



Pan-genes at MaizeGDB

Ethy Cannon

March 11th, 2026



What is a pan-gene?

Briefly: a set of related gene models across multiple accessions within a species or clade.

At MaizeGDB, a pan-gene contains not only related gene models, but also genetically-mapped gene loci that have been experimentally associated with specific gene models.

The screenshot shows the MaizeGDB website interface. At the top, there is a blue header with the MaizeGDB logo on the left, a search bar with a dropdown menu set to 'all data', and a 'Download' button on the right. Below the header is a green navigation bar with links for 'Home', 'About', 'Contact', 'Genomes', 'Tools', 'Data Centers', 'Explore MaizeGDB', and 'Feedback'. The main content area is a grid of icons representing various database features and tools. On the right side, there are sections for 'Reference Assembly', 'Contribute data', and 'MaizeGDB News'. The 'Reference Assembly' section includes icons for 'B73 ASSEMBLY', 'B73 ANNOTATION', and 'ALL GENOMES'. The 'Contribute data' section has buttons for 'Contribute your data' and 'Make your data FAIR'. The 'MaizeGDB News' section contains several news items with dates and titles.

Reference Assembly



Common genome assembly/annotation tasks | ▾

Contribute data

[Contribute your data](#) [Make your data FAIR](#)

MaizeGDB News

26, January 2026: The deadline to submit [Emerson and McClintock Award](#) nominations has been extended to **March 16th, 2026!**

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[more news](#) | [archived news](#)

Database

Last update: February 10, 2026
Next update: March 10, 2026

Pan-gene analysis

Pan-gene analyses look at sequence similarity and synteny to group similar gene models into pan-genes.

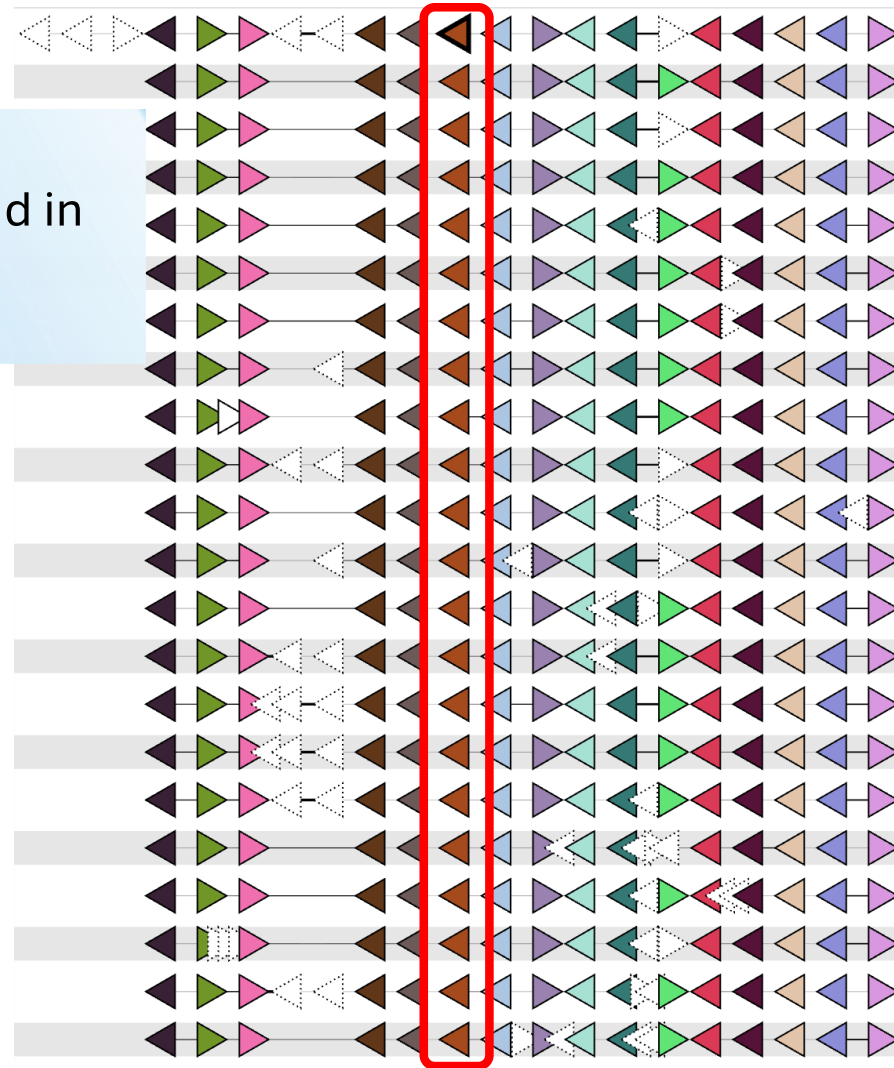
The MaizeGDB pan-genes are calculated using the Pandagma pipeline (<https://github.com/legumeinfo/pandagma>), developed by Steven Cannon for the Legume Information System.

