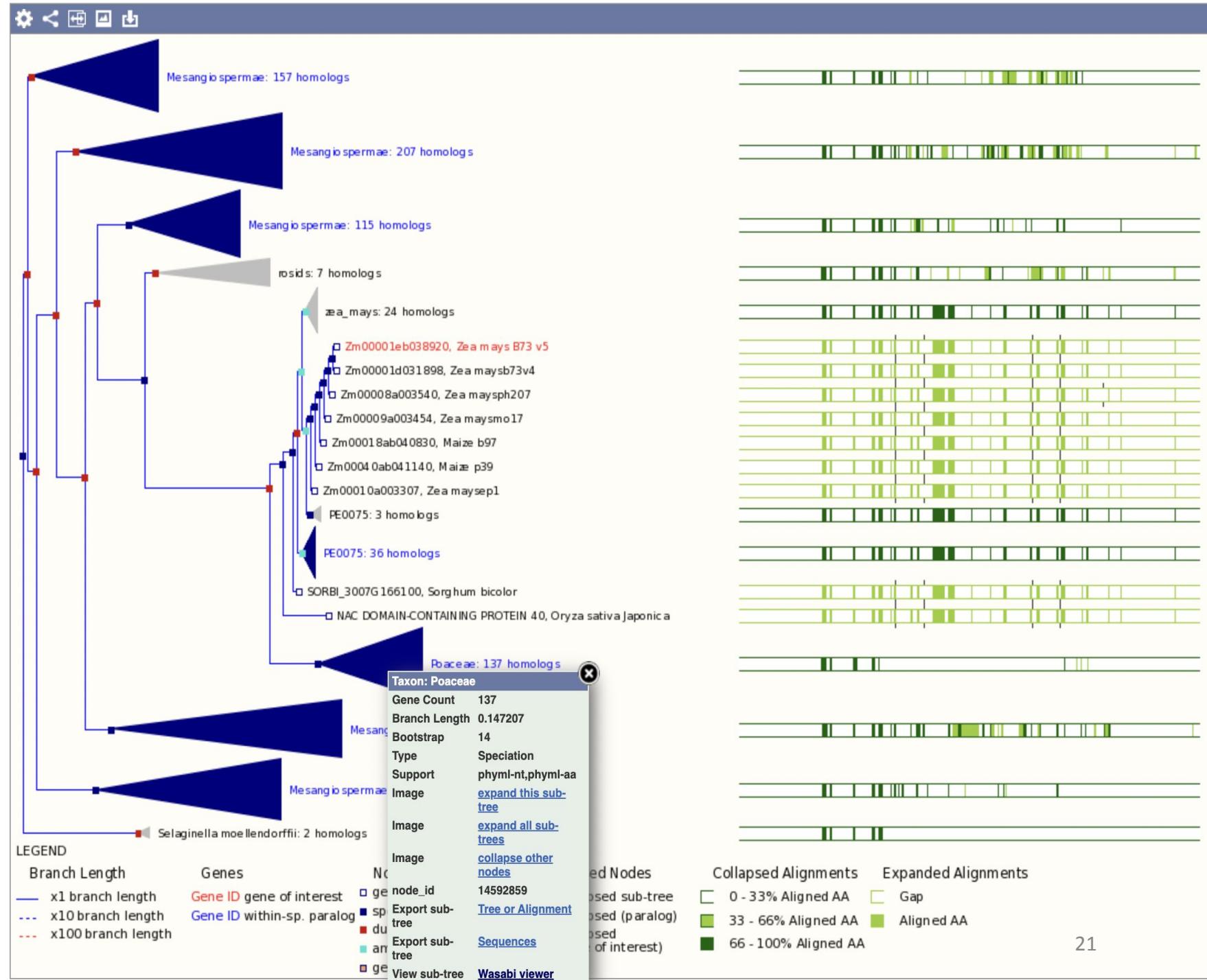
Gene Tree | Paralogs

19

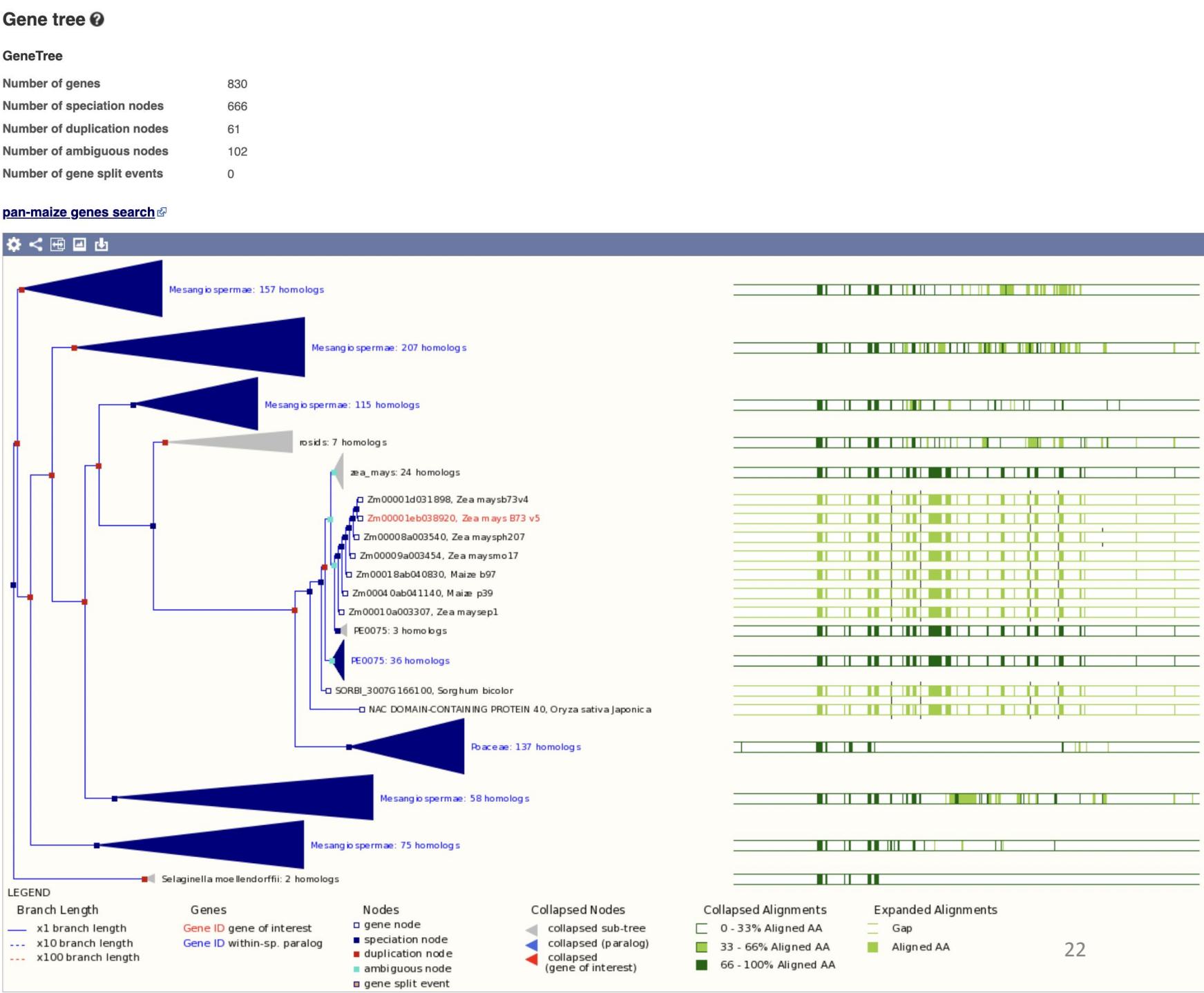
Ensembl Treeview



Ensembl Treeview Details



Ensembl Treeview Details



Gene Expression Atlas

Zm00001eb038920 [Zea mays B73 v5](#)

Zm00001d031898

Model Species Homolog

NAC078 *Arabidopsis thaliana*

NAC domain-containing protein 78

Location Expression Homology Pathways Papers Xrefs

All Studies

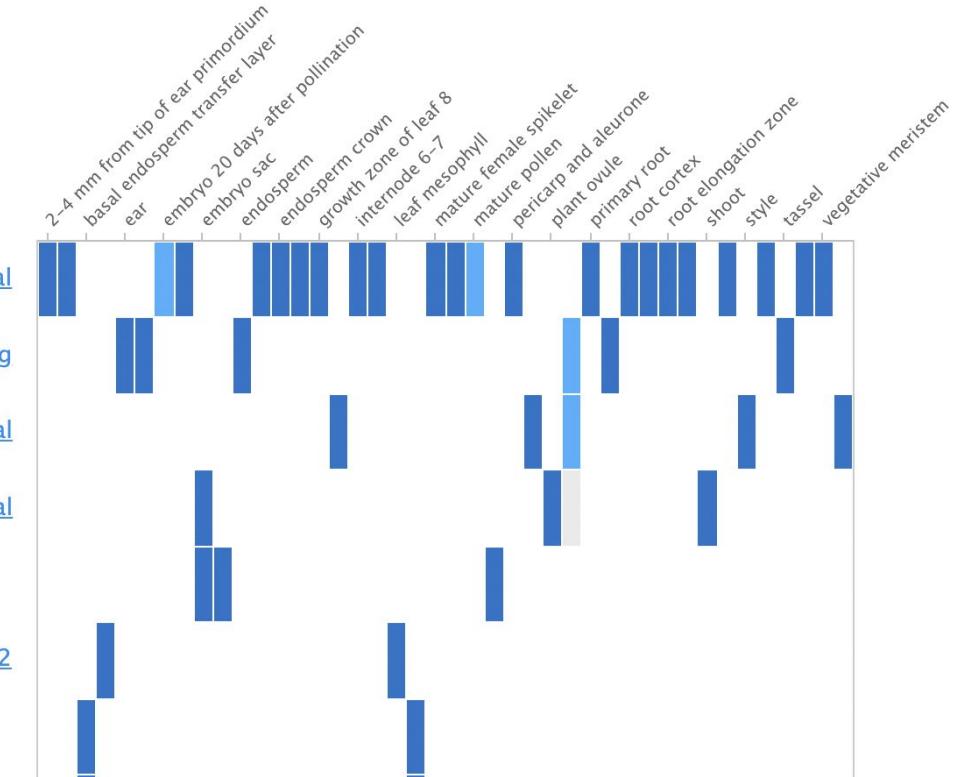
Reference Study (all paralogs)

