Citrus Genome Database

Resources for citrus genomics, genetics, breeding and disease research

Using the Citrus Genome Database for Genetics, Genomics, and Breeding Research

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What is CGD?

Single website

Can be tailored to community needs

Easy-to-use tools and searches

www.citrusgenomedb.org

Open-source database platform with numerous modules

Genetics
- Genetic Markers
- Genetic Maps
- QTLs
- MapViewer

Genomics
- Genes & Transcripts
- JBrowse
- BLAST
- Synteny Viewer
- CitrusCyc
- Expression Data

Breeding
- BIMS
- GRIN Phenotype Data
- Analysis Tools

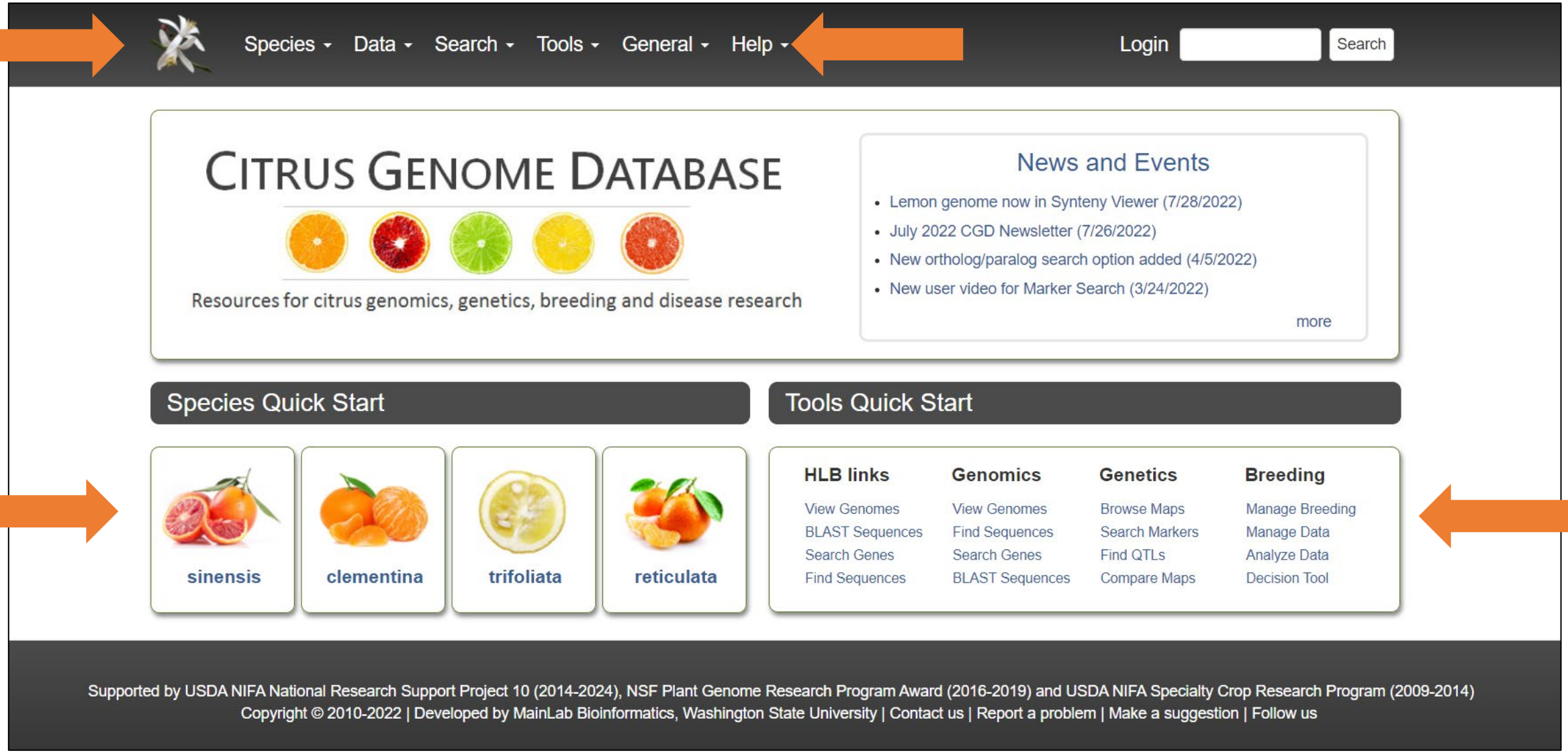
Available data

Data Type	Count
Genetic Maps	85
Genetic Markers	60,407
QTL	673
Traits	153
Phenotypic Measurements	23,070
Trait Descriptors	38
Transcripts/Unigenes	124,389
Genes	366,169
mRNA	649,803

Genomes

Citrus and related species	***Ca.* Liberibacter and related species**
C. clementina v1.0	*Ca.* L. asiaticus gxpsy
C. sinensis v1.1	*Ca.* L. asiaticus psy62
C. sinensis v2.0	*Ca.* L. asiaticus A4
C. maxima (*C. grandis*) v1.0	*Ca.* L. asiaticus Ishi-1
C. ichangensis (*C. cavaleriei*) v1.0	*Ca.* L. asiaticus JXGC
C. medica v1.0	*Ca.* L. americanus Sao Paulo
C. reticulata v1.0	*Ca.* L. africanus PTSAPSY
C. limon v1.0 (primary and alternative)	*Ca.* L. solanacearum CLso-ZC1
Poncirus trifoliata v1.3.1	*L. crescens* BT-1
Fortunella hindsii v1.0	*L. crescens* BT-0
Atalantia buxifolia v1.0	