Cannon SB, Le H, Weeks N, Brendzen J. *Pandagma: a tool for identifying pan-gene sets and gene families at desired evolutionary depths and accommodating whole-genome duplications*. *Bioinformatics*, 40:9, 2024, DOI: 10.1093/bioinformatics/btae526.

The screenshot displays the MaizeGDB website interface. At the top, the MaizeGDB logo is visible on the left, and a search bar with a dropdown menu (currently set to 'all data') is on the right. Below the logo, a navigation menu includes 'Home', 'About', and 'Contact'. A secondary menu contains 'Genomes', 'Tools', 'Data Centers', 'Explore MaizeGDB', and 'Feedback'. The main content area features a 'Reference Assembly' section with icons for '873 ASSEMBLY', '873 ANNOTATION', and 'ALL GENOMES'. Below this is a 'Contribute data' section with buttons for 'Contribute your data' and 'Make your data FAIR'. A 'MaizeGDB News' section contains two news items: one from January 2026 regarding award nomination deadlines and another from November 2025 regarding registration and contest submissions. At the bottom, there are links for 'more news | archived news' and a 'Database' section with update dates: 'Last update: February 10, 2026' and 'Next update: March 10, 2026'. The page number '3' is located in the bottom right corner.

Pan-gene example: phyC1

A highly conserved photo receptor found in plants.

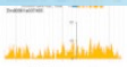


How can pan-genes be useful in breeding?

- Find corresponding, or non-corresponding genes across accessions of interest.
- Copy number variation (CNV) as this often affects important traits, like disease resistance.

Genomes ▾ Tools ▾ Data Centers ▾ Explore MaizeGDB Feedback

Welcome to MaizeGDB! A long-term, federally funded informatics service to researchers focused on the crop plant and model organism *Zea mays*.
 If you use MaizeGDB in your research, please cite us.



JBrowse



GBrowse



NAM Genomes



PanAnd Genomes



BLAST



qTeller




MaizoMine



Protein Structure




Maize Meeting




Maize Genetics Cooperation



Hot New Papers



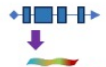
Downloads




Mutants and Phenotypes




Pan-genes



Gene Center




Artificial Intelligence









Reference Assembly



873 ASSEMBLY



873 ANNOTATION



ALL GENOMES

Common genome assembly/annotation tasks | ▾

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Database 5

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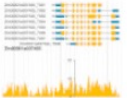

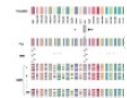

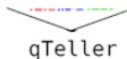





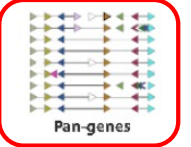



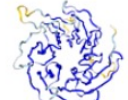
maizeGDB
MAIZE GENETICS AND GENOMICS DATABASE

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Welcome to MaizeGDB!
MaizeGDB is a community-oriented, long-term, federally funded project focused on the crop plant and model organism *Zea mays*.
If you use MaizeGDB in your research, please cite us.

Quick Links

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Database
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Simple search: go directory to a pan-gene.

Advanced search for sets of pan-genes. For example:

- Conserved pan-genes
- Variable pan-genes
- Pan-genes with members in specific assemblies
- Pan-genes lacking members specific assemblies

Pan-Gene Data In MaizeGDB

[Simple pan-gene search](#) [Advanced pan-gene search](#) [Downloads](#) [Phylogenetic tree](#) [Explore](#) [Information](#) [Definitions](#)

Introduction

The pan-gene and gene family datasets presented in this data center were calculated by MaizeGDB staff. Details about the analyses are in the information section below and in each pan-gene record page.

Note that different pan-gene and gene family analyses will produce different results, and that the accuracy of the results are impacted by assembly and annotation quality.

We welcome comments, error reports, and suggestions. Please use the [feedback form](#).

Simple Search

This search form allows you to find pan-genes by locus symbol, gene model ID, transcript ID, or protein ID.

(see example [gene model query](#) or [locus query](#))

Advanced Search

Check the boxes next to the fields you want to search; if you just want to find records that have any value for that attribute, check the box and leave the criteria alone.