Showing 9 experiments:

By experiment type ▾

Filters

Download ▾



Paralog Expression

Zm00001eb038920 [Zea mays B73 v5](#)

Zm00001d031898

Model Species Homolog

NAC078 *Arabidopsis thaliana*

NAC domain-containing protein 78

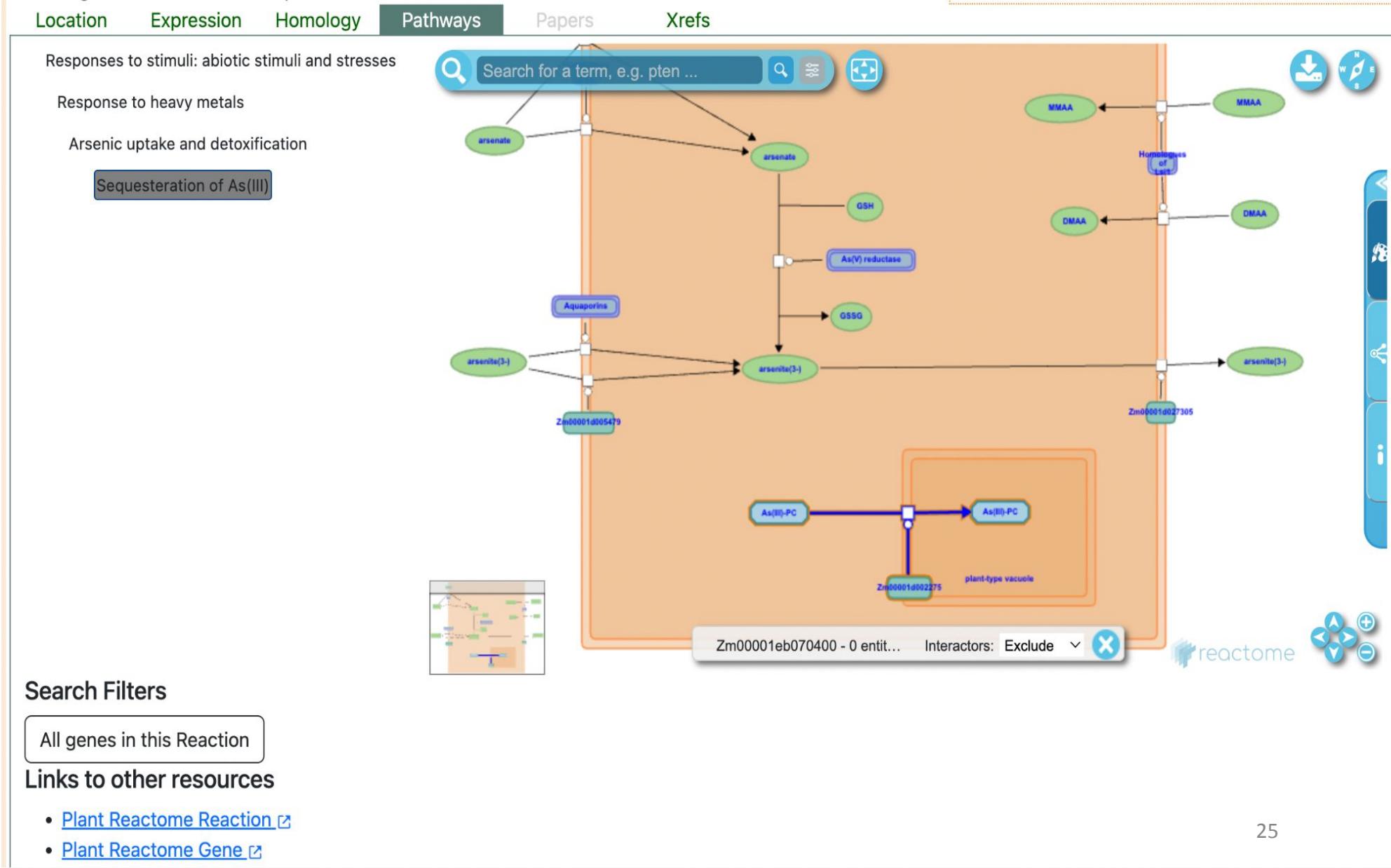


mrpa5 Zm00001eb070400

[Zea mays B73 v5](#)GRMZM2G084181, Zm00001d002275, protein5
multidrug resistance-associated protein5ABCC2 *Arabidopsis thaliana*

ABC transporter C family member 2

Plant Reactome



Publications

br2 Zm00001eb038710 [Zea mays B73 v5](#)

GRMZM2G315375, Zm00001d031871, brachytic2

Location Expression Homology Pathways

Papers

Xrefs

Curated publications

This gene has been described in the literature:

Curation		
PubMed link	source	Title/Description
29720555	geneRIF	PGP1 transcription is up-regulated by Aluminum stress.PGP1 role in root growth.
31881837	geneRIF	findings suggest that low auxin levels mediated by BR2/PGP1 in the intercalary meristem region are crucial for internode elongation

Model Species Homolog
ABCB1 *Arabidopsis thaliana*

ABC transporter B family member 1

Location View

Zm00001eb038920 [Zea mays B73 v5](#)

Zm00001d031898

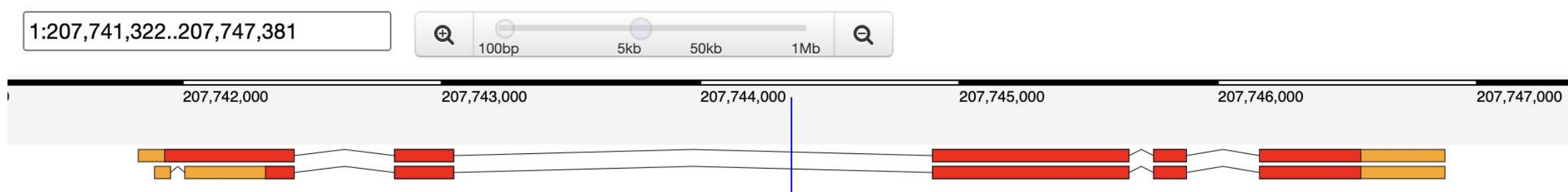
Model Species Homolog

NAC078 *Arabidopsis thaliana*

NAC domain-containing protein 78

Location Expression Homology Pathways Papers Xrefs

Currently viewing: 1:207741322-207747381 [Reset](#)



Search Filters

All on Chromosome 1

All within 1:207741322-207747381

Links to other resources

- [Ensembl Browser ↗](#)
- [MaizeGDB ↗](#)

Ensembl Browser View

Zea mays B73 v5 (Zm-B73-REFERENCE-NAM-5.0) ▾ Location: 1:207,741,827-207,746,876 Gene: Zm00001eb038920

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**
 - GO: Biological process
 - GO: Cellular component
 - GO: Molecular function
- Phenotypes**
- Genetic Variation**
 - Variant table
 - Variant image
 - Structural variants
- Gene expression**
- Regulation**
- External references**
- Supporting evidence**
- ID History**
 - Gene history
- Gramene Search

[Configure this page](#)

[Custom tracks](#)

[Export data](#)

[Share this page](#)

[Bookmark this page](#)

Gene: Zm00001eb038920

Description
Location
About this gene
Transcripts

Zm00001e003884
Chromosome 1: 207,741,827-207,746,876 forward strand.

This gene has 2 transcripts ([splice variants](#)), [44 orthologues](#) and [21 paralogues](#).

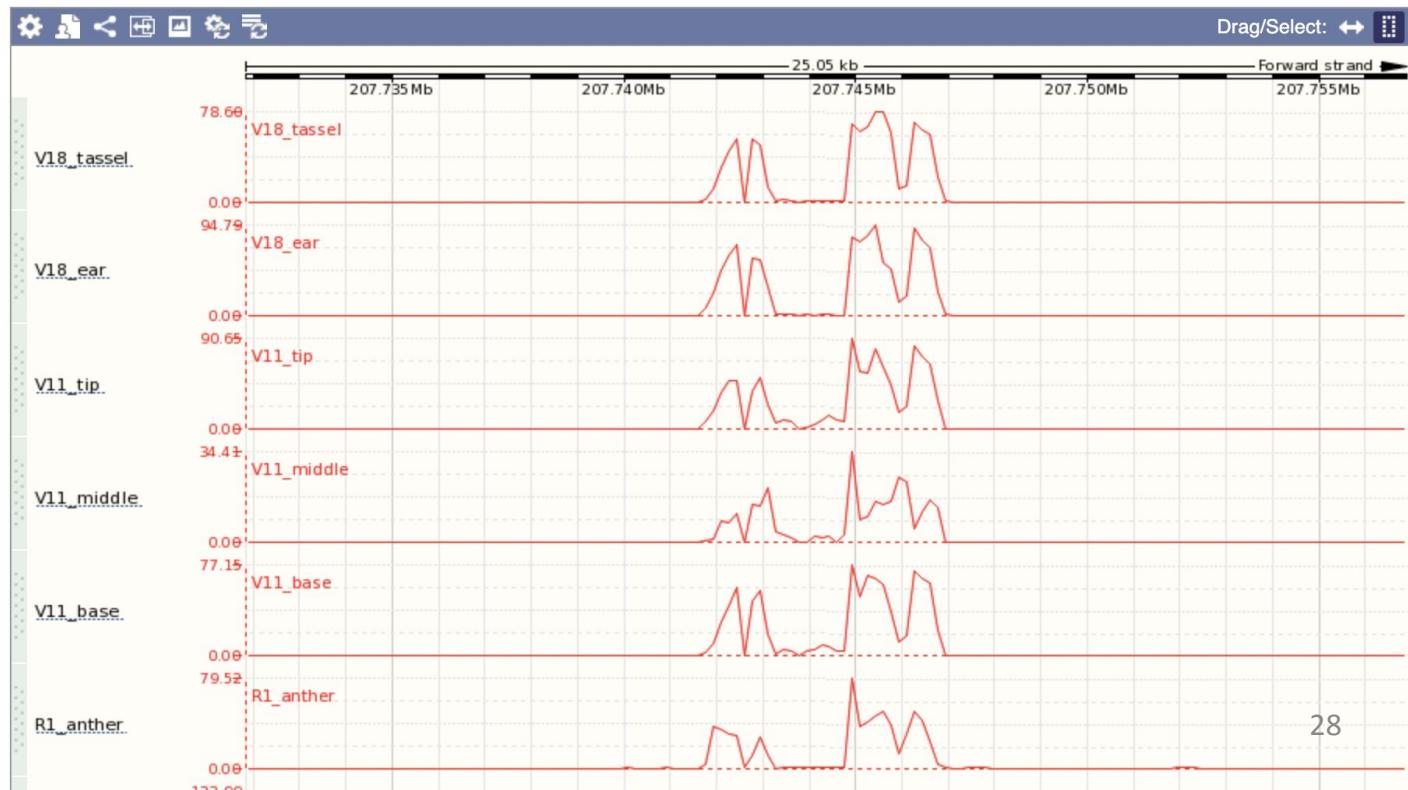
[Show transcript table](#)

Summary

Gene type Protein coding

Annotation method Gene annotation by warelab in CSHL through an automated, evidence-based method combining 3rd party software including Mikado, BRAKER and PASA

Go to [Region in Detail](#) for more tracks and navigation options (e.g. zooming)



Splice Variants and Transcript Comparisons

Gramene MAIZE BLAST Tools Help Feedback Gramene Search

Search Zea mays B73 v5... 