Homepage


Species
Data
Search
Tools
General
Help
Login
Search
CITRUS GENOME DATABASE
Resources for citrus genomics, genetics, breeding and disease research
News and Events
Lemon genome now in Synteny Viewer (7/28/2022)
July 2022 CGD Newsletter (7/26/2022)
New ortholog/paralog search option added (4/5/2022)
New user video for Marker Search (3/24/2022)
more
Species Quick Start
sinensis
clementina
trifoliata
reticulata
Tools Quick Start
HLB links
View Genomes
BLAST Sequences
Search Genes
Find Sequences
Genomics
View Genomes
Find Sequences
Search Genes
BLAST Sequences
Genetics
Browse Maps
Search Markers
Find QTLs
Compare Maps
Breeding
Manage Breeding
Manage Data
Analyze Data
Decision Tool
Supported by USDA NIFA National Research Support Project 10 (2014-2024), NSF Plant Genome Research Program Award (2016-2019) and USDA NIFA Specialty Crop Research Program (2009-2014)
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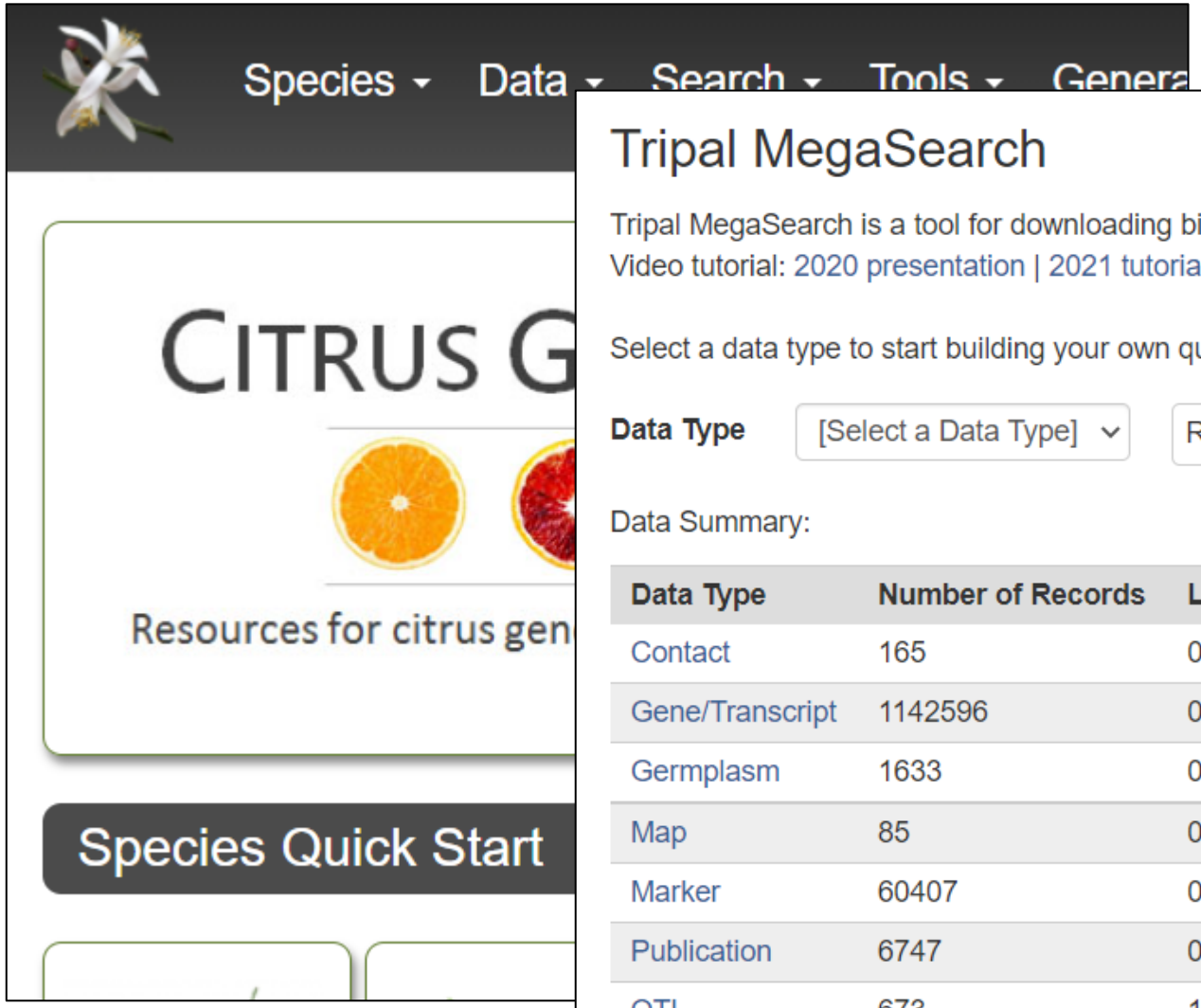
Searching the data



Tripal MegaSearch

Tripal MegaSearch is a tool for downloading biological data. (Current limit per download: 1,000,000 records. 200,000 FASTA sequences.)
Video tutorial: 2020 presentation | 2021 tutorial (Gene/Transcript) | 2022 tutorial (QTL)

Select a data type to start building your own query and download data in bulk:

Data Type [Select a Data Type] Reset

Data Summary:

Data Type	Number of Records	Last Updated
Contact	165	07/26/2021
Gene/Transcript	1142596	06/23/2022
Germplasm	1633	08/04/2021
Map	85	07/14/2022
Marker	60407	06/23/2022
Publication	6747	07/14/2022
QTL	673	10/11/2021

Searching the data

Select a data type to start building your own query and download data in bulk:

Data Type Gene/Transcript Reset

1,142,596 Gene/Transcript. *Note: actual rows in downloaded file depend on the selected fields.*

Query

Sequence Type Any Clear Refresh Count

Genome

Genome Name Any
Atalantia buxifolia genome v1.0
Ca. L. africanus PTSAPSY genome
Ca. L. americanus Sao Paulo genome

Chromosome/Scaffold Any

Start >

Stop >

Transcriptome/Other Dataset

Transcriptome/Dataset Any

Organism Any

Genome Any

Chromosome/Scaffold Any

Start >

Stop >

Downloadable Fields

View FASTA CSV TSV

Sequence retrieval

Gene/Transcript name

Name contains

Choose File No file chosen

Functional Annotation

All contains

BLAST contains

KEGG contains

InterPro contains

GO Term contains

GenBank Keyword contains

Downloadable Fields

View FASTA CSV TSV

Sequence retrieval

Warning: this may take hours if too many sequences are being downloaded. Please do not start two sequence retrieval jobs at the same time.