Search for pan-genes:

- in the pan-gene analysis Any
- that contain the gene model(s)
- that are associated with a gene locus
- that are associated with protein(s)
- that are associated with a trait
- that have at least members
- that have fewer than members
- that have members in at least % of annotations
- that have members in no more than % of annotations
- that contain members from annotations for these assemblies

Zd-Gigi-REFERENCE-PanAnd-1.0
Zd-Momo-REFERENCE-PanAnd-1.0
Zh-RIMHU001-REFERENCE-PanAnd-1.0
Zm-B73-REFERENCE-GRAMENE-4.0
Zm-B73-REFERENCE-NAM-5.0
Zm-W22-REFERENCE-NRGENE-2.0
Zm-PH207-REFERENCE_NS-UIUC_UMN-1.0
- that do not contain members from annotations for these assemblies

Zd-Gigi-REFERENCE-PanAnd-1.0
Zd-Momo-REFERENCE-PanAnd-1.0
Zh-RIMHU001-REFERENCE-PanAnd-1.0
Zm-B73-REFERENCE-GRAMENE-4.0
Zm-B73-REFERENCE-NAM-5.0
Zm-W22-REFERENCE-NRGENE-2.0
Zm-PH207-REFERENCE_NS-UIUC_UMN-1.0

Limit number of results to (upper limit on results is 2,000 records)

Some cautions about pan-genes:

- Pan-gene analyses are at the mercy of the quality of the gene model annotation.
- The analyses will encounter ambiguities that will need to be resolved, which can introduce errors. For example, by selecting the longer gene model if two are overlapping.
- Biology....

Example: **rp1** - resistance to *Puccinia sorghi*

This is a complex disease-resistance locus with considerable CNV.

Simple Search

This search form allows you to find pan-genes by locus symbol, gene model ID, transcript ID, or protein ID.

(see example gene model query or locus query)

Pan-gene and gene family information for gene model Zm00111aa044643 (LOC103640712, LOC109939211, nbs1, nbs104, rp1, Zm00001d023326)

[Zea mays pan-gene](#) [Genome context](#) **LOC103640712** [LOC109939211](#) [nbs1](#) [nbs104](#) [rp1](#) [Zm00001d023326](#)

Gene name: [See full locus page](#)

Synonyms: disease resistance protein RGA2, Rp1-like protein **Linkage group:** 10

Pan-gene association support:

[GRMZM2G443939](#): Gene Model - MaizeGDB

[Zm00001d023323](#): Gene Model - MaizeGDB

[Zm00001eb405910](#): Gene Model - MaizeGDB. **Warning: this gene model is in a different pan-gene**

NCBI Gene:

[103640712](#)

There is no description for this locus.

Comments:

Annotation: Attributed to Lai J, et al. Genome Res, 2004 Oct. PMID 15466291 by NCBI (per [NCBI](#))

Map Note: B73 bp coordinates support Genetic cM (EHC Feb 2023) (per [Staff](#))

Gene Products:

none

Pan-Zea Information

There are multiple ways to define and generate a **pan-genome**. Here we refer to a "pan-genome analysis" of multiple genome annotations to group gene models by sequence similarity and syntenic position, to identify core gene models (present in all annotations), common, rare, and orphan gene models (present in only one).

A **pan-gene** is the set of gene models generated by the analysis that appear to have the same function.

Bulk downloads can be found [here](#).

Details about this MaizeGDB/Pandagma pan-gene analysis and its statistics are provided below.

ALERT

There may be some errors in this pan-gene. Pan-gene analyses continue to evolve and improve, but remain subject to gene model annotation quality, and complexities of genome structure. For example, split, merged, or otherwise miss-annotated gene models may be incorrectly included or excluded. Note also that the MaizeGDB pan-gene analysis is optimized to limit false negatives rather than false positives.

Discrepancies with hand-curated gene model associations by MaizeGDB curators

There are discrepancies between hand-curated gene model associations for **LOC103640712** and the membership of this pan-gene.

Expected via hand-curation: [GRMZM2G443939](#), [Zm00001d023323](#), [Zm00001eb405910](#)

Missing from pan-gene: [Zm00001eb405910](#)

[Zm00001eb405910](#) is not in any pan-gene.

There are discrepancies between hand-curated gene model associations for **LOC109939211** and the membership of this pan-gene.

Expected via hand-curation: [AC152495.1_FG003](#), [Zm00001d023327](#), [Zm00001eb405870](#)

Missing from pan-gene: [AC152495.1_FG003](#), [Zm00001eb405870](#)

[AC152495.1_FG003](#) is not in any pan-gene.

[Zm00001eb405870](#) is not in any pan-gene.

There are discrepancies between hand-curated gene model associations for **nbs1** and the membership of this pan-gene.

Expected via hand-curation: [AC152495.1_FG017](#) (split model), [GRMZM5G879178](#) (split model), [Zm00001d023320](#), [Zm00001eb405880](#), [Zm00032ab423330](#)

Missing from pan-gene: [AC152495.1_FG017](#), [Zm00001eb405880](#), [Zm00032ab423330](#)

[AC152495.1_FG017](#) is not in any pan-gene.

[Zm00001eb405880](#) is not in any pan-gene.

[Zm00032ab423330](#) is not in any pan-gene.

There are discrepancies between hand-curated gene model associations for **nbs104** and the membership of this pan-gene.

