



<https://www.gramene.org>

Rel #66 (Dec. 2022)

Plant genomes: 128

Gene family trees: 152K

Pairwise DNA alignments: 278

Synteny maps: 79

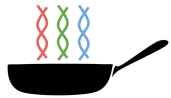
Species with genetic variation: 15

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.



Rel #2 (July 2021)
Maize genomes: 26
Gene trees: 31K

maize-pangenome.gramene.org



Rel #3 (May 2022)
Grape genomes: 18
Gene trees: 28K

vitis.gramene.org



Rel #6 (Jan. 2023)
Rice genomes: 28
Gene trees: 38K

oryza.gramene.org



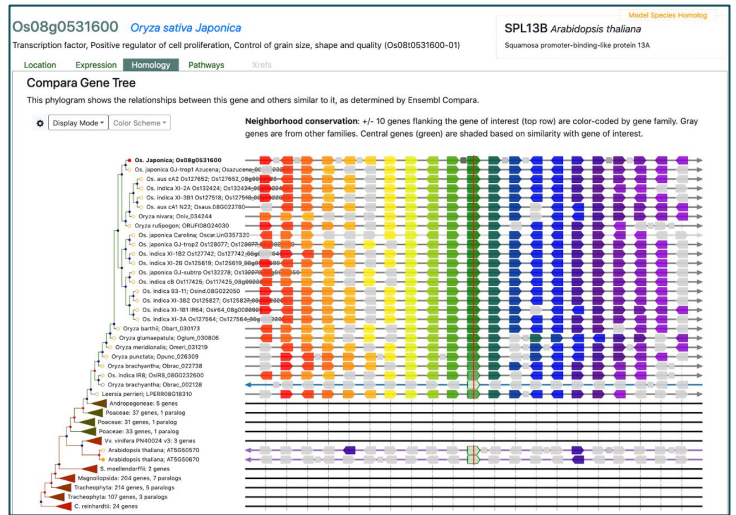
Rel #5 (Dec. 2022)
Sorghum genomes: 28
Gene trees: 44K
61M SNPs and EMS mutations
Publications DB & research highlights

sorghumbase.org

Contact us for data integration, training and support or to partake in our community curation projects:

<https://www.gramene.org/feedback>

Tools



Neighborhood Conservation View. This view allows researchers to identify structural variants and presence/absence variation in a conserved region. For each gene in the tree 10 flanking genes are displayed and color coded by gene family or shaded based on similarity to the gene of interest.

Cite Gramene:

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



CLIMtools

Environment × Genome × Phenotype Associations



SINCE 2021

<https://www.gramene.org/CLIMtools>

Version 2 (May 2022)
Arabidopsis accessions: 2999
Climate Variables: 473

Climate GWAS and TWAS
RiboSNitch† prediction



Rice CLIMTools *coming in 2023*

AraCLIM V2

Interactive spatial analysis web tool via a database of local Arabidopsis environments

CLIMGeno V2

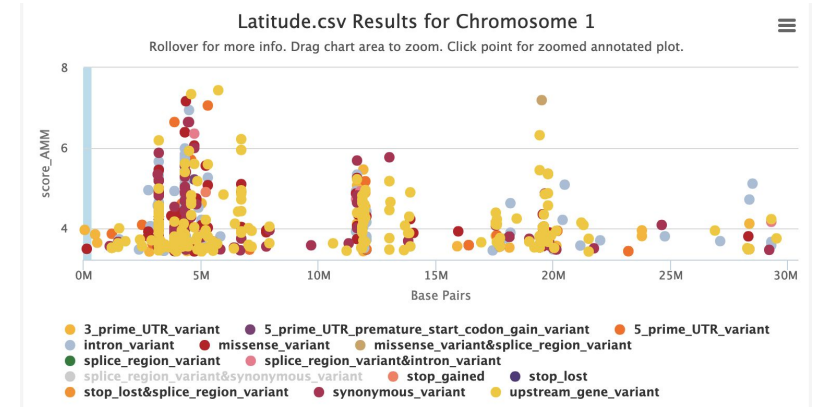
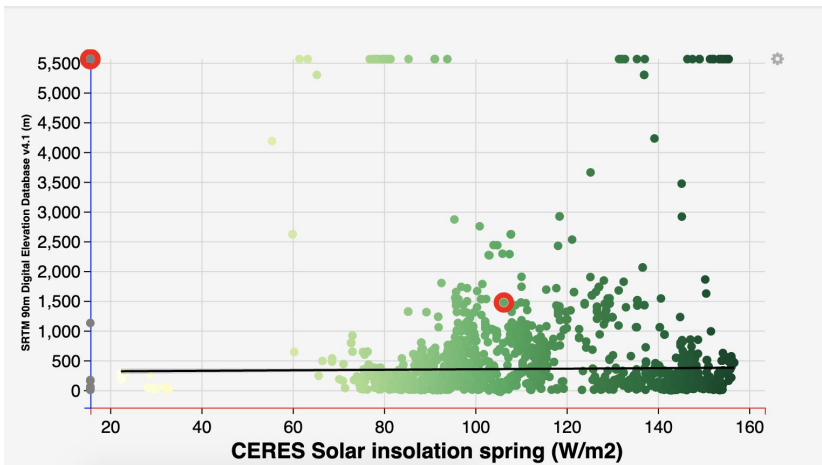
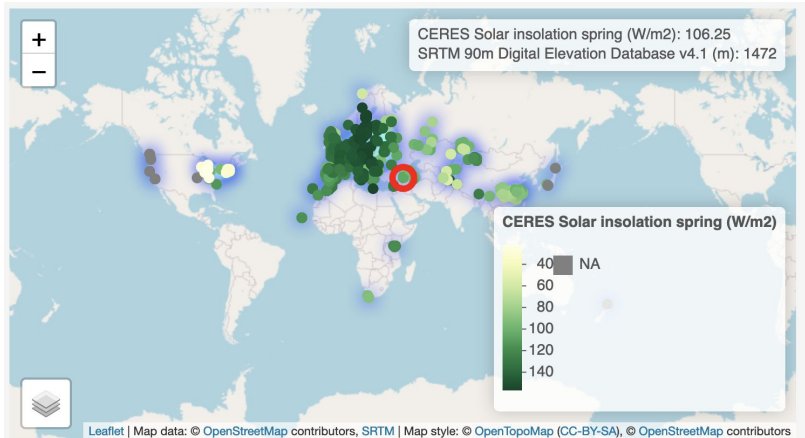
Genetic variation associated with an environmental variable of interest

GenoCLIM V2

Environmental variation associated with a gene or variant of interest

T-CLIM V2

Association between natural variation in transcript abundance of a gene and an environmental variable



† RiboSNitches are SNPs that change RNA structure between the reference and the alternative SNP.

Cite ClimTools: Ferrero-Serrano *et al* (2022)
10.1186/s13059-022-02656-4