Upstream bases **Downstream bases**

Retrieve

- [x] All Fields
- [x] Name
- [x] Unique Name
- [x] Organism

MapViewer

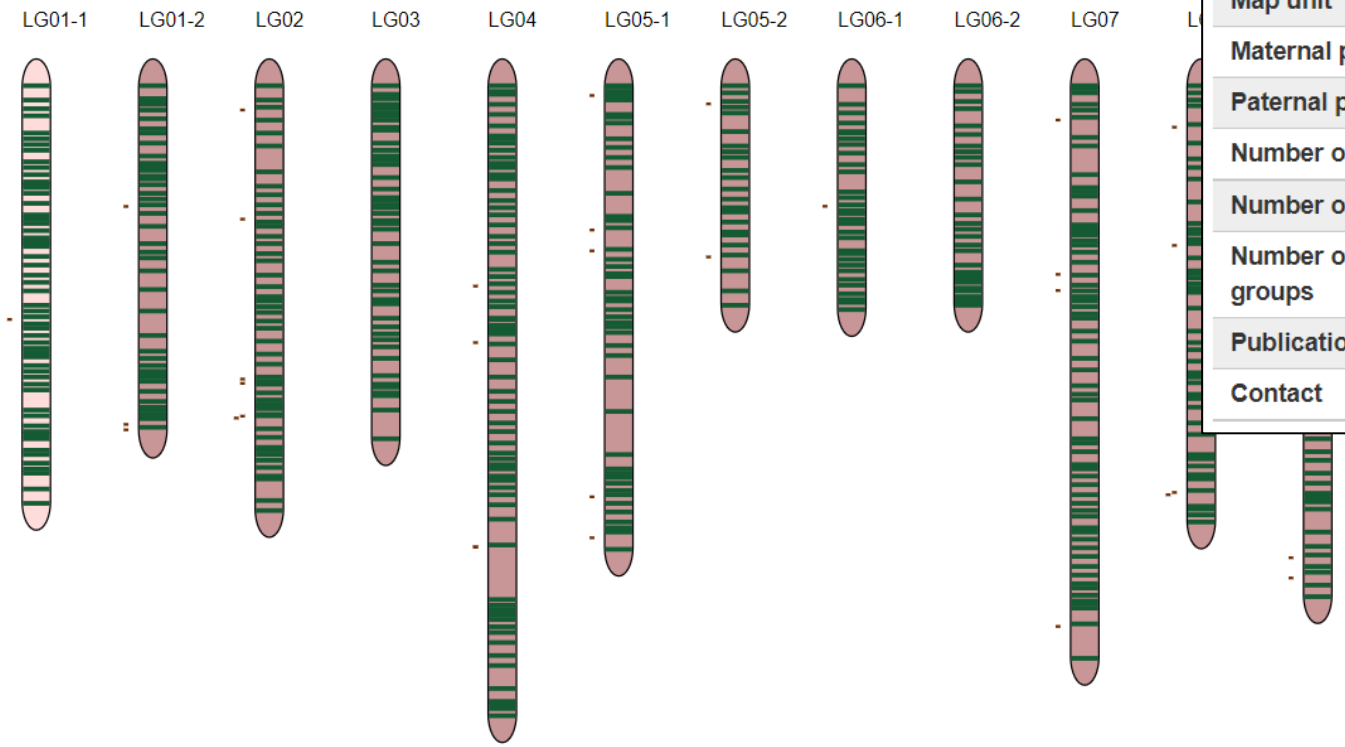
Citrus-C_sunki/Rubidoux-F1-Rubidoux-2020

- Map Overview
- View Map
- Contact
- Map Loci
- Map QTL
- Publication
- Stock

Map Overview

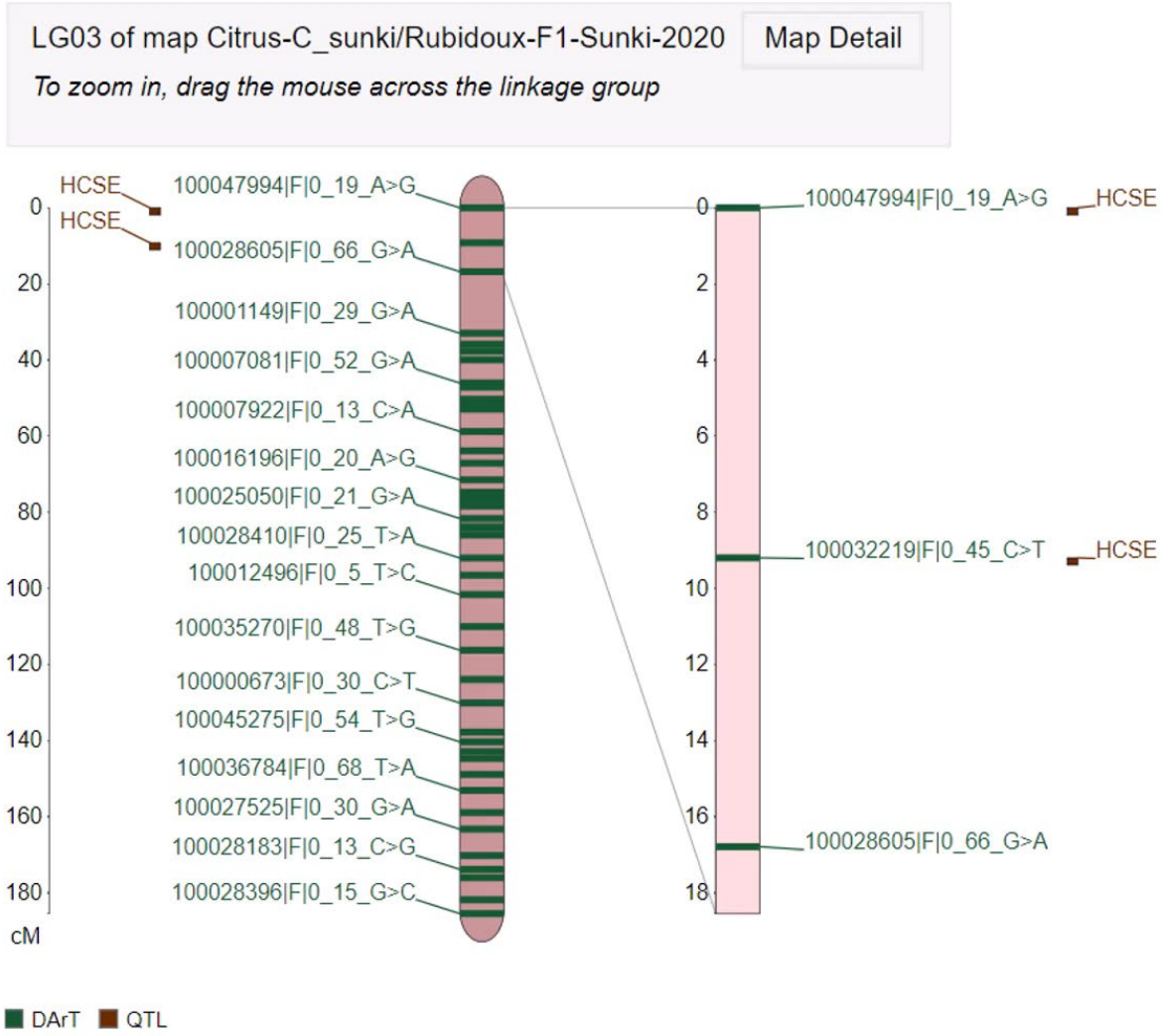
Click on any linkage group to explore this map further. You will be taken to MapViewer and leave this page.