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ALERT

ANALYSIS DETAILS AND STATISTICS

Information about this pan-gene analysis

Description	Generated by MaizeGDB using the Pandagma pipeline
Analysis software	Pandagma Aug-25
Source	MaizeGDB
Date	2025-08-18 00:00:00
Number of annotations	65

Summary of annotations and assemblies included in the analysis

Assembly name	Annotation name	# of gene models	Min length	Max length	Ave length	% placed in pan-genes
Zm-B73-REFERENCE-NAM-5.0	Zm00001eb.1	39744	87	16278	1088.8	83.4
Zm-B73-REFERENCE-GRAMENE-4.0	Zm00001d.2	49202	9	15804	1053.7	73.3
Zm-B97-REFERENCE-NAM-1.0	Zm00018ab.1	40368	135	16278	1077.9	85.7
Zm-CML103-REFERENCE-NAM-1.0	Zm00021ab.1	40013	93	16278	1080.6	89.3
Zm-CML228-REFERENCE-NAM-1.0	Zm00022ab.1	41577	45	16278	1076	86.6
Zm-CML247-REFERENCE-NAM-1.0	Zm00023ab.1	40383	84	15201	1082.4	88.4
Zm-CML277-REFERENCE-NAM-1.0	Zm00024ab.1	40325	105	16278	1077.7	89.4
Zm-CML322-REFERENCE-NAM-1.0	Zm00025ab.1	41122	105	16278	1067	87.2
Zm-CML333-REFERENCE-NAM-1.0	Zm00026ab.1	40428	72	16278	1080.3	88.3
Zm-CML52-REFERENCE-NAM-1.0	Zm00019ab.1	40473	126	16278	1087.6	87.6
Zm-CML69-REFERENCE-NAM-1.0	Zm00020ab.1	40272	120	16278	1062.3	88.8
Zm-HP301-REFERENCE-NAM-1.0	Zm00027ab.1	39785	69	16278	1085.4	90.1
Zm-IT14H-REFERENCE-NAM-1.0	Zm00028ab.1	40290	69	16278	1074.6	89.8

▶ ALERT

ANALYSIS DETAILS AND STATISTICS

301 members!

▼ GENE MODEL MEMBERS

This pan-gene contains 301 members representing 65 of 65 assemblies.
The exemplar gene model is shown in **bold text**.

Gene model	Assembly	Annotation	Chromosome
+ GRMZM2G003625	B73 RefGen_v3	5b+	Chr10
+ GRMZM2G349565	B73 RefGen_v3	5b+	Chr10
+ GRMZM2G443939	B73 RefGen_v3	5b+	Chr10
+ GRMZM5G879178	B73 RefGen_v3	5b+	Chr10
+ AC152495.1_FGTT002	B73 RefGen_v3	5b+	chr10
+ AC152495.1_FGTT003	B73 RefGen_v3	5b+	chr10
+ AC152495.1_FGTT010	B73 RefGen_v3	5b+	chr10
+ Zd00001ab044170	Zd-Gigi-REFERENCE-PanAnd-1.0	Zd00001ab.1	chr10
+ Zd00001ab044172	Zd-Gigi-REFERENCE-PanAnd-1.0	Zd00001ab.1	chr10
+ Zd00001ab044174	Zd-Gigi-REFERENCE-PanAnd-1.0	Zd00001ab.1	chr10
+ Zd00001ab044177	Zd-Gigi-REFERENCE-PanAnd-1.0	Zd00001ab.1	chr10
+ Zd00001ab044178	Zd-Gigi-REFERENCE-PanAnd-1.0	Zd00001ab.1	chr10
+ Zd00003ab046185	Zd-Momo-REFERENCE-PanAnd-1.0	Zd00003ab.1	chr10
+ Zd00003ab046186	Zd-Momo-REFERENCE-PanAnd-1.0	Zd00003ab.1	chr10
+ Zd00003ab046188	Zd-Momo-REFERENCE-PanAnd-1.0	Zd00003ab.1	chr10
+ Zd00003ab046191	Zd-Momo-REFERENCE-PanAnd-1.0	Zd00003ab.1	chr10
+ Zd00003ab046192	Zd-Momo-REFERENCE-PanAnd-1.0	Zd00003ab.1	chr10
+ Zh00001ab048222	Zh-RIMHU001-REFERENCE-PanAnd-1.0	Zh00001ab.1	chr10
+ Zh00001ab048223	Zh-RIMHU001-REFERENCE-PanAnd-1.0	Zh00001ab.1	chr10
+ Zm00056aa042431	Zm-A188-REFERENCE-KSU-1.0	Zm00056aa.1	chr10
+ Zm00056aa042436	Zm-A188-REFERENCE-KSU-1.0	Zm00056aa.1	chr10
+ Zm00056aa042441	Zm-A188-REFERENCE-KSU-1.0	Zm00056aa.1	chr10
+ Zm00056aa042445	Zm-A188-REFERENCE-KSU-1.0	Zm00056aa.1	chr10
+ Zm00056aa042447	Zm-A188-REFERENCE-KSU-1.0	Zm00056aa.1	chr10
+ Zm00056aa042448	Zm-A188-REFERENCE-KSU-1.0	Zm00056aa.1	chr10
+ Zm00056aa042456	Zm-A188-REFERENCE-KSU-1.0	Zm00056aa.1	chr10
+ Zm00056aa042459	Zm-A188-REFERENCE-KSU-1.0	Zm00056aa.1	chr10
+ Zm00092aa041686	Zm-A632-REFERENCE-CAAS_FIL-1.0	Zm00092aa.1	chr10
+ Zm00092aa041687	Zm-A632-REFERENCE-CAAS_FIL-1.0	Zm00092aa.1	chr10
+ Zm00092aa041688	Zm-A632-REFERENCE-CAAS_FIL-1.0	Zm00092aa.1	chr10

