

# CITRUS GENOME DATABASE



Resources for citrus genomics, genetics, breeding and disease research

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## What's new in CGD?

### ***New Training Videos***

- [How to download protein sequences](#) (1:27 mins)
- [How to use the ortholog/paralog search](#) (2:02 mins)

### ***New Data and Functionality***

- *C. sinensis* cv. Jinhong genome
- Citrus SNP genotyping array probes added
- *C. aurantiifolia* long read transcriptome added to Blast and database

## New data added in second quarter of 2024

### **Genome and transcriptome**

- Wang et al. [Phased genomics reveals hidden somatic mutations and provides insight into fruit development in sweet orange](#). Horticulture research. 2024 Feb; 11(2):uhad268
- Paisey et al. [Long-reads-based transcriptome dataset from leaves of lime, \*Citrus aurantiifolia\* \(Christm.\) Swingle treated by ethephon and abscisic acid](#). Data in brief. 2023 Jun; 48:109167.

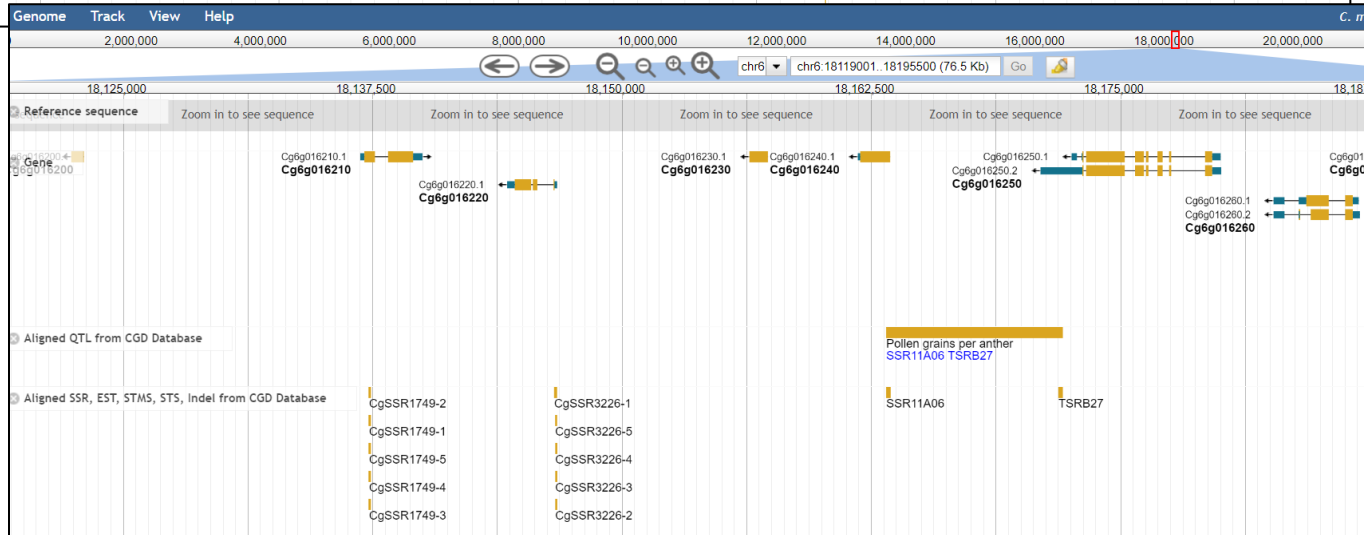
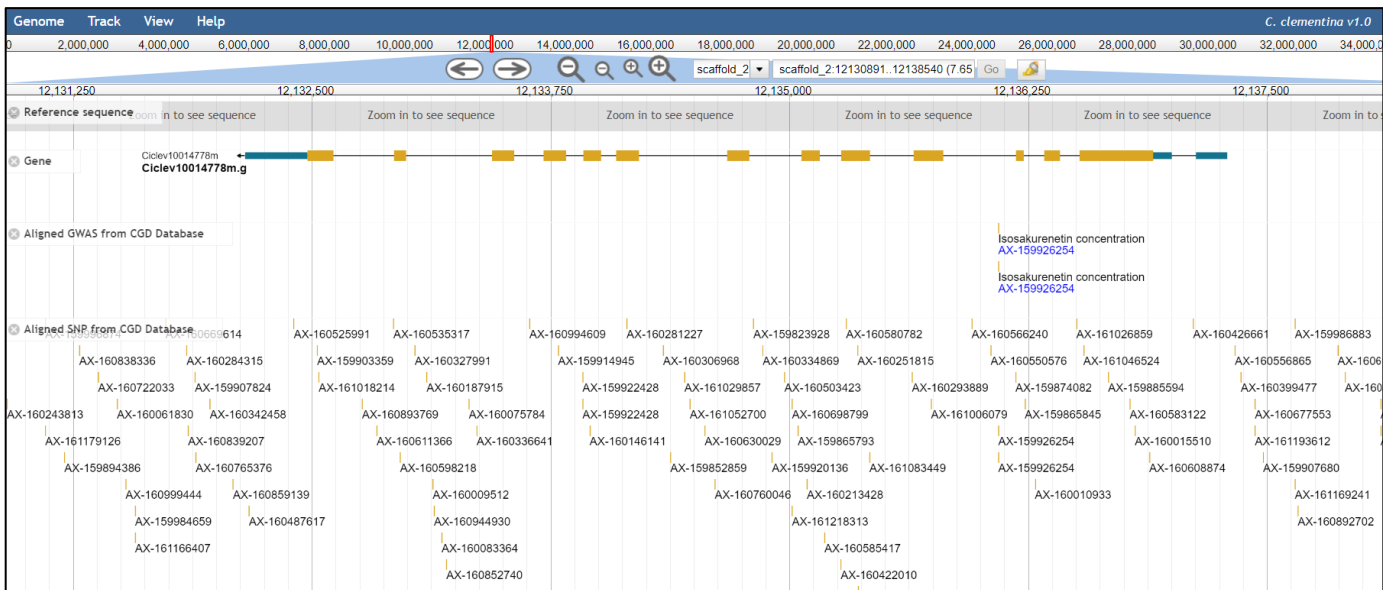
### **Genotyping probes and genome alignments**