Viewing genetic map Citrus-C_sunki/Rubidoux-F1-Rubidoux-2020



Name	Citrus-C_sunki/Rubidoux-F1-Rubidoux-2020
Species	Citrus spp.
Map type	genetic
Population type	F1
Population size	272
Map unit	cM
Maternal parent	Citrus sunki
Paternal parent	Rubidoux
Number of loci	568
Number of QTL	34
Number of linkage groups	12
Publication	[view all]
Contact	Maiara Curtolo

MapViewer


LG03 of map Citrus-C_sunki/Rubidoux-F1-Sunki-2020
Map Detail
To zoom in, drag the mouse across the linkage group
HCSE
HCSE
100047994|F|0_19_A>G
100028605|F|0_66_G>A
100001149|F|0_29_G>A
100007081|F|0_52_G>A
100007922|F|0_13_C>A
100016196|F|0_20_A>G
100025050|F|0_21_G>A
100028410|F|0_25_T>A
100012496|F|0_5_T>C
100035270|F|0_48_T>G
100000673|F|0_30_C>T
100045275|F|0_54_T>G
100036784|F|0_68_T>A
100027525|F|0_30_G>A
100028183|F|0_13_C>G
100028396|F|0_15_G>C
0
20
40
60
80
100
120
140
160
180
cM
100047994|F|0_19_A>G
HCSE
100032219|F|0_45_C>T
HCSE
100028605|F|0_66_G>A
0
2
4
6
8
10
12
14
16
18
DArT
QTL

MapViewer

Dot Plot

Select Reference Map:

Species Citrus grandis **Map** Citrus-Chandler-Ref-F1 **Linkage Group** LG1 Submit

Select Comparison Map: (View Correspondence Matrix)

☐ Show comparison map Download Table

Species Citrus grandis **Map** Citrus-Guanxi/Pingshan-Integrated-F1-2015 (3) **Linkage Group** LG4 (3) Submit

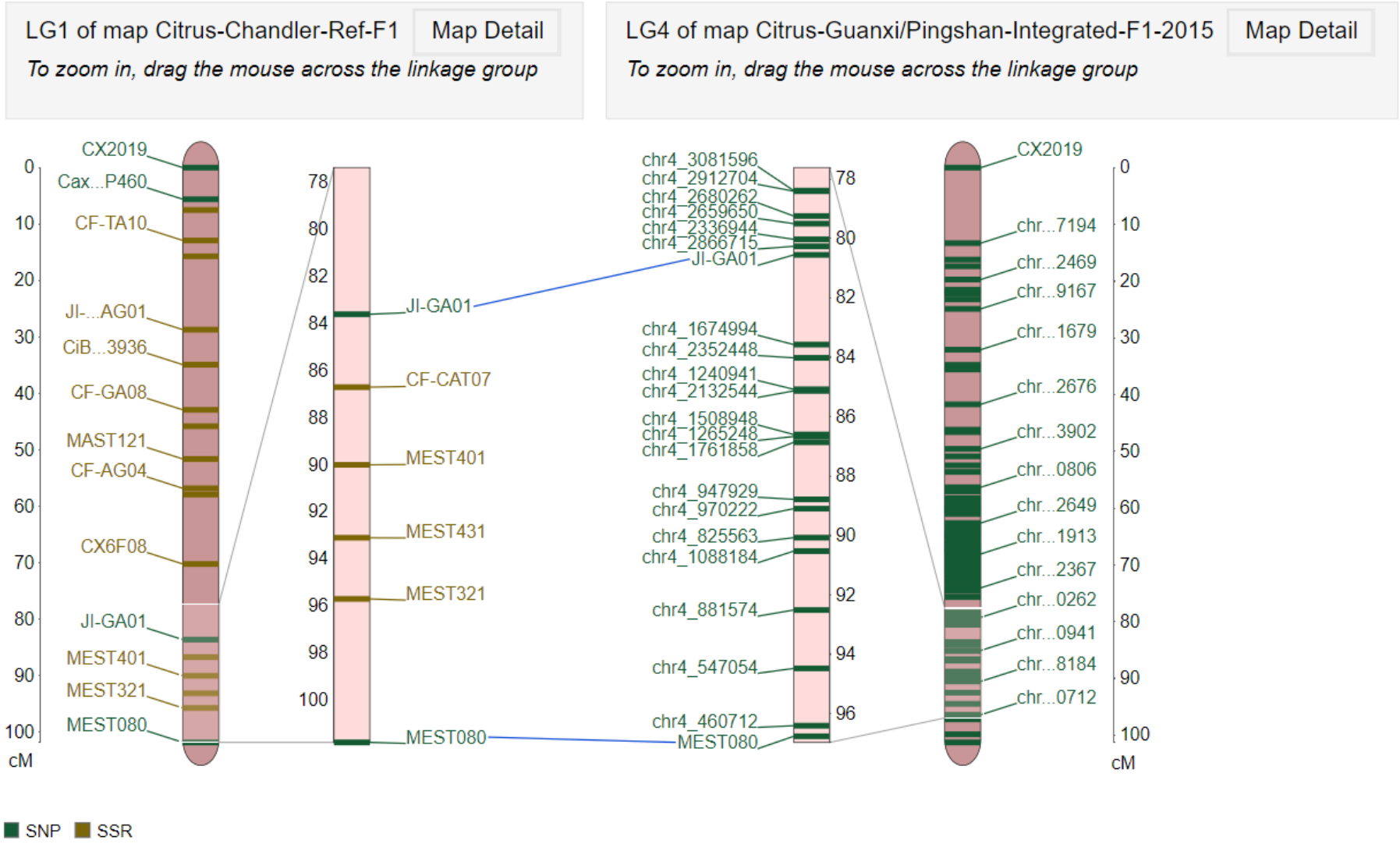
Display Settings:

Marker color SNP deepGreen Submit Reset

Marker visibility SNP SSR Show Submit Reset

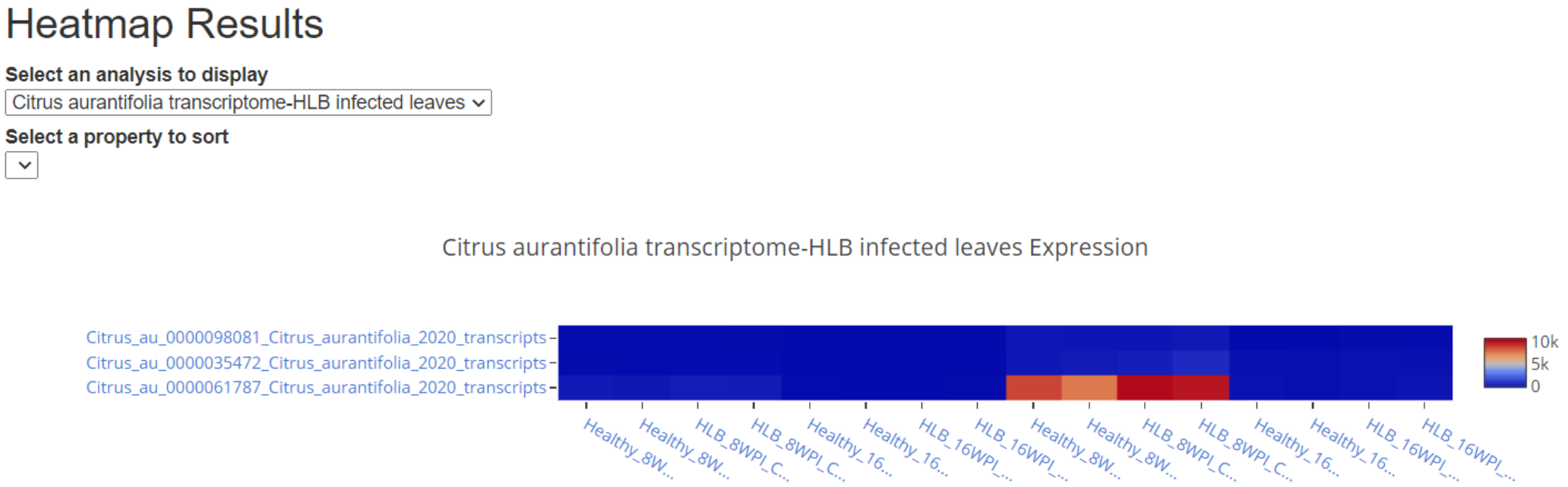
☑ Show ruler ☐ Show marker position ☐ Expand QTL Submit