5 copies

2 copies

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▶ ALERT

▶ ANALYSIS DETAILS AND STATISTICS

▶ GENE MODEL MEMBERS

▼ PAN-GENE ALIGNMENT

MSA Viewer

Instructions: Drag image or use top scroll bar to scroll.

Show CDS alignment Show protein alignment

[Expand](#) [Contract](#) [Select a color scheme](#) [Export alignment](#)

name

Z600001ab044170_T001
Z600001ab044172_T002
Z600001ab044174_T001
Z600001ab044177_T001
Z600001ab044178_T001
Z600003ab046185_T001
Z600003ab046186_T001
Z600003ab046188_T001
Z600003ab046191_T001
Z600003ab046192_T001
Zh00001ab048222_T001
Zh00001ab048223_T001
AC152495.1_FGT002_T002
AC152495.1_FGT003_T003
AC152495.1_FGT010_T010
GRMZM2G879178_T01
GRMZM2G443939_T02
GRMZM2G349565_T01
GRMZM2G003625_T01
Zm000014023317_T002
Zm000014023318_T065
Zm000014023320_T001
Zm000014023323_T002
Zm000014023326_T004
Zm000014023327_T004
Zm000014023329_T001



▶ PAN-GENE ALIGNMENT

▼ PAN-GENE PROTEIN DOMAINS

Pfam protein domain alignments

The table below shows the domains as they appear in order across the gene models.
If a domain is repeated in order, the repeat number is shown in square brackets.

```

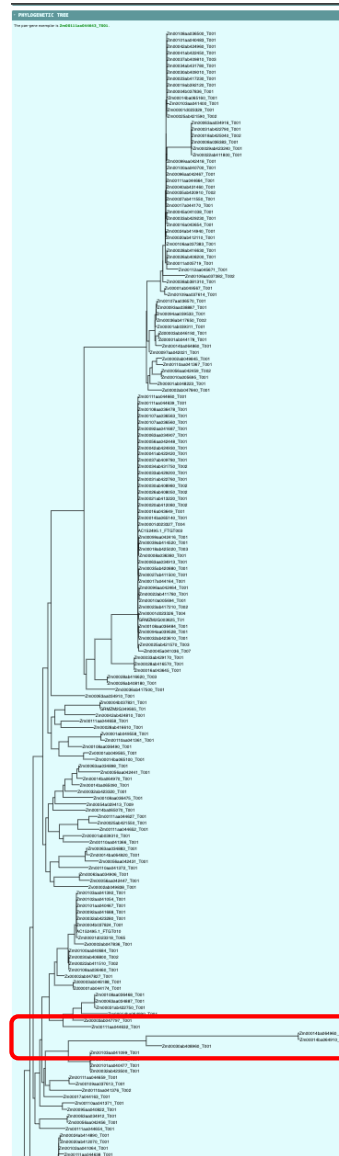
AC152495.1 FGTT002 --
AC152495.1 FGTT003 --
AC152495.1 FGTT010 --
GRMZM2G003625 T01 Rx_N => nSTAND1 => NB-ARC => NACHT => Rx_N => NB-ARC => LRR_4[2] => LRR_8 => LRR_4[2] => LRR_8 => LRR_4 => Rx_N => LI
GRMZM2G349565 T01 LRR_4[12]
GRMZM2G443939 T02 Rx_N[2] => nSTAND1 => NB-ARC => NACHT => Rx_N => LRR_8[2] => LRR_4 => LRR_8 => LRR_4[2] => LRR_8 => LRR_4[2] => Rx_N
GRMZM5G879176 T01 Rx_N => NACHT => AAA_16 => NB-ARC => NACHT => Rx_N => LRR_8 => LRR_4[2] => LRR_8 => LRR_4[2] => LRR_8 => LRR_4 => Rx
Zm00001d023317 T002 AAA_16 => nSTAND1 => NB-ARC => NACHT => LRR_8 => LRR_4[2] => LRR_8 => LRR_4 => nSTAND1 => LRR_4 => LRR_8 => LRR_4
Zm00001d023318 T007 Acetyltransf_1 => PPR[2] => Cation_ATPase
Zm00001d023320 T001 Rx_N => AAA_16 => NB-ARC => NACHT => DUF815 => TIR_2[2] => LRR_8 => LRR_4[2] => LRR_8 => LRR_4[2] => LRR_8 => LRR_4
Zm00001d023323 T002 Rx_N[2] => nSTAND1 => NB-ARC => NACHT => Rx_N => LRR_8[2] => LRR_4 => LRR_8 => LRR_4[2] => LRR_8 => LRR_4[2] => Rx_N
Zm00001d023326 T004 THH1_TOM1-3_dom => CRAL_TRIO_N => Rx_N => nSTAND1 => NB-ARC => NACHT => Rx_N => NB-ARC => LRR_4[2] => LRR_8 => LF
Zm00001d023327 T004 THH1_TOM1-3_dom => CRAL_TRIO_N => Rx_N => nSTAND1 => NB-ARC => NACHT => Rx_N => NB-ARC => LRR_4[2] => LRR_8 => LF