Zea mays B73 v5 (Zm-B73-REFERENCE-NAM-5.0) ▾ Location: 1:207,741,827-207,746,876 Gene: Zm00001eb038920

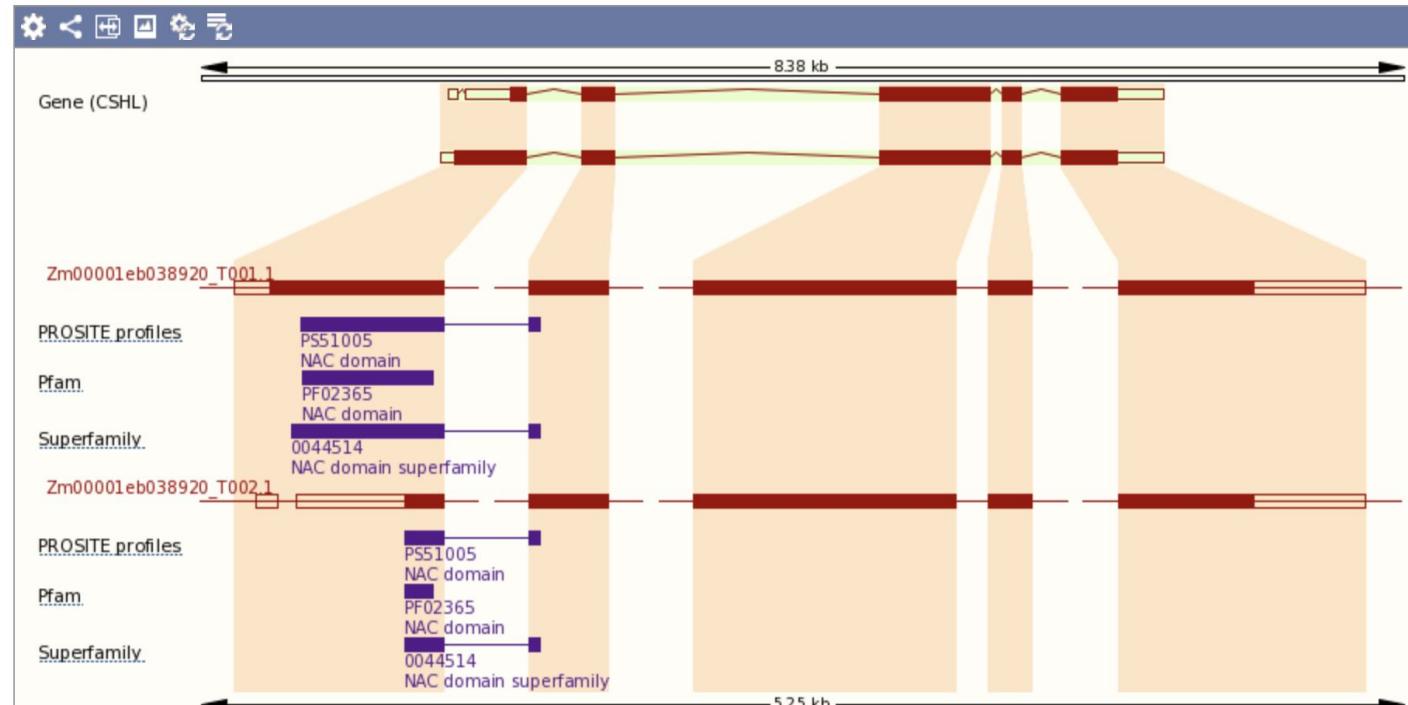
Gene-based displays

- Summary
 - Splice variants** (selected)
 - Transcript comparison
 - Gene alleles
- Sequence
 - Secondary Structure
 - Gene families
 - Literature
- Plant Compara
 - Genomic alignments
 - Gene tree
 - Gene gain/loss tree
 - Orthologues
 - Paralogues
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 - GO: Biological process
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 - GO: Molecular function
- Phenotypes
- Genetic Variation
 - Variant table
 - Variant image
 - Structural variants
- Gene expression
- Regulation
- External references
- Supporting evidence
- ID History
 - Gene history
- Gramene Search

Gene: Zm00001eb038920

Description: Zm00001e003884
 Location: Chromosome 1: 207,741,827-207,746,876 forward strand.
 About this gene: This gene has 2 transcripts (splice variants), 44 orthologues and 21 paralogues.
 Transcripts: Show transcript table

Splice variants ?



Configuring the display

Tip: use the 'Configure this page' link on the left to customise the protein domains displayed above.

Configure this page

Custom tracks

Export data

Share this page

Bookmark this page

Sequence Information—Rapid Views and Porting

The screenshot shows the Gramene website interface for Zea mays B73 v5. The top navigation bar includes links for MAIZE, BLAST, Tools, Help, Feedback, Gramene Search, Login/Register, and a search bar. The main content area is for gene **Zm00001eb038920**. The left sidebar contains a hierarchical menu under "Gene-based displays" with sections like Summary, Splice variants, Transcript comparison, Gene alleles, Sequence (which is currently selected), Secondary Structure, Gene families, Literature, Plant Compara, Pan-taxonomic Compara, Ontologies, Genetic Variation, ID History, and various export and sharing options. The right side shows a detailed view of the gene, including its description (Zm00001e003884), location (Chromosome 1: 207,741,827-207,746,876 forward strand), and transcripts (2 transcripts, 44 orthologues, 21 paralogues). A "Marked-up sequence" section highlights exons (Zm00001eb038920 exons) and shows the sequence starting with >chromosome: Zm-B73-REFERENCE-NAM-5.0:1:207741227:207747476:1.

Sequence Downloads: FASTA or RTF

Download sequence

File name:

File format:

Settings

Sequences to export:

Select/deselect all
 cDNA (transcripts)
 Coding sequences (CDS)
 Amino acid sequences
 5' UTRs
 3' UTRs
 Exons
 Introns
 Genomic sequence

5' Flanking sequence (upstream): * (Maximum of 1000000)

3' Flanking sequence (downstream): * (Maximum of 1000000)

Fields marked * are required

Guide to file formats

FASTA

Text sequence(s):
DNA and/or amino acids

```
>11_dna_chromosome_chromosome:GRCm38:11:10:  
ZAGGGGAAGCCACAAAGGGGATCCCTAGTAGGGCTACTTGC  
TCYGGCCCTCAAGACAGAATCTCCCCACATTGGCAGTTGGC  
ZCGAGTATGAGGCAAGGCTCAAGGGCTGAGGGCCGGTTGTAGT  
TTCTTAATCCCTGTAGACTTACCCCTCCGGGCGGCCGCTGGAC
```

RTF

Marked-up sequence,
with or without variants

```
ATTAGCCAACAAAAAGCAAACACGGG  
GAGTCCTTCCCACAAACATGGGCAT  
TCTTAGGGAGTRAGAATATTGATGCC  
TTTTTAGGGTAATGTGGCTTCCGT
```

Sequence Downloads: FASTA or RTF

Download sequence

File name: Zea_maysb73_Zm00001eb038920

File format: RTF (Word-compatible)

Settings

5' Flanking sequence (upstream): 600 * (Maximum of 1000000)

3' Flanking sequence (downstream): 600 * (Maximum of 1000000)

Number of base pairs per row: 60 bps

Additional exons to display: Core exons

Orientation of additional exons: Display exons in both orientation

Show variants: No

Hide variants longer than 10bp:

Hide variants by frequency (MAF): Don't hide

Filter variants by consequence type:

- No filter
- 3 prime UTR variant
- 5 prime UTR variant
- Coding sequence variant
- Downstream gene variant

Hide individual variant sources:

- No filter
- Hide HapMap2
- Hide Panzea_2.7GBS

Ontology Descriptions and Links

Gramene MAIZE BLAST Tools Help Feedback Gramene Search Search Zea mays B73 v5... 

Zea mays B73 v5 (Zm-B73-REFERENCE-NAM-5.0) ▾ Location: 1:207,741,827-207,746,876 Gene: Zm00001eb038920

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
 - ⊖ **GO: Biological process**
 - ⊖ GO: Cellular component
 - ⊖ GO: Molecular function
- ⊖ Phenotypes
- ⊖ Genetic Variation
 - ⊖ Variant table
 - ⊖ Variant image
 - ⊖ Structural variants
 - ⊖ Gene expression
 - ⊖ Regulation
 - ⊖ External references
 - ⊖ Supporting evidence
- ⊖ ID History
 - ⊖ Gene history
- Gramene Search

Gene: Zm00001eb038920

Description	Zm00001e003884
Location	<u>Chromosome 1: 207,741,827-207,746,876</u> forward strand.
About this gene	This gene has 2 transcripts (splice variants), 44 orthologues and 21 paralogues .
Transcripts	Show transcript table

GO: Biological process 

Accession	Term	Evidence	Annotation Source	Transcript IDs
GO:0006355	regulation of transcription, DNA-templated	IEA	InterPro:NAC-dom , InterPro:NAC dom_sf	Zm00001eb038920_T002 Zm00001eb038920_T001

[Contact Us](#) | [Help](#)

Maize PanGenome release 3 - Feb 2023 © [EMBL-EBI](#)

 [Configure this page](#)