MapViewer

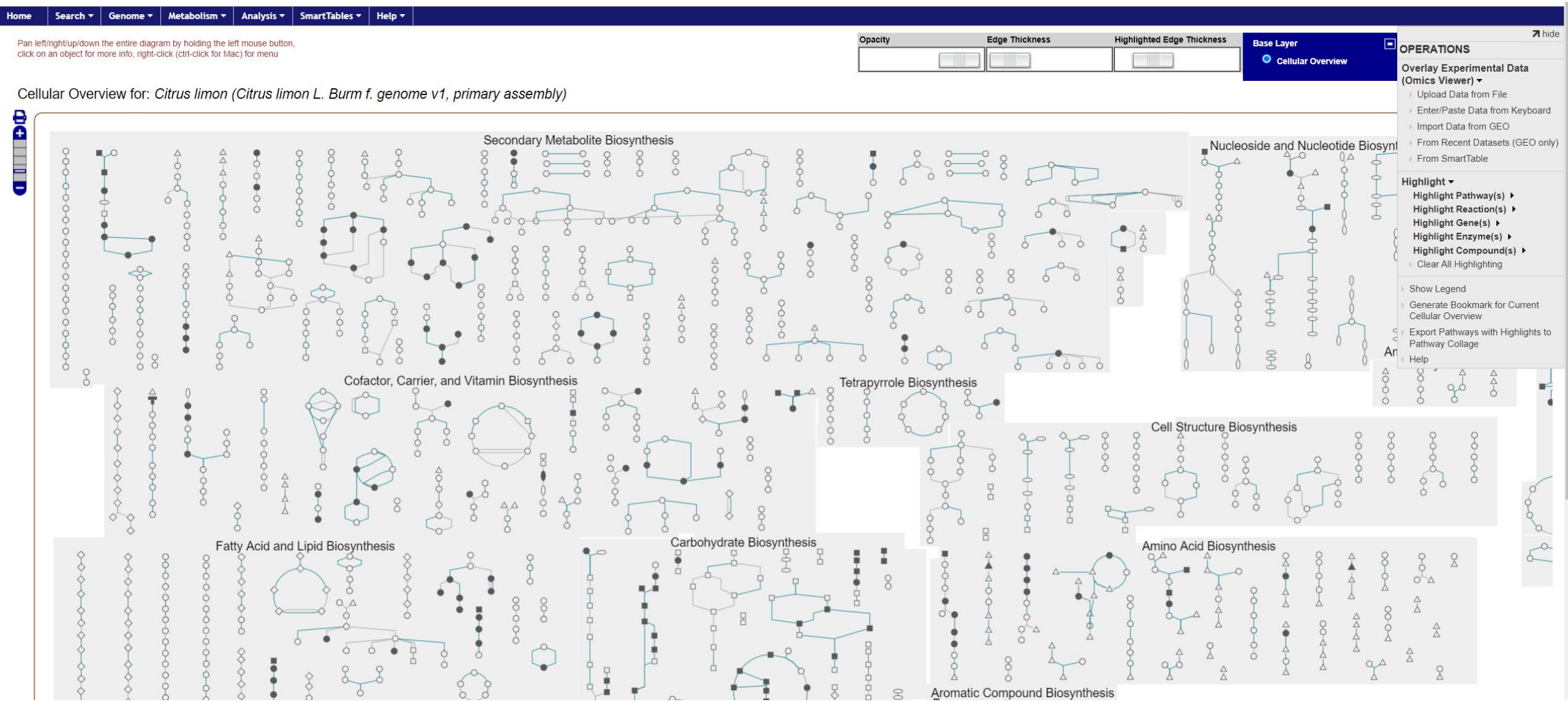

LG1 of map Citrus-Chandler-Ref-F1
Map Detail
To zoom in, drag the mouse across the linkage group
LG4 of map Citrus-Guanxi/Pingshan-Integrated-F1-2015
Map Detail
To zoom in, drag the mouse across the linkage group
CX2019
Cax...P460
CF-TA10
JI-...AG01
CiB...3936
CF-GA08
MAST121
CF-AG04
CX6F08
JI-GA01
MEST401
MEST321
MEST080
cM
JI-GA01
CF-CAT07
MEST401
MEST431
MEST321
MEST080
chr4_3081596
chr4_2912704
chr4_2680262
chr4_2659650
chr4_2336944
chr4_2866715
JI-GA01
chr4_1674994
chr4_2352448
chr4_1240941
chr4_2132544
chr4_1508948
chr4_1265248
chr4_1761858
chr4_947929
chr4_970222
chr4_825563
chr4_1088184
chr4_881574
chr4_547054
chr4_460712
MEST080
CX2019
chr...7194
chr...2469
chr...9167
chr...1679
chr...2676
chr...3902
chr...0806
chr...2649
chr...1913
chr...2367
chr...0262
chr...0941
chr...8184
chr...0712
cM
SNP
SSR

Genome Tools

- JBrowse to view the genome assemblies and annotations
- BLAST to search the genome scaffolds, mRNA, CDS, protein sequences and transcriptome sequences
- Expression Heatmap tool to view transcriptome data



CitrusCyc



www.citrusgenomedb.org

Synteny Viewer

Search Syntenic Blocks

Search blocks by a given location.

Organism Type

omes Plant

Genome:

Citrus limon L. Burm f. genome v1.0 - Primary

Chromosome/Scaffold:

Chr01_pri

Choose (a) genome(s) for comparison:

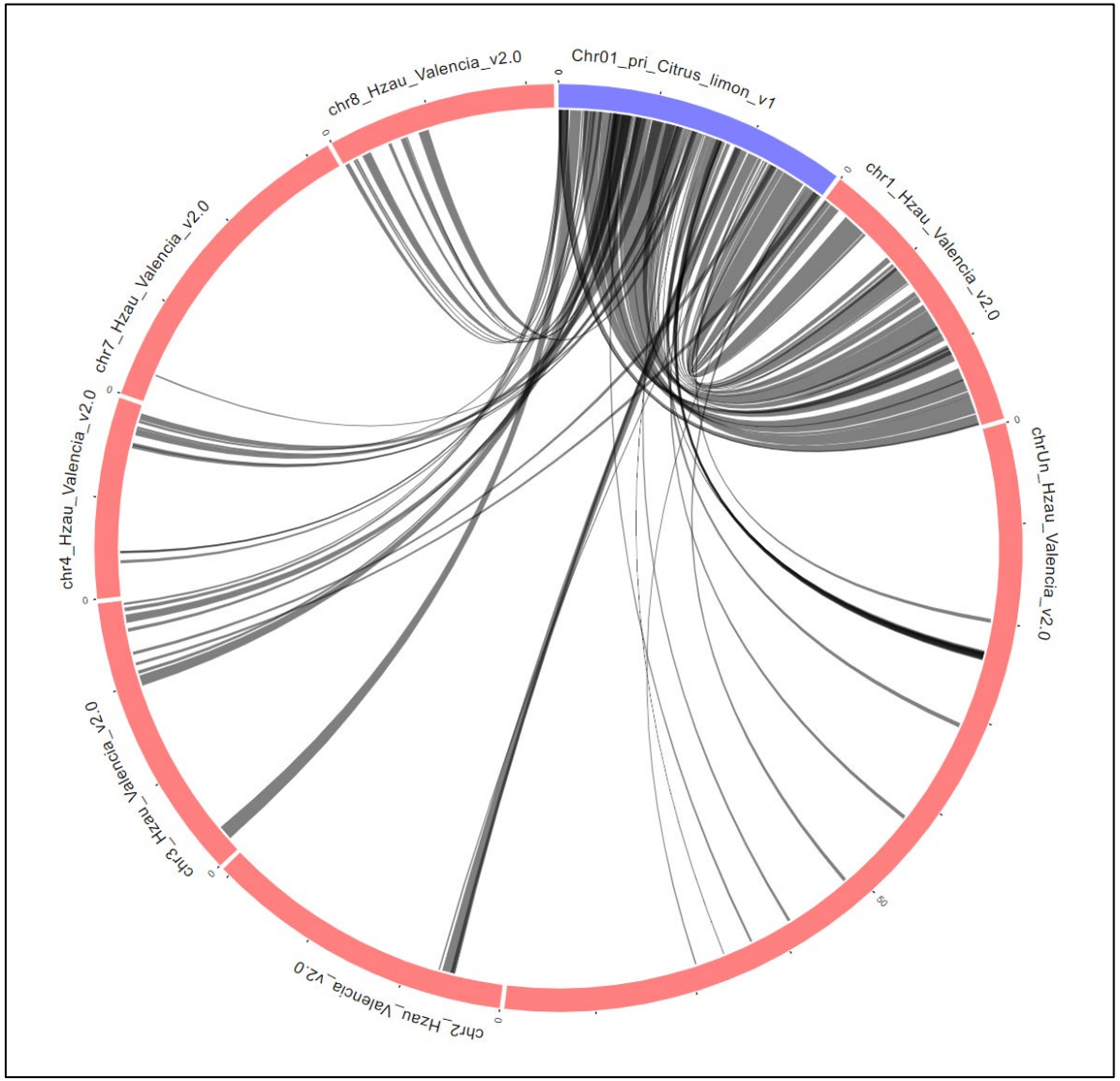
- [ ] Citrus clementina genome v1.0 (JGI)
- [ ] Citrus limon L. Burm f. genome v1.0 - Alternative
- [ ] Citrus limon L. Burm f. genome v1.0 - Primary
- [ ] Citrus maxima (C. grandis) genome v1.0
- [ ] Citrus sinensis genome v1.1 (JGI)
- [x] Citrus sinensis genome v2.0 (HZAU)
- [ ] Fortunella hindsii genome v1.0
- [ ] Poncirus trifoliata genome v1.3.1 (JGI)