Zm00001d023329 T001 Rx_N => nSTAND3 => NACHT => AAA_16[2] => nSTAND3 => NB-ARC => NACHT => NB-ARC => LRR_8 => LRR_4[2] => LRR_8 => LRR
Zm00001eb405860 T001 Rx_N => AAA_16[2] => nSTAND1 => NB-ARC => NACHT => Rx_N => LRR_8 => LRR_4[3] => nSTAND1 => LRR_4 => LRR_8 => LRR
Zm00004b037824 T001 Rx_N => AAA_16[2] => nSTAND1 => NB-ARC => NACHT => Rx_N => LRR_4[5] => Rx_N => LRR_4[7]
Zm00004b037827 T001 Rx_N => AAA_16 => NB-ARC => NACHT => DUF815 => TIR_2[2] => LRR_8[3] => Rx_N => LRR_8[2] => NB-ARC => AAA_16 => DUF8
Zm00004b037829 T001 Rx_N[2] => nSTAND1 => NB-ARC => NACHT => Rx_N => LRR_8[2] => LRR_4 => LRR_8 => LRR_4[2] => LRR_8 => LRR_4[2] => Rx_N
Zm00004b037831 T001 LRR_4[12]
Zm00004b037836 T001 Rx_N => nSTAND3 => NACHT => AAA_16[2] => nSTAND3 => NB-ARC => NACHT => NB-ARC => LRR_8 => LRR_4[2] => LRR_8 => LRR
Zm00008a036380 T001 Rx_N => NB-ARC[3] => LRR_8[2] => Rx_N => LRR_8[2]
Zm00008a036383 T001 Rx_N => nSTAND3 => NACHT => AAA_16[2] => nSTAND3 => NB-ARC => NACHT => TIR_2 => Rx_N => TIR_2 => NB-ARC
Zm00018ab424890 T004 Rx_N => AAA_16 => nSTAND1 => NB-ARC => NACHT => Rx_N => LRR_8[2] => LRR_4[2] => LRR_8 => LRR_4[2] => LRR_8 => LRR_
Zm00018ab425010 T001 Rx_N => nSTAND3 => NACHT => AAA_16[2] => nSTAND3 => NB-ARC => NACHT => Rx_N => LRR_8[2] => LRR_4 => LF
Zm00018ab425020 T003 Rx_N => nSTAND1 => NB-ARC => NACHT => Rx_N => NB-ARC => LRR_4[2] => LRR_8 => LRR_4[2] => LRR_8 => LRR_4 => Rx_N =>
Zm00018ab425040 T002 Rx_N => nSTAND3 => NACHT => AAA_16 => Rx_N => DUF815 => AAA_16 => nSTAND3 => NB-ARC => NACHT => DUF815 => TIR_2
Zm00019ab392100 T001 LRR_8 => LRR_4[2] => LRR_8 => LRR_4 => LRR_8 => LRR_4[3] => LRR_8 => LRR_4[3] => LRR_8 => LRR_4[2] => LRR_8 => LRR_4
Zm00019ab392120 T001 Rx_N => nSTAND3 => NACHT => AAA_16[2] => nSTAND3 => NB-ARC => NACHT => NB-ARC => LRR_8 => LRR_4[2] => LRR_8 => LR
Zm00020ab412030 T004 AAA_16 => nSTAND1 => NB-ARC => NACHT => LRR_8[2] => LRR_4 => LRR_8 => LRR_4[2] => LRR_8 => LRR_4[2] => LRR_8 => LR
Zm00020ab412070 T001 Rx_N => nSTAND3 => NACHT => AAA_16[2] => nSTAND3 => NB-ARC => NACHT => Rx_N => LRR_4[3] => nSTAND3 =>
Zm00020ab412080 T002 Rx_N => nSTAND1 => NB-ARC => NACHT => Rx_N => NB-ARC => LRR_4[2] => LRR_8 => LRR_4[2] => LRR_8 => LRR_4 => Rx_N =>
Zm00020ab412110 T001 Rx_N => nSTAND3 => NACHT => AAA_16[2] => nSTAND3 => NB-ARC => NACHT => NB-ARC => LRR_8 => LRR_4[2] => LRR_8 => LR
    
```

Protein domains are calculated by HMMscan.

