

# GENOME DATABASE FOR ROSACEAE



Resources for Rosaceae Research Discovery and Crop Improvement

July 2022

Welcome to the July 2022 issue of the GDR newsletter. This newsletter is issued to inform users about **new or updated data and tools in GDR**. In addition to new and updated data, each issue will provide more detailed information in the specific **featured tool/data** section.

## New Genome Assemblies

Data from **three whole genome assemblies of *Fragaria* and the whole genome assembly of the cultivated hawthorn** have been added to GDR this past quarter. Access data from [Gene Search](#), [MegaSearch](#), [Synteny Viewer](#), [JBrowse](#), [BLAST](#) as well as the individual genome pages linked below.

- [Fragaria vesca Yellow Wonder](#)
- [Fragaria x ananassa FL15.89-25](#)
- [Fragaria chiloensis](#)
- [cultivated hawthorn Crataegus pinnatifida var. major](#)

## Updated corresponding Matrices in MapViewer

View the Correspondence Matrix and browse correspondences between genetic maps

When the Submit button is clicked, a new correspondence matrix page will appear to allow browsing correspondence between species and one genetic map.

Species:  Map:

Compare To

Species:  Map:

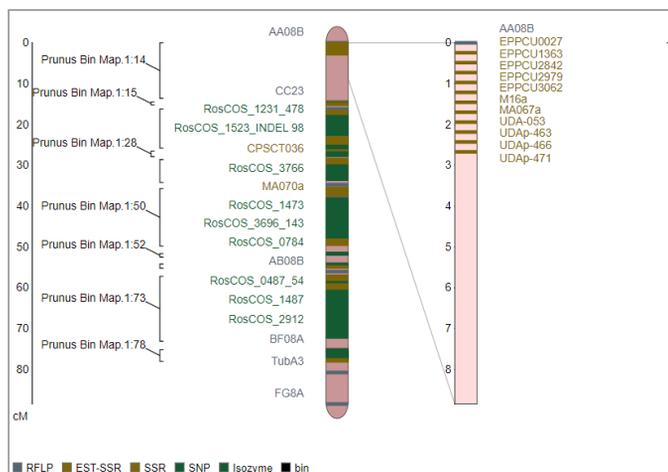
View the Correspondence Matrix and browse correspondences between whole genomes and maps

When the Submit button is clicked, a new correspondence matrix page will appear to allow browsing correspondence between

Whole Genome:

## New Bin Map display in MapViewer

- [Example bin map](#)
- [Example page of a bin and associated markers](#)



### Matrix between genetic maps

Prunus-TxE-peachV2.0

	LG1	LG2	LG3	LG4	LG5	LG6	LG7	LG8
Prunus Bin Map	156	92	102	62	92	114	108	100
Prunus-TE-F2	124	120	52	112	116	108	96	44

### Matrix between the whole genome and maps

Malus x domestica GDDH13 v1.1 Whole Genome Assembly & Annotation

	Chr00_GDDH13v1.1	Chr01_GDDH13v1.1	Chr02_GDDH13v1.1	Chr03_GDDH13v1.1	Chr04_GDDH13v1.1	Chr05_GDDH13v1.1	Chr06_GDDH13v1.1
Apple-BB-F1	62	559	1002	668	1147	1218	814
Apple-B-F1-2014	0	5	12	11	9	4	5

## More tutorial videos are available

[How to use MegaSearch for QTL](#) and [How to use BLAST](#) short tutorials were made available this past quarter. Go to [the manual page](#) or our [YouTube channel](#).

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## Featured Data and Tools

### New GDR search interfaces

A couple years ago, we added [MegaSearch](#) to GDR. MegaSearch was an additional way for users to search the data in GDR and also allowed further refinement to the displayed/downloaded search results over the traditional searches on GDR.

Since [MegaSearch](#) works so well, we have decided to transition most searches within GDR to MegaSearch. Not only is this an improvement in database usability, but also helps GDR run more efficiently which will help with performance.

If you have used some of the GDR searches in the past month, you probably noticed a change in the interfaces. We are still working on some of the searches, but MegaSearch is being used for the following data types:

- Genes and Transcripts
- Germplasm
- Genetic Maps
- Genetic Markers
- Publications
- QTL

Either click on the individual data search links, or select MegaSearch to start a search

### Tripal MegaSearch

Tripal MegaSearch is a tool for downloading biological data. (Current limit per download: 1000 records)  
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

Data Summary:

Data Type	Number of Records	Last Updated
Contact	374	02/22/2022
Gene/Transcript	8156048	07/12/2022
Germplasm	22571	02/22/2022
Map	387	07/14/2022
Marker	4260647	06/23/2022
Publication	9819	07/14/2022
QTL	4353	02/22/2022

# MegaSearch Interfaces

## Genes and Transcripts

[Watch the video!](#)

The image displays four overlapping screenshots of the MegaSearch web application interface, each representing a different search category. Each screenshot includes a 'Data Type' dropdown, a 'Reset' button, and a 'Downloadable Fields' panel on the right. The 'Gene/Transcript' interface shows search criteria like 'Sequence Type', 'Genome', and 'Chromosome/Scaffold'. The 'Germplasm' interface features an 'Organism' dropdown and a 'Name' search field. The 'QTL' interface includes a 'Type' dropdown and a 'Trait' search field. The 'Marker' interface has a 'Marker Type' dropdown and a 'Marker Name' search field. Each interface also includes a 'Query' section with various filters and a 'Downloadable Fields' panel with checkboxes for fields like 'Name', 'Accession', 'Map', and 'Start'. A blue callout box with the text 'Watch the video!' is overlaid on each screenshot.

### Germplasm

### QTL [Watch the video!](#)

### Genetic Maps

### Genetic Markers

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