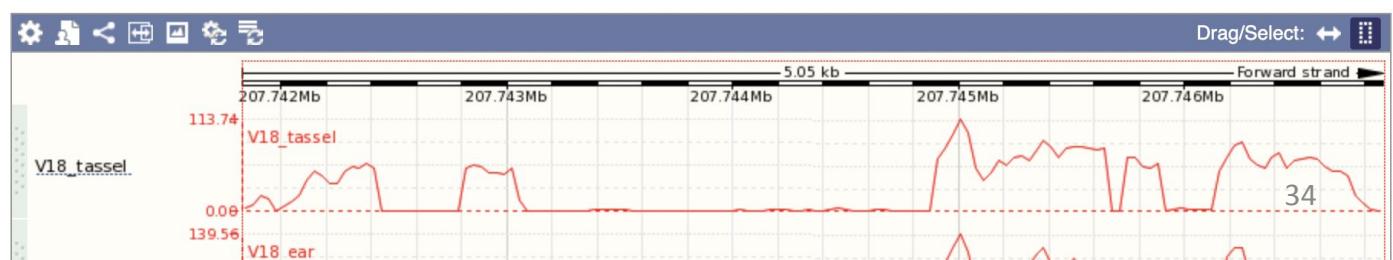
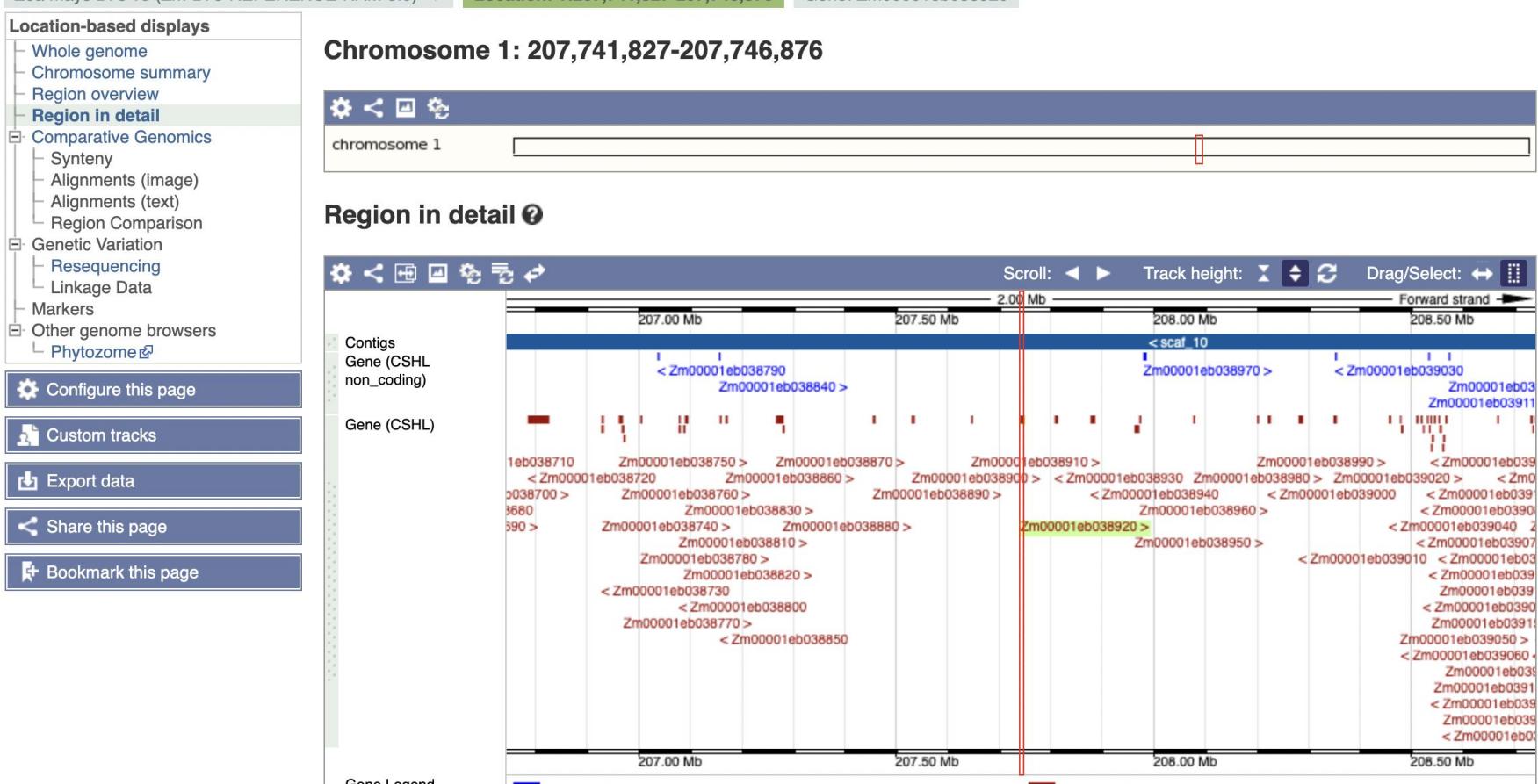
 [Custom tracks](#)

 [Export data](#)

 [Share this page](#)

 [Bookmark this page](#)

Regional Sequence Details



Customizable Browser Tracks

Configure Region Image Configure Overview Image Configure Chromosome Image Personal Data

Find a track

Active tracks

Favourite tracks

Track order

Search results

Sequence and assembly (2/4)

Genes and transcripts (2/3)

Variation (26/29)

Regulation (10/10)

Repeat regions (0/17)

Information and decorations (10/11)

Display options

Manage configurations

Reset configuration

Reset track order

Custom tracks

Select from available configurations: Default

Variation

Enable/disable all tracks

Sequence variants (all sources)
 Panzea_2.7GBS variants
 HapMap2 variants

Enable/disable all Sequence variants

All failed variations
 External NAM_Zm-B97_SV
 External NAM_Zm-CML103_SV
 External NAM_Zm-CML228_SV
 External NAM_Zm-CML247_SV
 External NAM_Zm-CML277_SV
 External NAM_Zm-CML322_SV
 External NAM_Zm-CML333_SV
 External NAM_Zm-CML52_SV
 External NAM_Zm-CML69_SV
 External NAM_Zm-HP301_SV
 External NAM_Zm-II14H_SV
 External NAM_Zm-Ki11_SV
 External NAM_Zm-Ki3_SV
 External NAM_Zm-Ky21_SV
 External NAM_Zm-M162W_SV
 External NAM_Zm-M37W_SV
 External NAM_Zm-Mo18W_SV
 External NAM_Zm-Ms71_SV
 External NAM_Zm-NC350_SV
 External NAM_Zm-NC358_SV
 External NAM_Zm-Oh43_SV
 External NAM_Zm-Oh7B_SV
 External NAM_Zm-P39_SV
 External NAM_Zm-Tx303_SV
 External NAM_Zm-Tzi8_SV

35

Incorporate Non-coding Features

Configure Region ImageConfigure Overview ImageConfigure Chromosome ImagePersonal Data

Find a track

- Active tracks**
- Favourite tracks
- Track order
- Search results
- Sequence and assembly (2/4)
- Genes and transcripts (2/3)
- Variation (28/29)
- Regulation (10/10)
- Repeat regions (4/17)**
- Information and decorations (10/11)
- Display options
- Manage configurations**
- Reset configuration**
- Reset track order**
- Custom tracks**

Select from available configurations:

Current unsavedSave current configuration

Repeat regions

Enable/disable all tracks

- All repeats
- Low complexity (Dust)
- Repeats
- LTRs
- Low complexity regions
- RNA repeats
- Satellite repeats
- Simple repeats
- Type I Transposons/LINE
- Type I Transposons/SINE
- Type II Transposons
- Unknown
- Repeats
- LTRs
- Type I Transposons/LINE
- Type II Transposons
- Tandem repeats (TRF)

Key

 Track style	 External data
 Forward strand	 User-added track
 Reverse strand	
 Favourite track	
 Track information	

Please note that the content of external tracks is not the responsibility of the Ensembl project.

URL-based tracks may either slow down your ensembl browsing experience OR may be unavailable as these are served and stored from other servers elsewhere on the Internet.



Personal Data Incorporation

Configure Region Image Configure Overview Image Configure Chromosome Image Personal Data

Custom tracks
Track Hub Registry Search
Manage Configurations

Your data

Search for public track hubs

Add a custom track

Name for this data (optional):

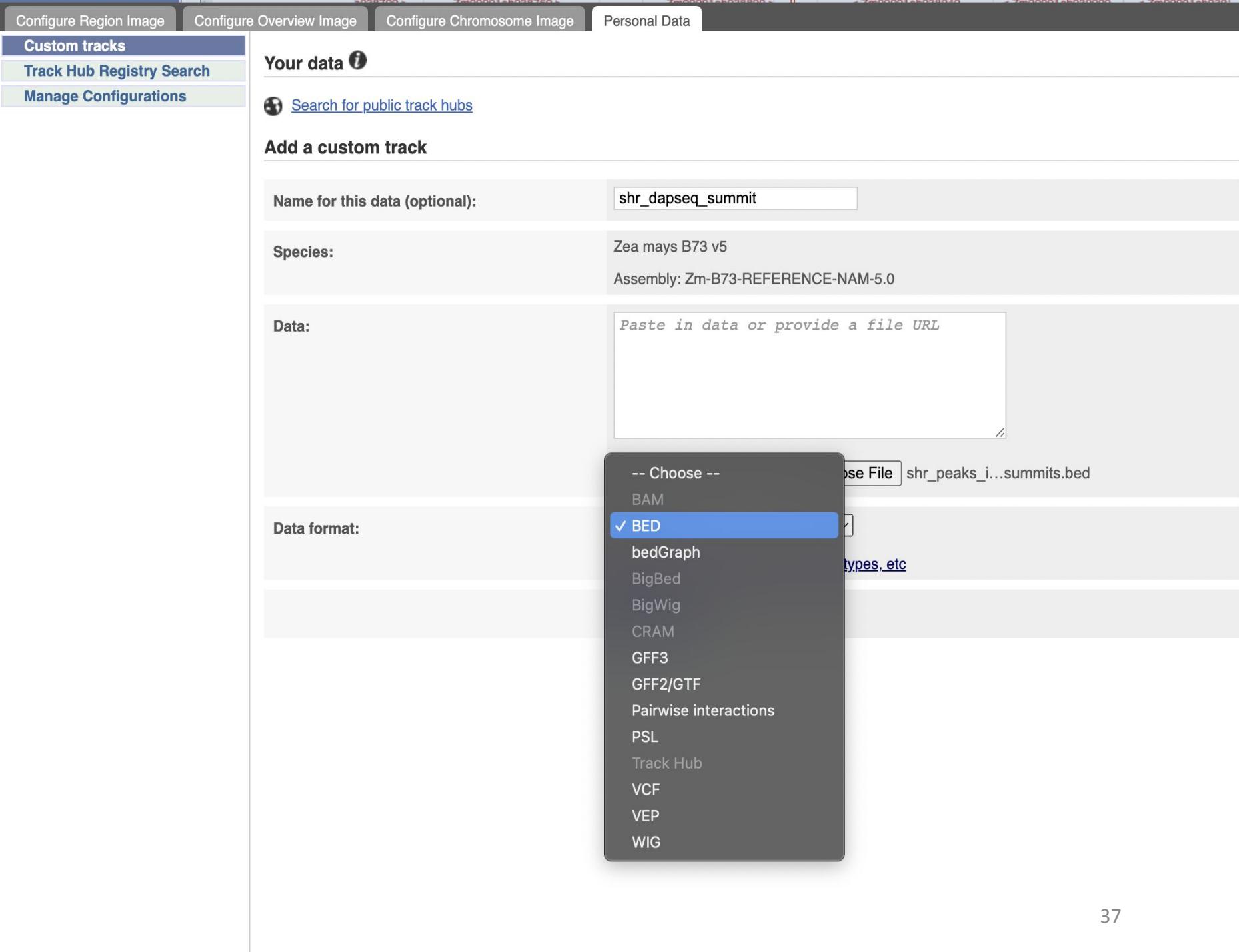
Species: Zea mays B73 v5
Assembly: Zm-B73-REFERENCE-NAM-5.0