- Hiraoka et al. [Development and Assessment of SNP Genotyping Arrays for Citrus and Its Close Relatives](#). Plants (Basel, Switzerland). 2024 Feb 29; 13(5).
- PCR primer-based markers have been aligned to the genomes listed below and used to map QTL with those associated markers. Find out more on next page.
  - *Citrus clementina* genome v1.0 (JGI)
  - *Citrus sinensis* genome v1.1 (JGI)
  - *Citrus sinensis* Di-Haploid Sweet Orange (DHSO) v3.0 (HZAU)
  - *Citrus maxima* (*C. grandis*) genome v1.0
  - *Citrus sinensis* cv. Valencia DVS\_A genome v1.0
  - *Citrus limon* cv. Eureka genome v1.0
  - *Citrus australis* genome v1.0 (UQ)
  - *Citrus australasica* CRC3672 genome v1
  - *Poncirus trifoliata* acc. ZK8 v1.0 (HZAU)
  - *Fortunella hindsii* S3y-45 genome v2.0

# Aligned markers and new JBrowse tracks

CGD is always looking for ways to take existing data and make it more useful for researchers. Using primer sequences from PCR-based markers (SSR, EST, etc.) in the database, and a short sequence BLAST analysis along with filtering, we have aligned the marker primers to representative genomes of each species. The aligned positions are stored under the marker record. We have then mapped QTLs which are associated with aligned markers to genomes.

We have also added four new JBrowse tracks. One track is SNPs mapped to the genome. The second track is the aligned markers with PCR primers. And the last two tracks are aligned QTL either from provided genome positions or based on aligned markers associated with the QTL and GWAS with stored positions.



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