Definitions:

Accession	Name	Description
PF13173	AAA_14	AAA domain
PF13191	AAA_16	AAA ATPase domain
PF13401	AAA_22	AAA domain
PF00583	Acetyltransf_1	Acetyltransferase (GNAT) family
PF03765	CRAL_TRIO_N	CRAL/TRIO, N-terminal domain
PF13246	Cation_ATPase	Cation transport ATPase (P-type)
PF05673	DUF815	Protein of unknown function (DUF815)
PF07011	EIF4	Early Flowering 4 domain
PF23286	LRR_13	Disease resistance protein RPS4B-like, leucine-rich repeats
PF23598	LRR_14	Leucine-rich repeat region
PF12799	LRR_4	Leucine Rich repeats (2 copies)
PF13855	LRR_8	Leucine rich repeat
PF23622	LRR_At1g61320_AtMIF1	At1g61320/AtMIF1, LRR domain

Phylotree of the pan-gene members



› INSERTIONS

› METABOLIC PATHWAYS

› EXPRESSION

› PROTEINS, PROTEOMICS, AND PROTEIN STRUCTURE

› SNPS AND TRAITS

› FUNCTION

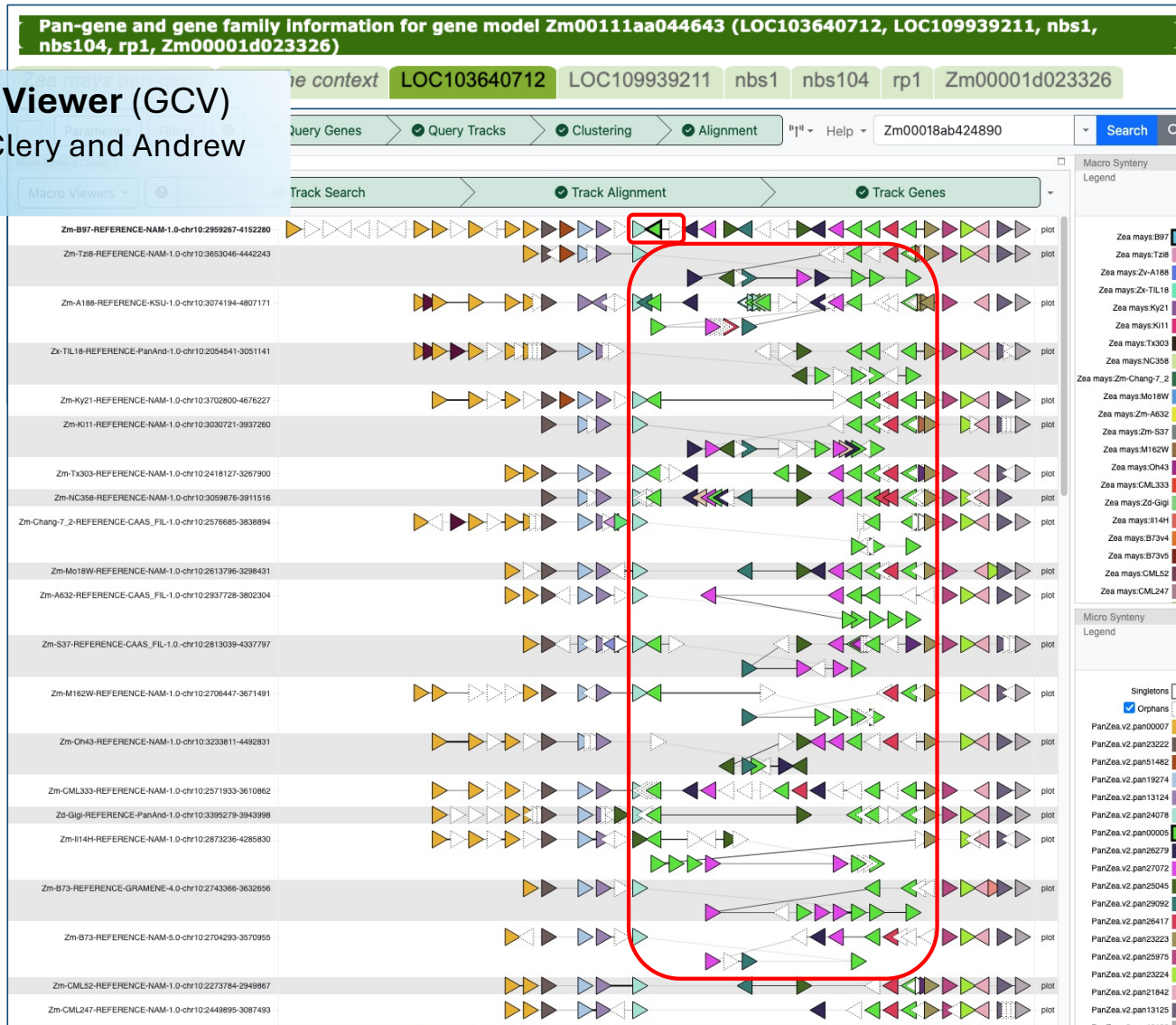
› SEQUENCE

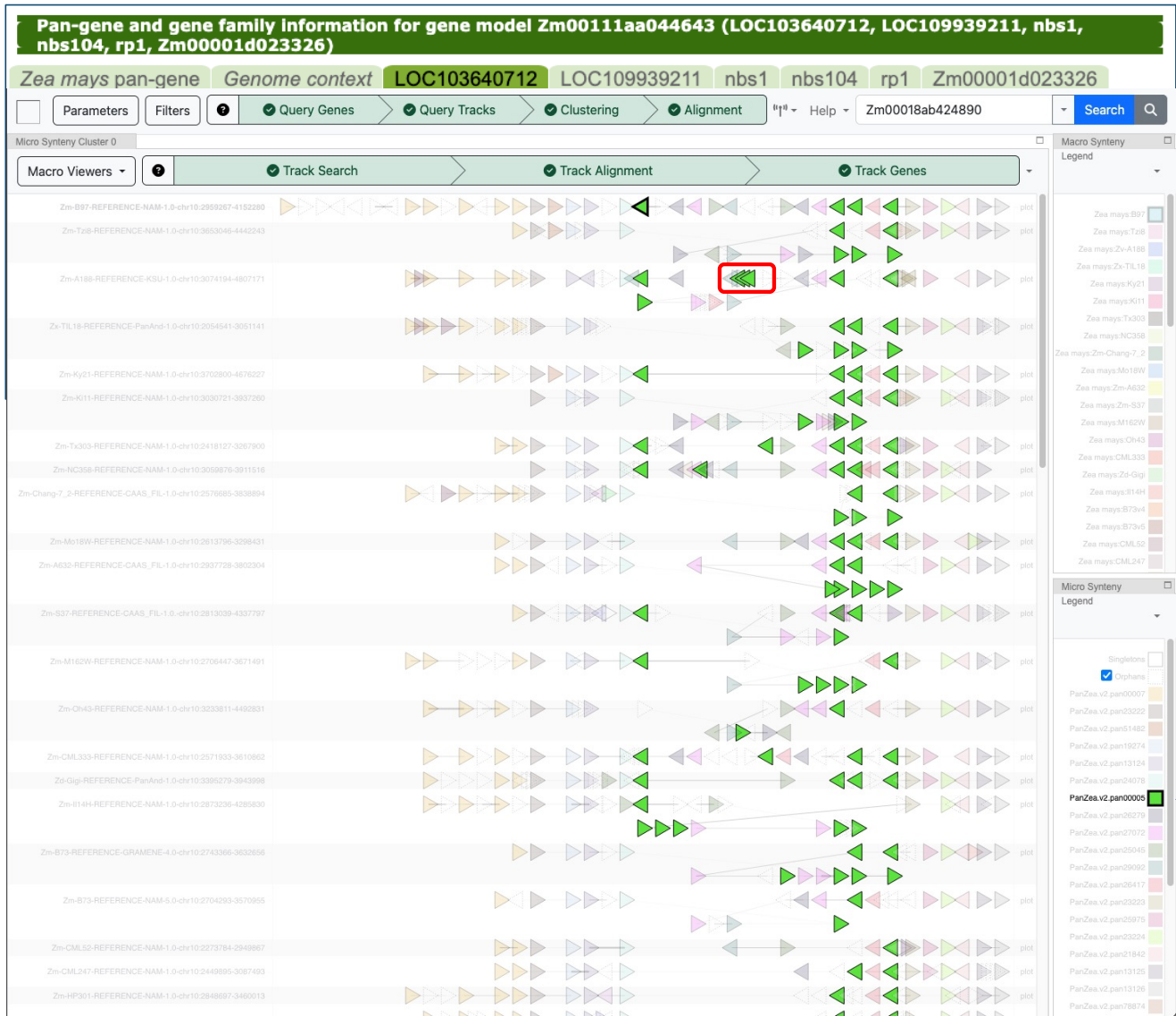
› DOWNLOADS

› 3RD PARTY COMPARATIVE VIEWERS

Pan-gene and gene family information for gene model Zm00111aa044643 (LOC103640712, LOC109939211, nbs1, nbs104, rp1, Zm00001d023326)

Genome Context Viewer (GCV)
Developed by Alan Clery and Andrew Farmer for LIS.





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Questions?