Data: *Paste in data or provide a file URL*

-- Choose -- shr_peaks_i...summits.bed

BED bedGraph BigBed BigWig CRAM GFF3 GFF2/GTF Pairwise interactions PSL Track Hub VCF VEP WIG

File types, etc



Personal Data Incorporation

Configure Region Image Configure Overview Image Configure Chromosome Image Personal Data

Find a track

- Active tracks
- Favourite tracks
- Track order
- Search results
- Your data (3/3)**
- Sequence and assembly (2/4)
- Genes and transcripts (2/3)
- Variation (28/29)
- Regulation (10/10)
- Repeat regions (4/17)
- Information and decorations (10/11)
- Display options
- Manage configurations
- Reset configuration
- Reset track order
- Custom tracks

Select from available configurations:

Current unsaved

Your data

Enable/disable all tracks

Custom shr_dapseq_summit
 Custom scl23_dapseq_summits
 Custom scl3_dapseq_summit

Key

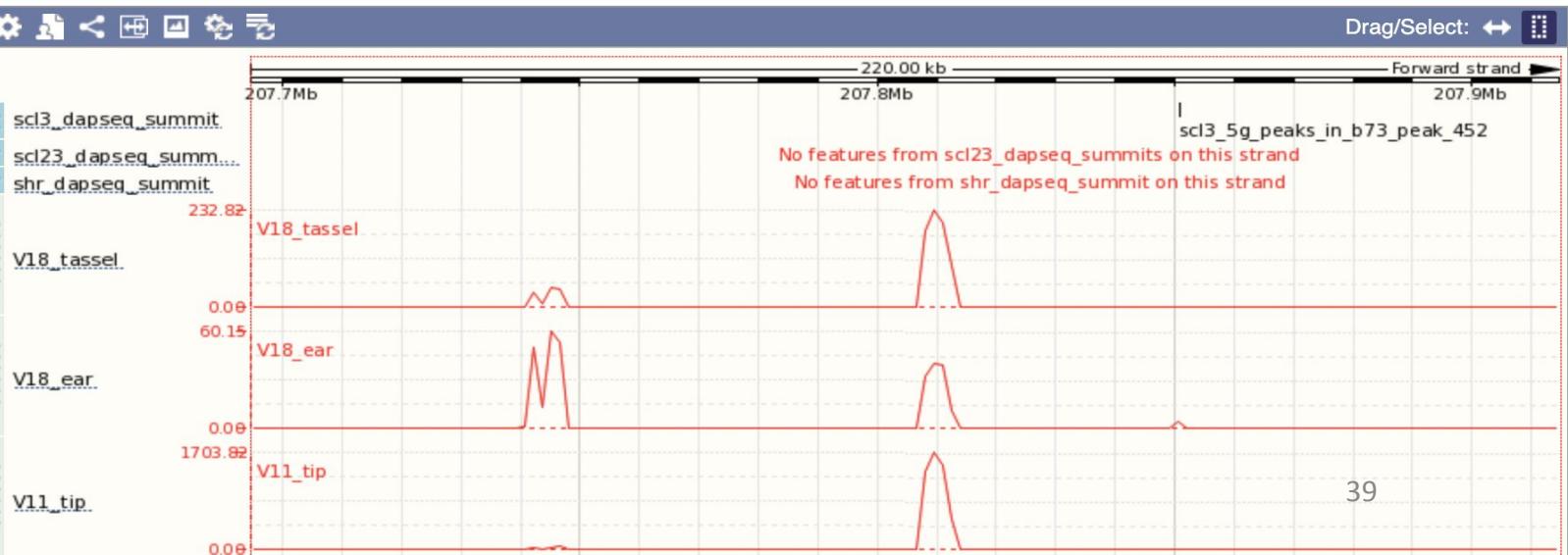
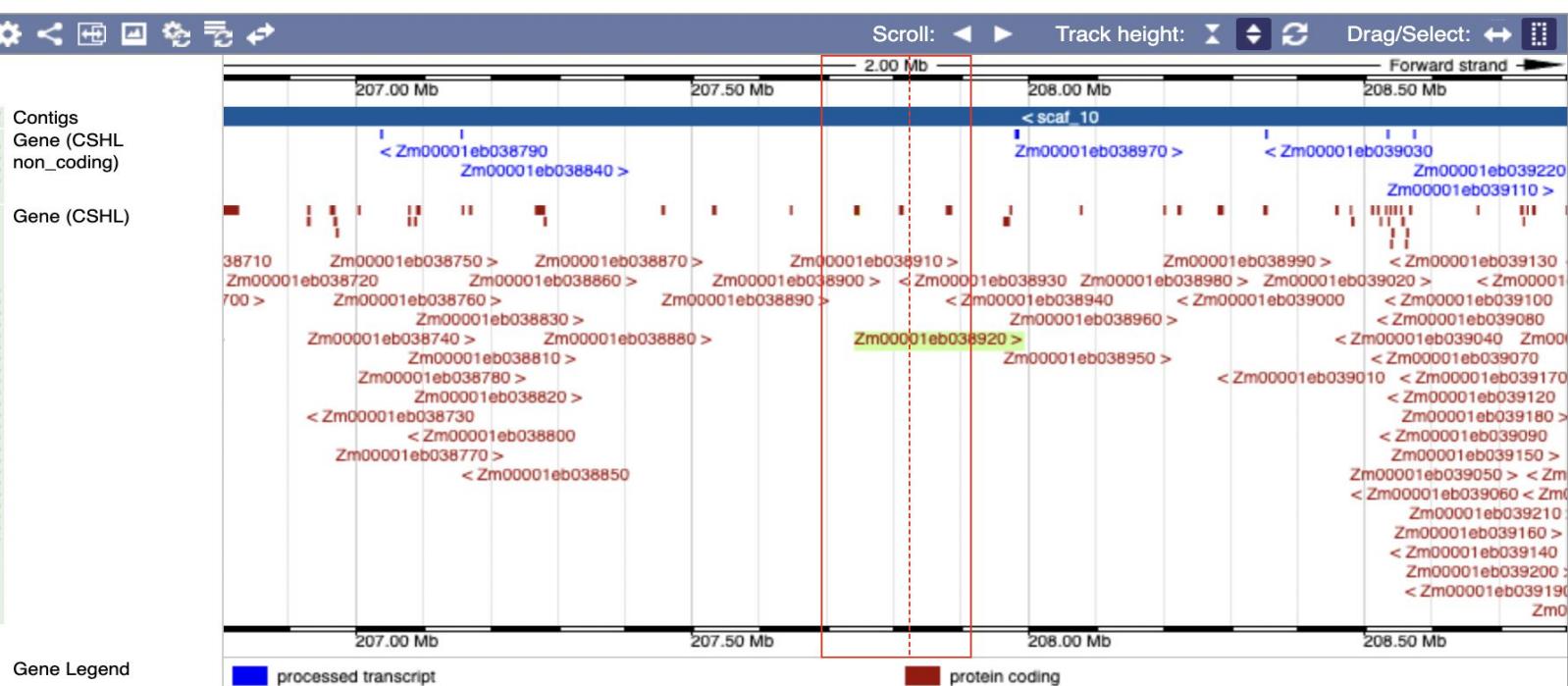
 Track style  External External data
 F Forward strand  Custom User-added track
 R Reverse strand
 Favourite track
 I Track information

Please note that the content of external tracks is not the responsibility of the Ensembl project.

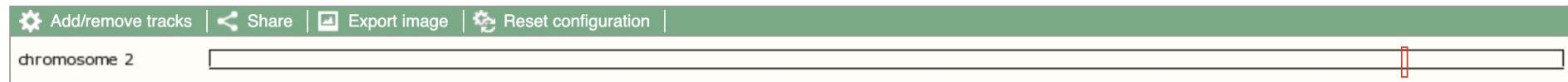
URL-based tracks may either slow down your ensembl browsing experience OR may be unavailable as these are served and stored from other servers elsewhere on the Internet.

★ 
★ 
★ 

Personal Data Incorporation



Chromosome 2: 214,332,705-215,332,705



Synteny ?