or

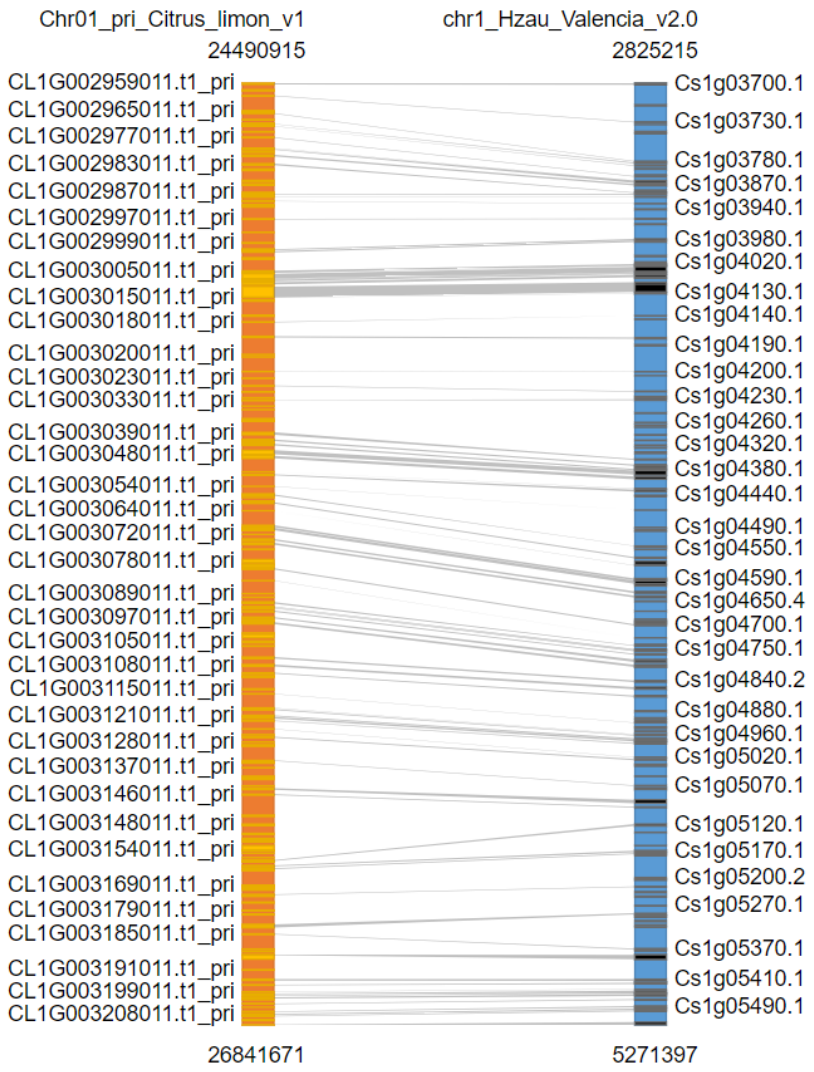
Search a block by its ID.

Example: 'cccmB003' or 'cmcsiB100'

Search



Synteny Viewer



Gene A
CL1G002959011
CL1G002961011
CL1G002962011
NA
NA
CL1G002964011
CL1G002965011
CL1G002966011
NA
NA
NA
CL1G002967011
CL1G002969011
CL1G002970011
NA
CL1G002971011
CL1G002972011
CL1G002973011

CL1G002959011.t1_pri

- Transcript Overview
- Alignments
- Analyses
- Annotated Terms
- Homology
- InterPro
- Relationships
- Sequences

Annotated Terms

The following terms have been associated with this mRNA:

Vocabulary: **INTERPRO**

Term	Definition
IPR006685	MscS_channel
IPR023408	MscS_dom_sf
IPR016688	MscS-like_plants/fungi
IPR010920	LSM_dom_sf

Vocabulary: **Cellular Component**

Term	Definition
GO:0016020	membrane

Vocabulary: **Biological Process**

Term	Definition
GO:0055085	transmembrane transport

Ortholog/Paralog Search

Ortholog/Paralo

Retrieve orthologs/paralo
assemblies/annotations o
mRNAs are not available.

