

<https://www.gramene.org>

Rel #66 (Dec. 2022)

Plant genomes: 128

Gene family trees: 152K

WG Pairwise DNA alignments: 278

Synteny maps: 79

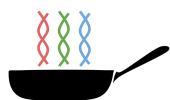
Species with genetic variation: 17

Species with baseline gene expression: 28

Curated rice pathways: 320

Species with orthology-based pathway projections: 120

Support for community curation of gene structures



PanGenomes

For each pan genome site, gene trees were built with a minimum of 7 outgroup species. Expression data and pathways are available for the reference genomes.



maize-pangenome.gramene.org

Rel #3 (March 2023)

Maize genomes: 41

Gene trees: 36K



oryza.gramene.org

Rel #6 (Jan. 2023)

Rice genomes: 28

Gene trees: 38K



vitis.gramene.org

Rel #3 (May 2022)

Grape genomes: 18

Gene trees: 28K



sorghumbase.org

Rel #5 (Dec. 2022)

Sorghum genomes: 28

Gene trees: 44K

61M SNPs and EMS mutations

Publications DB & research highlights



Curated gene functions from the literature (354 Z. mays, 4006 O. sativa, 7184 A. thaliana) enable searches with TO/PO terms, and returns associated PMIDs in a new Publications tab

lox9 Zm00001eb005920 [Zea mays](#)

GRMZM2G017616, Zm00001d027893, lpxoxyenase9

Location Expression Homology Pathways Papers Xrefs

Curated publications

This gene has been described in the literature:

PubMed link	Curation source	Title/Description
19817885	geneRIF	The oxidation of 20:2 and 22:2 by 9-LOX afforded low yields of racemic 11-, 12-, 14-, and 15-hydroperoxides.
20673209	geneRIF	Lox9 was stable form pH 4.5 to 9.5 with a maximum activity at pH7.5.

LOX4 *Arabidopsis thaliana*

PLATLH2 domain-containing lipoxygenase family protein

Tools



Comparative pathway analysis of JA signaling in rice vs 4 species in Gramene's Plant Reactome

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

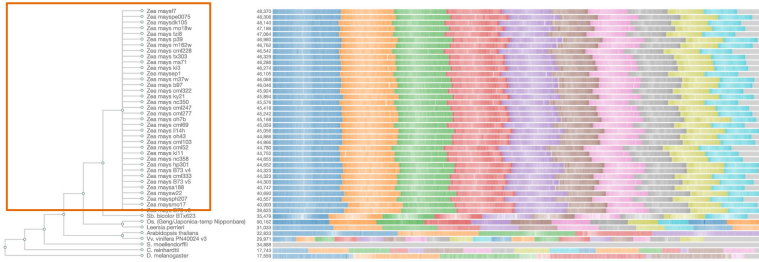
Contact us for data integration, training and support or to partake in our community curation projects: <https://www.gramene.org/feedback>

Cite Gramene: Tello-Ruiz *et al* (2021) 10.1093/nar/gkaa979



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

41 Maize genomes, 3 versions of B73, 7 outspecies



Structural variation for NAM genomes (B73 v5 browser)



Gene curation interface

This is the gene tree containing Zm0001eb009920. Gene name: *lox9*. Description: *lipoxygenase9*.

Curation Instructions

Mark genes as okay or flag genes that you might think have issues and choose a reason from the drop down menu. When finished, enter your email address and submit.

The reason for flagging a gene model is optional, but you may indicate whether there is a gain (G), loss (L) or no change (L) in the beginning, middle, and end of the gene model.

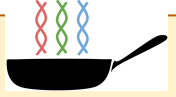
For example L... means there is a loss at the 5' end.

Display Mode: Color Scheme: Alignment overview: Proteins color-coded by InterPro domain. Resize slider to navigate.

Curate: [List of genes with status indicators like 'Curate', 'Flag', 'OK', and a dropdown menu to 'Choose a reason']

Curation of the gene tree containing *lox9* (lipoxygenase 9). Genes are marked as 'okay' or 'flag' for potential annotation issues with an option to choose a reason for it from the drop down menu. G indicates a gain, L is a loss and (L) indicates no change in the beginning, middle, and end of the gene model.

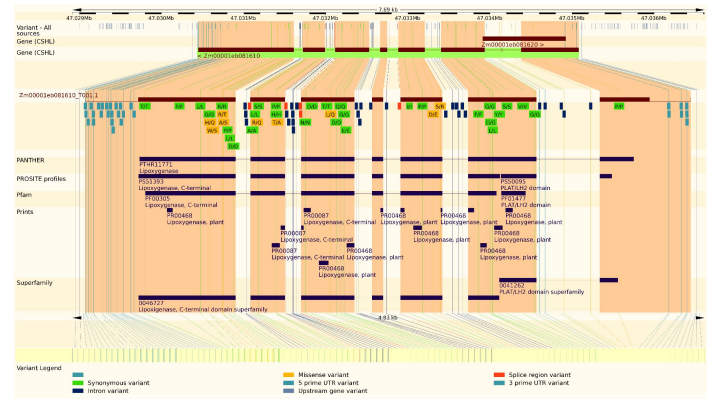
Release #3 (March 2023)



Maize PanGenome

- Maize genomes: 41
- Gene family trees: 36K with ortholog & paralog calls
- Integrated curated gene functions from the literature enable searches by TO/PO terms
- List of publications associated with curated genes in search results
- Genetic variation (Hapmap2 & Panzea) & structural variation for the NAM genomes overlaid in the B73 v5
- Variation & effect prediction
- 25 RNA-Seq baseline & 55 differential gene expression studies for B73 v5
- Orthology-projected pathways: 267 in v5 (268 in v4) including carotenoid biosynthesis
- Manually curated B73 v4 gene models mapped to v5
- Gene curation user interface
- Blast service
- Programmatic access
- Quick start guide

Genetic variation with color-coded functional effect predictions overlaid on the protein's domain structure



Contact us:

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

Community Engagement

- Engagement and training
- Support for data standards
- Integrated access via data federation