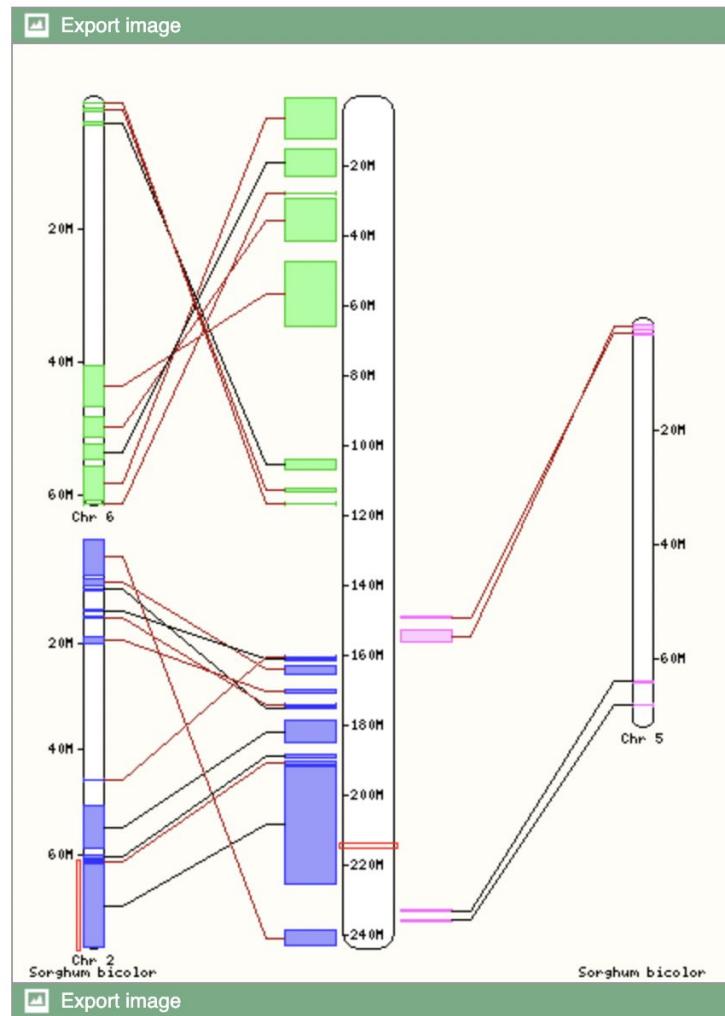
Synteny between **Zea mays** chromosome 2 and **Sorghum bicolor**

Change species:

Sorghum bicolor ▾ Go

Change chromosome:

2 ▾ Go



Ensemble Browser View

Zea mays B73 v5 (Zm-B73-REFERENCE-NAM-5.0) ▾ Location: 1:207,741,827-207,746,876 Gene: Zm00001eb038920

Gene-based displays

- Summary**
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- Regulation**
- External references**
- Supporting evidence**
- ID History**
 - Gene history
- Gramene Search

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Gene: Zm00001eb038920

Description
Location
About this gene
Transcripts

Zm00001e003884
Chromosome 1: 207,741,827-207,746,876 forward strand.

This gene has 2 transcripts ([splice variants](#)), [44 orthologues](#) and [21 paralogues](#).

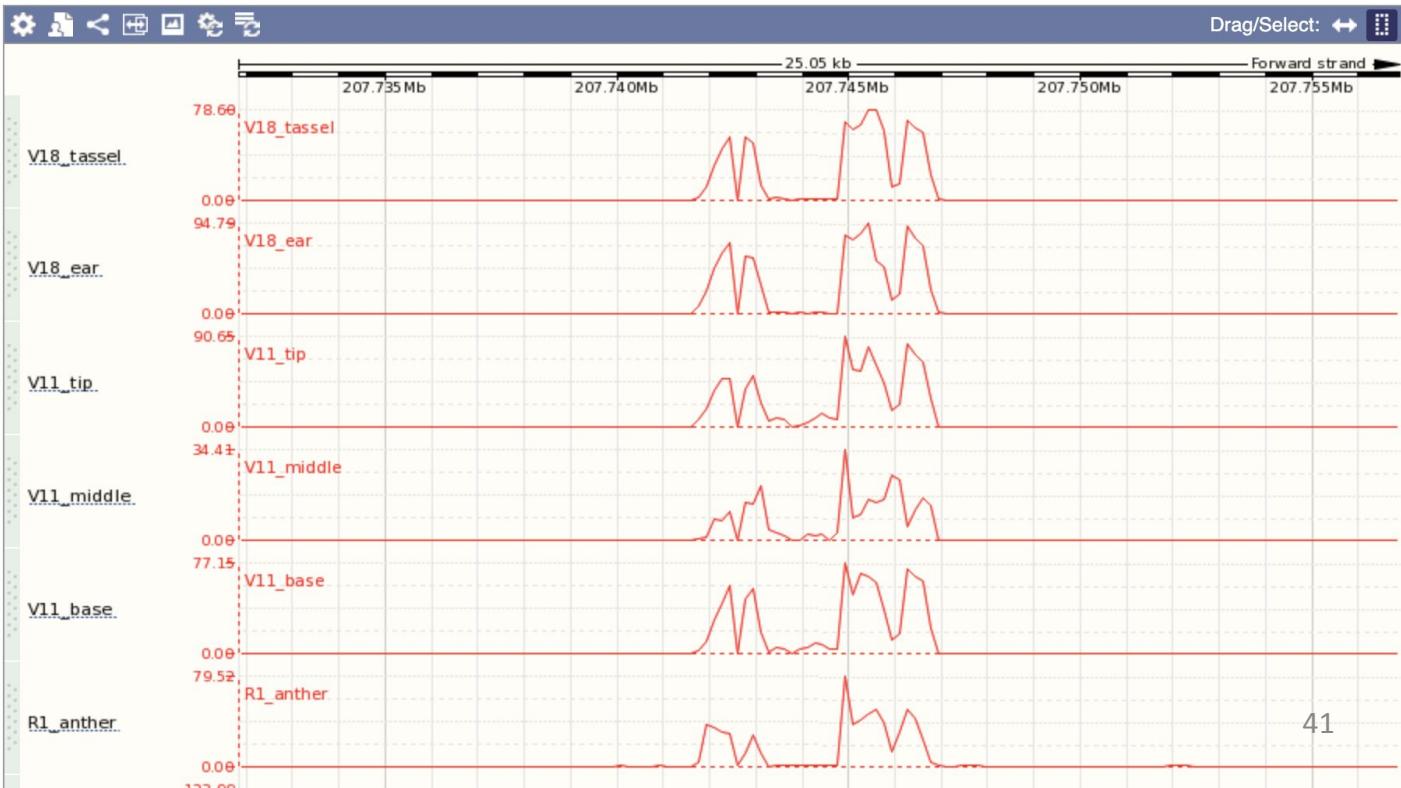
[Show transcript table](#)

Summary

Gene type Protein coding

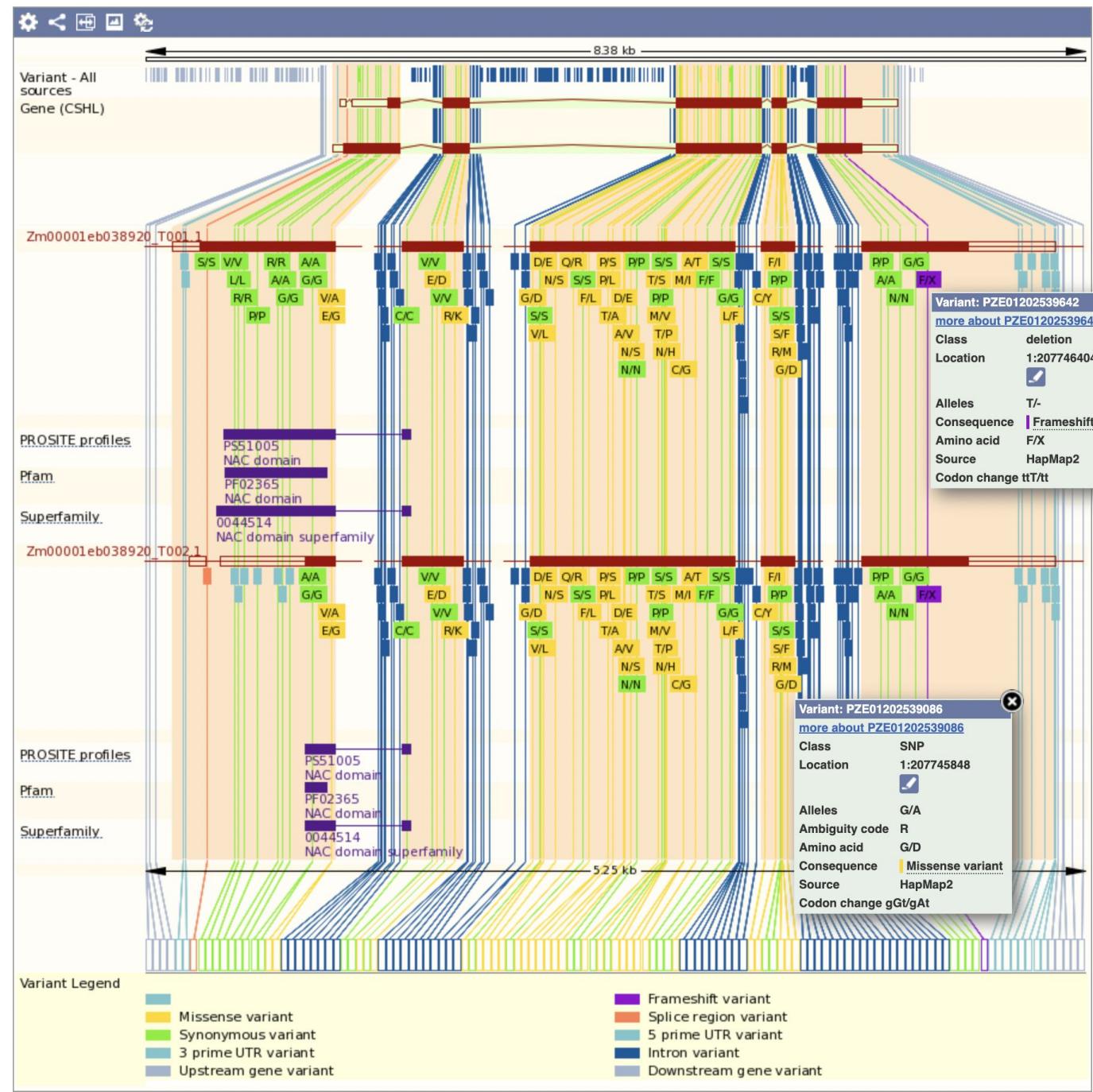
Annotation method Gene annotation by warelab in CSHL through an automated, evidence-based method combining 3rd party software including Mikado, BRAKER and PASA

Go to [Region in Detail](#) for more tracks and navigation options (e.g. zooming)



Variation Data

Variant image ?



Variant table



This table shows known variants for this gene. Use the 'Consequence Type' filter to view a subset of these.