Genome

Chromosome/Scaffold

Gene/Transcript Name

Compare to

Chromosome/Scaffold

Search Reset

1280 records were returned

Download Table

#	Genome1	Chromosome/Scaffold1	Ortholog/Paralog1	Genome2	Chromosome/Scaffold2	Ortholog/Paralog2	Associated Gene
1	Citrus limon L. Burm f. genome v1.0 - Primary	Chr01_pri	CL1G000004011.t1_pri	Citrus sinensis genome v2.0 (HZAU)	chr1	Cs1g26860.2	Cs1g26860
2	Citrus limon L. Burm f. genome v1.0 - Primary	Chr01_pri	CL1G000006011.t1_pri	Citrus sinensis genome v2.0 (HZAU)	chr1	Cs1g26850.1	Cs1g26850
3	Citrus limon L. Burm f. genome v1.0 - Primary	Chr01_pri	CL1G000007011.t1_pri	Citrus sinensis genome v2.0 (HZAU)	chr1	Cs1g26840.1	Cs1g26840
4	Citrus limon L. Burm f. genome v1.0 - Primary	Chr01_pri	CL1G000009011.t1_pri	Citrus sinensis genome v2.0 (HZAU)	chr1	Cs1g26820.1	Cs1g26820
5	Citrus limon L. Burm f. genome v1.0 - Primary	Chr01_pri	CL1G000010011.t1_pri	Citrus sinensis genome v2.0 (HZAU)	chr1	Cs1g26810.1	Cs1g26810
6	Citrus limon L. Burm f. genome v1.0 - Primary	Chr01_pri	CL1G000011011.t1_pri	Citrus sinensis genome v2.0 (HZAU)	chr1	Cs1g26800.1	Cs1g26800
7	Citrus limon L. Burm f. genome v1.0 - Primary	Chr01_pri	CL1G000013011.t1_pri	Citrus sinensis genome v2.0 (HZAU)	chr1	Cs1g26790.1	Cs1g26790
8	Citrus limon L. Burm f. genome v1.0 - Primary	Chr01_pri	CL1G000016011.t1_pri	Citrus sinensis genome v2.0 (HZAU)	chr1	Cs1g26780.1	Cs1g26780
9	Citrus limon L. Burm f. genome v1.0 - Primary	Chr01_pri	CL1G000018011.t1_pri	Citrus sinensis genome v2.0 (HZAU)	chr1	Cs1g26770.1	Cs1g26770
10	Citrus limon L. Burm f. genome v1.0 - Primary	Chr01_pri	CL1G000020011.t1_pri	Citrus sinensis genome v2.0 (HZAU)	chr1	Cs1g26760.1	Cs1g26760
11	Citrus limon L. Burm f. genome v1.0 - Primary	Chr01_pri	CL1G000022011.t1_pri	Citrus sinensis genome v2.0 (HZAU)	chr1	Cs1g26750.1	Cs1g26750
12	Citrus limon L. Burm f. genome v1.0 - Primary	Chr01_pri	CL1G000025011.t1_pri	Citrus sinensis genome v2.0 (HZAU)	chr1	Cs1g26740.1	Cs1g26740

BIMS

- Breeding Information Management System
- Tool to manage private breeding programs with multiple users via user accounts
  - Traits
  - Locations
  - Crosses
  - Accessions
  - Trials
- Compatible with Android Field Book App for digital data collection
- Citrus phenotype data from USDA-GRIN available to all users (no account required)

BIMS

Citrus-GRIN | Program | Hello Anonymous | Site Home | Log in

- About BIMS
- Help
- Manage Breeding
  - Program
  - Trait
  - Location
  - Cross
  - Accession
  - Trial
- Search
- Field Book Management
- Data Analysis

Manage Trait

Instructions

To create a trait descriptor, expand 'Trait Admin Menu' and click 'Add'. Trait descriptor data in file can also be loaded in 'Data Import' section (trait data in the template) or in 'Field Book Management' section (trait data in .trt file downloaded from the Field Book App). If you click one of the trait descriptors on the left, you can see the details of the trait as well as statistics of the trait values of all the accessions in your program. You can delete the trait descriptor by clicking 'Delete' but all the trait values for the trait descriptors will be deleted as well. You can edit the details of the trait descriptor such as trait name, format and definition by clicking 'Edit'.

Traits

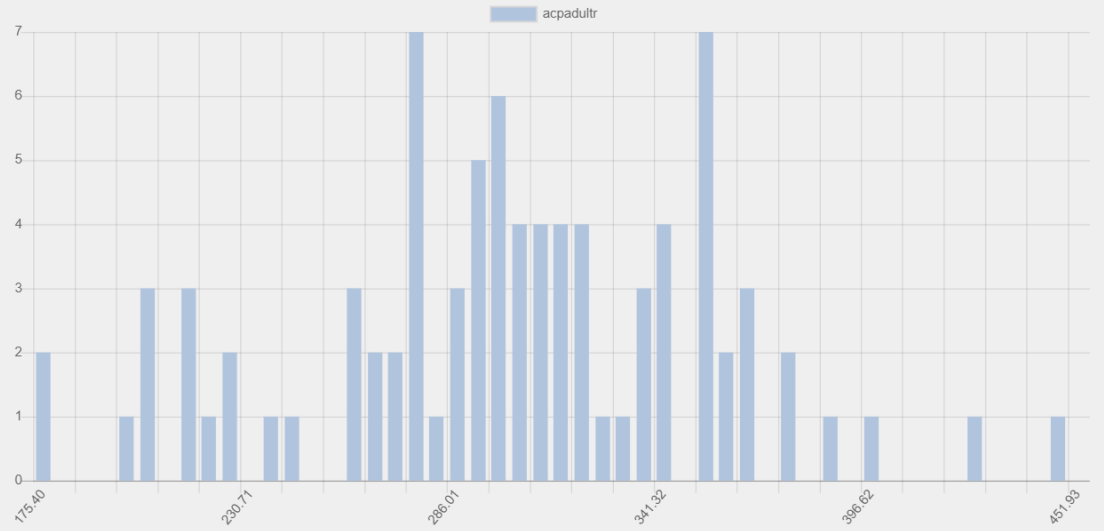
acpadultm
acpadultr
acpeggm
acpeggr
acpnymphm
acpnymphr
aroma
epicarpadh
epicarptex
flav
fruitaxmat
fruitaxrip
fruitcolor
fruitlngth

Click a trait to see the details.

Trait Details

*Click **here** to go Data Analysis → Statistical Analysis to view stats from multiple datasets.*

Name	acpadultr
Alias	*N/A*
Format	numeric
Definition	This is a statistical measurement calculated as the F-approximation of the Friedman test (Ipe 1987) and the associated Rank Sum multiple comparison test (PROC GLM, SAS Institute 2008).
# data points	86



# Data	Min	Max	Mean	STD

Funding and Acknowledgements

Citrus Research Community

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