Filter SIFT: All Consequences: Splice donor variant...(5/26) Location: All Source: All Evidence: All Filter Other Columns

Variant ID	Chr: bp	Alleles	Class	Source	Evidence	Clin. Sig.	Conseq. Type	AA		AA co-ord	SIFT	Transcript
								AA	AA			
PZE01202539642	1:207746404	T/-	deletion	HapMap2	-	-	Frameshift variant	F/X	620	-	0.00	Zm00001eb038920_T001.1
PZE01202539642	1:207746404	T/-	deletion	HapMap2	-	-	Frameshift variant	F/X	490	-	0.00	Zm00001eb038920_T002.1
PZE01202535654	1:207742416	T/C	SNP	HapMap2	-	-	Missense variant	V/A	163	0.83	1	Zm00001eb038920_T001.1
PZE01202535657	1:207742419	A/G	SNP	HapMap2	-	-	Missense variant	E/G	164	0.00	1	Zm00001eb038920_T001.1
PZE01202536187	1:207742949	G/T	SNP	HapMap2	-	-	Missense variant	E/D	211	0.8	1	Zm00001eb038920_T001.1
PZE01202536252	1:207743014	G/A	SNP	HapMap2	-	-	Missense variant	R/K	233	0.00	1	Zm00001eb038920_T001.1
PZE01202538142	1:207744904	G/A	SNP	HapMap2	-	-	Missense variant	G/D	246	0.00	1	Zm00001eb038920_T001.1
PZE01202538177	1:207744939	G/C	SNP	HapMap2	-	-	Missense variant	V/L	258	0.17	43	Zm00001eb038920_T001.1
PZE01202538185	1:207744947	T/G	SNP	HapMap2	-	-	Missense variant	D/E	260	0.15	43	Zm00001eb038920_T001.1

Variant table



This table shows known variants for this gene. Use the 'Consequence Type' filter to view a subset of these.

Filter SIFT: All

Consequences: Splice donor variant...(5/26)

Location: All

Source: All

Evidence: All

Filter Other Columns

Consequences					(5/26 on)	
	Chr:	Turn All Off	PTV	PTV & Missense	Only Exonic	Turn All On
PTV = Protein Truncating Variant						
PZE01202539642	1:20	Transcript ablation	(0) Off	Inframe deletion	(0) Off	5 prime UTR variant (11) Off
PZE01202539642	1:20	Splice donor variant	(0) On	Missense variant (87) On	3 prime UTR variant (24) Off	Non coding transcript exon variant (0) Off
PZE01202535654	1:20	Splice acceptor variant	(0) On	protein altering variant (0) Off	Intron variant (559) Off	0.83 Zm00001eb038920 T001.1
PZE01202535657	1:20	Stop gained	(0) On	Splice region variant (1) Off	NMD transcript variant (0) Off	1 Zm00001eb038920 T001.1
PZE01202536187	1:20	Frameshift variant	(3) On	Incomplete terminal codon variant (0) Off	Non coding transcript variant (0) Off	0.8 Zm00001eb038920 T001.1
PZE01202536252	1:20	Stop lost	(0) Off	Stop retained variant (0) Off	Upstream gene variant (1524) Off	1 Zm00001eb038920 T001.1
PZE01202536252	1:20	Start lost	(0) Off	Synonymous variant (76) Off	Downstream gene variant (123) Off	1 Zm00001eb038920 T001.1
PZE01202538142	1:20	Transcript amplification	(0) Off	Coding sequence variant (0) Off		1 Zm00001eb038920 T001.1
PZE01202538177	1:20	Inframe insertion	(0) Off	Mature miRNA variant (0) Off		0.17 Zm00001eb038920 T001.1
<input type="button" value="Apply »"/> <input type="button" value="Cancel"/>						

PZE01202538185	1:207744947	T/G	SNP	HapMap2	-	-	Missense variant	D/E	260	0.15	Zm00001eb038920 T001.1
PZE01202538226	1:207744988	A/G	SNP	HapMap2	-	-	Missense variant	N/S	274	0.57	Zm00001eb038920 T001.1
PZE01202538295	1:207745057	A/G	SNP	HapMap2	-	-	Missense variant	Q/R	297	0.04	Zm00001eb038920 T001.1
PZE01202538353	1:207745115	T/A	SNP	HapMap2	-	-	Missense variant	F/L	316	0.66	Zm00001eb038920 T001.1
PZE01202538423	1:207745185	C/T	SNP	HapMap2	-	-	Missense variant	P/S	340	0.04	Zm00001eb038920 T001.1
PZE01202538424	1:207745186	C/T	SNP	HapMap2	-	-	Missense variant	P/L	340	0.05	Zm00001eb038920 T001.1

Variant displays**Explore this variant**

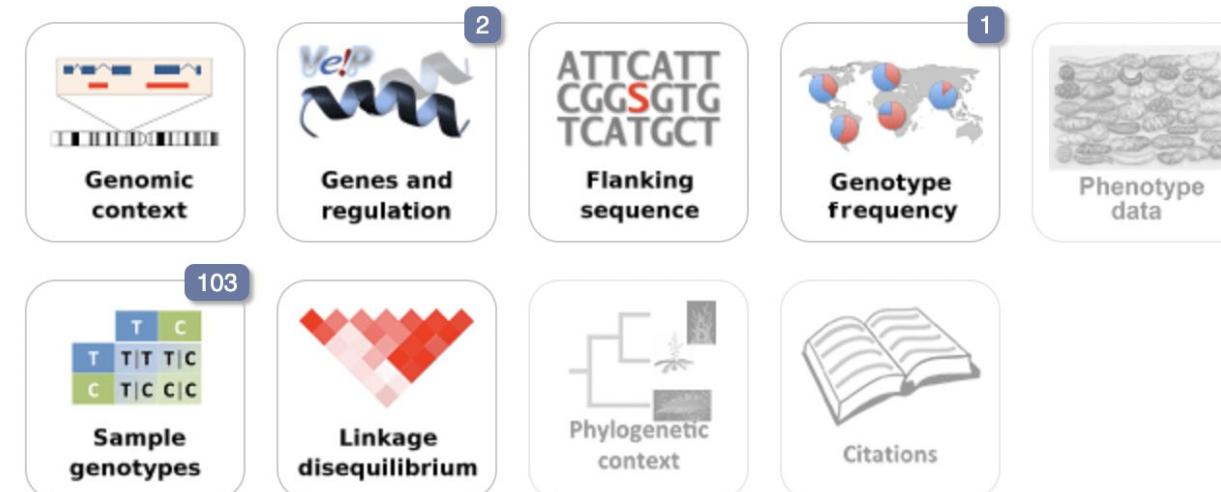
- Genomic context
 - |- Genes and regulation
 - |- Flanking sequence
- Genotype frequency
- Phenotype data
- Sample genotypes
- Linkage disequilibrium
- Phylogenetic context
- Citations

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

Gramene is produced in
collaboration with Ensembl Plants

PZE01202539642 DELETION**Most severe consequence****Frameshift variant** | [See all predicted consequences](#)**T/-**Chromosome **1:207746404** (forward strand) | [View in location tab](#)This variant has 5 HGVS names - [Show](#) ▾

Remapped to Zm-B73-REFERENCE-NAM-5.0

This variant overlaps [2 transcripts](#) and has [103 sample genotypes](#).**About this variant****Explore this variant ?****Using the website**

- Video: [Browsing SNPs and CNVs in Ensembl](#)
- Video: [Clip: Genome Variation](#)
- Video: [BioMart: Variation IDs to HGNC Symbols](#)
- Exercise: [Genomes and SNPs in Malaria](#)

Reference materials

- [Variation Quick Reference card](#)

Most severe consequence

[See all predicted consequences](#)

Alleles

T/-

Location

Chromosome 1:207746404 (forward strand) | [View in location tab](#)

HGVS names

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

Original source

Remapped to Zm-B73-REFERENCE-NAM-5.0

About this variant

This variant overlaps [2 transcripts](#) and has [103 sample genotypes](#).

Sample genotypes

Search for a sample:

(e.g. NA18507)

[\[back to top\]](#)

Genotypes for Zmays

Show All <input type="button" value="▼"/> entries	Show/hide columns	<input type="text" value="Filter"/>
Sample	Genotype (forward strand)	Description
TDD39103:TD	-I-	-
BKN011:MZ	-IT	-
BKN016:MZ	-IT	-
BKN022:MZ	-IT	-
BKN029:MZ	-IT	-
BKN032:MZ	-IT	-
BKN033:MZ	-IT	-
BKN034:MZ	-IT	-
CML202:MZ	-IT	-
CML341:MZ	-IT	-
CML418:MZ	-IT	-
CML505:MZ	-IT	-
H16:MZ	-IT	-
TIL02:TEO	-IT	-
TIL03:TEO	-IT	-
TIL04-TIP285:TEO	-IT	-
VL0512447:MZ	-IT	-
W22:MZ	-IT	-
B73:MZ	TTT	-
B97:MZ	TTT	-
BKN009:MZ	TTT	-

Variant displays**Explore this variant**

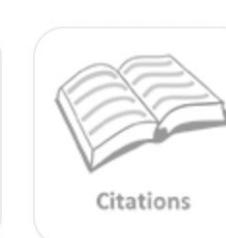
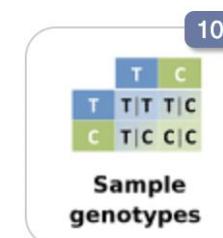
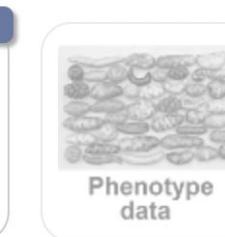
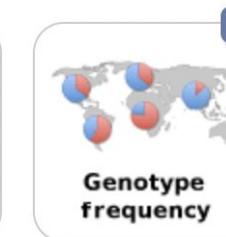
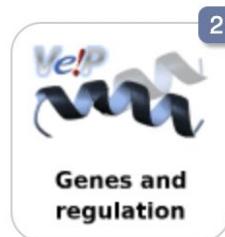
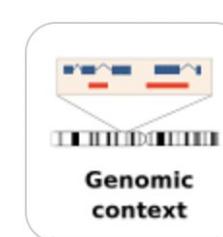
- Genomic context
 - |- Genes and regulation
 - |- Flanking sequence
- Genotype frequency
- Phenotype data
- Sample genotypes
- Linkage disequilibrium
- Phylogenetic context
- Citations

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collaboration with Ensembl Plants

PZE01202539642 DELETION**Most severe consequence**[See all predicted consequences](#)**Frameshift variant****T/-**Chromosome **1:207746404** (forward strand) | [View in location tab](#)This variant has 5 HGVS names - [Show](#)

Remapped to Zm-B73-REFERENCE-NAM-5.0

This variant overlaps [2 transcripts](#) and has [103 sample genotypes](#).**About this variant****Explore this variant ?****Using the website**

- Video: [Browsing SNPs and CNVs in Ensembl](#)
- Video: [Clip: Genome Variation](#)
- Video: [BioMart: Variation IDs to HGNC Symbols](#)
- Exercise: [Genomes and SNPs in Malaria](#)

Reference materials

- [Variation Quick Reference card](#)

PZE01202539642 DELETION

Most severe consequence	 See all predicted consequences
	Frameshift variant
Alleles	T/-
Location	Chromosome 1:207746404 (forward strand) View in location tab
HGVS names	This variant has 5 HGVS names - Show 
Original source	Remapped to Zm-B73-REFERENCE-NAM-5.0
About this variant	This variant overlaps 2 transcripts and has 103 sample genotypes .

Genotype frequency

Frequency data (1)

Show/hide columns					Filter	
Population	Allele: frequency (count)	Genotype: frequency (count)			Genotype detail	
Zmays	T: 0.909 (189) -: 0.091 (19)	TIT: 0.827 (86)	-I-: 0.010 (1)	-IT: 0.163 (17)	Show	



Zea mays B73 v5 (Zm-B73-REFERENCE-NAM-5.0) ▾

Location: 1:207,741,827-207,746,876

Gene: Zm00001eb038920

Variant: PZE01202539642

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](#)

PZE01202539642 DELETION

Most severe consequence

Frameshift variant | [See all predicted consequences](#)

Alleles

T/-

Location

Chromosome 1:207746404 (forward strand) | [View in location tab](#)

HGVS names

This variant has 5 HGVS names - [Show](#) +

Original source

Remapped to Zm-B73-REFERENCE-NAM-5.0

About this variant

This variant overlaps [2 transcripts](#) and has [103 sample genotypes](#).

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](#) [3 prime UTR](#) **Focus variant** [Intronic](#) [Synonymous](#)

Markup loaded

AAG~~R~~TTGAAGTAT~~Y~~AGAY~~G~~WT~~T~~TGT~~T~~TGAGAATCTAGCTAAC~~T~~CT~~R~~CTTA~~T~~TGG
GGCAG~~R~~GT~~T~~TAT~~A~~TCAGCTGG~~C~~AY~~G~~CATTTC~~C~~TGG~~C~~RT~~K~~AGCT~~K~~ACAC~~C~~TGAA~~A~~GG
~~A~~Y~~T~~ATTG~~T~~TGACAAG~~T~~TTTG~~T~~TG~~C~~Y~~T~~TGTTCCACAG~~A~~GT~~G~~CAGG~~C~~TAAGAG~~T~~ACTA
TTGGAAAGGGATTG~~T~~TAAAG~~A~~TTTG~~G~~ACTCAATCTCG~~C~~CCCC~~M~~GCTTTTG~~C~~TGGAG
AATTCCCAGC~~M~~AT~~C~~ACC~~G~~CAAATCTTGG~~C~~T~~C~~AT~~A~~TTCTGGGGGGCCCCAA~~Y~~ACAC
TCCAT~~G~~TTTCTG~~C~~TGAAGT~~G~~AT~~C~~CG~~G~~TAGGAAG~~T~~TAGCT~~G~~T~~C~~CTCTGG~~Y~~GCAGATA
AGT~~GGG~~CGCTG~~C~~AAAAGG~~A~~TCAGG~~C~~ATGG~~G~~AGCTGG~~C~~T~~T~~[**T/-**]TCTGCAG~~A~~TTTG~~G~~
CCTGATAACCG~~T~~CTTCACTGTGG~~C~~T~~C~~AACACC~~A~~T~~C~~CCG~~G~~GT~~C~~T~~G~~GT~~G~~GT~~G~~C~~T~~
TG~~C~~CTTTCTT~~T~~TG~~T~~TG~~C~~GAATAATG~~C~~T~~T~~AGT~~G~~AGCT~~A~~T~~G~~GAGGT~~G~~GCAT~~G~~T~~G~~CATC
TATGGCAAGTAGCAGG~~C~~GT~~G~~TATTGG~~A~~TAAGATAAA~~T~~CTCATGACATTAGATAATCCA
GTGTTCTGAGG~~C~~AGACTCAACTGGGGCC~~T~~CTG~~C~~T~~G~~GT~~C~~T~~G~~TTAAATGTATTG~~C~~GTT~~G~~CAT
GGCGTGGACCTG~~T~~GGAGT~~G~~TCAGC~~A~~CTG~~C~~AGT~~A~~CCATT~~T~~TG~~C~~T~~G~~CAG~~C~~T~~G~~GAGAGCT
AATGGTGTATG~~T~~ATGAATTCSGT~~T~~TATTG~~T~~AGTAGT~~T~~ATGCAATTGCC~~T~~CATTGG~~T~~
TGTGATGAT~~K~~CCATTG~~C~~CATGG~~A~~

Zea mays B73 v5 (Zm-B73-REFERENCE-NAM-5.0) ▾

Location: 1:207,741,827-207,746,876

Gene: Zm00001eb038920

Variant: PZE01202539642

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
 - GO: Biological process
 - GO: Molecular function
 - GO: Cellular component
- Phenotypes
- Genetic Variation
 - Variant table
 - Variant image
 - Structural variants
- Gene expression
- Regulation
- External references
- Supporting evidence
- ID History
 - Gene history
- Gramene Search

[Configure this page](#)[Custom tracks](#)[Export data](#)[Share this page](#)[Bookmark this page](#)**Gene: Zm00001eb038920****Description**

Zm00001e003884

Location

Chromosome 1: 207,741,827-207,746,876 forward strand.

About this geneThis gene has 2 transcripts ([splice variants](#)), [44 orthologues](#) and [21 paralogues](#).**Transcripts**[Show transcript table](#)**Orthologues** [Download orthologues](#)**Summary of orthologues of this gene**

Click on 'Show details' to display the orthologues for one or more groups of species. Alternatively, click on 'Configure this page' to choose a custom list of species.

Species set	Show details	With 1:1 orthologues	With 1:many orthologues	With many:many orthologues	Without orthologues
All (42 species)	<input type="checkbox"/>	33	2	3	4
Chlorophyta (1 species)	<input type="checkbox"/>	0	0	0	1
Liliopsida (37 species)	<input type="checkbox"/>	33	2	0	2
Lycopodiophyta (1 species)	<input type="checkbox"/>	0	0	1	0
Eudicotyledons (2 species)	<input type="checkbox"/>	0	0	2	0

Selected orthologues

Show All entries		Show/hide columns						
Species	Type	Orthologue	dN/dS	Target %id	Query %id	GOC Score	WGA Coverage	High Confidence
Arabidopsis thaliana	Many-to-many	AT3G10480	n/a	24.90 %	19.61 %	n/a	n/a	n/a
		View Gene Tree	3:3,264,194-3,267,695:1					
			View Sequence Alignments					
Arabidopsis thaliana	Many-to-many	AT3G10490	n/a	29.05 %	19.61 %	n/a	n/a	n/a
		View Gene Tree	3:3,267,825-3,271,202:1					
			View Sequence Alignments					
Arabidopsis thaliana	Many-to-many	NAC053 (AT3G10500)	n/a	27.87 %	22.90 %	n/a	n/a	n/a
		View Gene Tree	3:3,271,217-3,274,176:1					
			View Sequence Alignments					
Arabidopsis thaliana	Many-to-many	AT5G04395	n/a	43.32 %	12.13 %	n/a	n/a	n/a
		View Gene Tree	5:1,241,555-1,242,374:1					
			View Sequence Alignments					



Zea mays B73 v5 (Zm-B73-REFERENCE-NAM-5.0) ▾

Location: 1:207,741,827-207,746,876

Gene: Zm00001eb038920

Variant: PZE01202539642

Gene-based displays

- Summary
 - Splice variants
 - Transcript comparison
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 - Gene tree
 - Gene gain/loss tree
 - Orthologues**
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- Gene expression
- Regulation
- External references
- Supporting evidence
- ID History
 - Gene history
- Gramene Search

Configure this page**Custom tracks****Export data****Share this page****Bookmark this page****Gene: Zm00001eb038920****Description**

Zm00001e003884

LocationChromosome 1: 207,741,827-207,746,876 forward strand.**About this gene**This gene has 2 transcripts ([splice variants](#)), [44 orthologues](#) and [21 paralogues](#).**Transcripts**[Show transcript table](#)**Orthologues** [Download orthologues](#)**Summary of orthologues of this gene**

Click on 'Show details' to display the orthologues for one or more groups of species. Alternatively, click on 'Configure this page' to choose a custom list of species.

Species set	Show details	With 1:1 orthologues	With 1:many orthologues	With many:many orthologues	Without orthologues
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Chlorophyta (1 species)	<input type="checkbox"/>	0	0	0	1
Liliopsida (37 species)	<input type="checkbox"/>	33	2	0	2
Lycopodiophyta (1 species)	<input type="checkbox"/>	0	0	1	0
Eudicots (2 species)	<input type="checkbox"/>	0	0	2	0

Selected orthologues

Show All entries		Show/hide columns		sorghum					
Species	Type	Orthologue	dN/dS	Target %id	Query %id	GOC Score	WGA Coverage	High Confidence	
Sorghum bicolor	1-to-many	SORBI_3007G166100 View Gene Tree View Sequence Alignments	0.24392	92.24 %	92.52 %	n/a	n/a	n/a	

Species without orthologues

4 species are not shown in the table above because they don't have any orthologue with Zm00001eb038920.

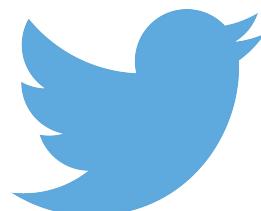
- Chlamydomonas reinhardtii
- Drosophila melanogaster
- Zea maysa188
- Zea maysb73v3

Get in touch!

- Slides, exercises, brochures, posters:
http://ftp.gramene.org/pub/gramene/outreach/maize_2023/
- Guides: <https://maize-pangenome.gramene.org/guides>
- E-mail: feedback@gramene.org
- Contact form: <https://maize-pangenome.gramene.org/feedback>
- Gramene YouTube channel & News blog
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Gramene - Exploring Function through Comparative
Genomics and Network Analysis
USDA-ARS-8062-21000-041-00D

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Crispin Taylor (ASPB)



Workshop Slideshow Access Information

Slides and other info are located here:

http://ftp.gramene.org/pub/gramene/outreach/maize_2023/



Gramene Protocol Book Chapters:

https://link.springer.com/protocol/10.1007/978-1-4939-3167-5_7



YouTube:

<https://www.youtube.com/@gramenedatabase3929>

