

# GENOME DATABASE FOR ROSACEAE



Resources for Rosaceae Research Discovery and Crop Improvement

October 2022

Welcome to the October 2022 issue of the GDR newsletter. This newsletter is issued to inform users about **new or updated data and tools in GDR**, and provide a summary from the quarterly Rosaceae Executive Committee (RosEXEC) meetings.

## New funding for GDR!

[New funding support from the USDA SCRI](#): Enabling genomic-assisted specialty crop breeding and research through advance database resources!

## Summary of RosEXEC meetings!

Our newsletter now provides a summary from the quarterly RosEXEC meetings! Check page 3!

## Registration for RGC11 Open!

Registration for RGC11 is now open. RGC11 will be held in Nelson, NZ on 13-16 March 2023. See the [website](#) to register, submit abstracts, etc.

## New tutorial videos available

[How to use MegaSearch for Genetic Maps](#) and [How to go from BLAST to mRNA details to JBrowse](#) short tutorials were made available this past quarter. See [the manual page](#) or our [YouTube channel](#).

## New Genome Assemblies

Data from **7 whole genome assemblies of Fragaria, Malus, Prunus, Pyrus, and Rubus** 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 x ananassa Florida Brilliance](#)
- [Fragaria x ananassa FL15.89-25](#)
- [Malus x domestica Honeycrisp](#)
- [Prunus dulcis Nonpareil](#)
- [Prunus humilis](#)
- [Pyrus communis d'Anjou](#)
- [Rubus idaeus Joan J](#)

## New Trait and Trait Descriptor Search

Now available: User [Trait Search](#) to find standardized trait terms using categories or keyword to access all the data associated with the trait term. Alternatively use the [Trait Descriptor Search](#) to find trait descriptors in publicly available phenotyping datasets and access associated data. [BIMS](#) also allows you to access publicly available phenotype data.

## Updated Trait Page

Access all the associated data from [a trait page](#) such as QTLs, Haplotype blocks, trait descriptors, publications, and phenotyping datasets.

Group	Descriptor
GRIN_APPLE	FRTFLSHFRM
GRIN_PFLUM	FIRMNESS
GRIN_RUBUS	FIRMNESS
GRIN_STRAWBERRY	FLESHFIRM
GRIN_APRICOT	FIRMNESS
GRIN_PEACH	FIRMNESS
STRAWBERRY_CRS	FRUIT_FIRMNESS
STRAWBERRY_CRS	SKIN_FIRMNESS
SWEET_CHERRY_CRS	Bulked_Fruit_Firmness
SWEET_CHERRY_CRS	Firmness_1
TART_CHERRY_CRS	Firmness
TART_CHERRY_CRS	Firmness_Firmtech

QTL/MTL	Linkage Group	Peak	Start	Stop	Dataset	MapViewer
GR-4.7-13	LG4	-	26.8	34.1	na	View
HB-C	Chr02	-	24.76	28.94	na	View
HB-D	Chr02	-	28.97	29.54	na	View
HB-E	Chr02	-	29.58	35.11	na	View
HB-F	Chr02	-	37.73	42.93	na	View
qFRFRM.232x1392-ch2F8.2009	VII-F.1	39.64	-	-	Agronomical and fruit quality traits-Amaya-2011	View
qFRFRM.232x1392-ch1F1.2009	VII-F.1	39.64	-	-	Agronomical and fruit quality traits-Amaya-2011	View
qFRFRM.A-ch1.1-Y1	1	-	60.3	76.29	SweetCherry-Firmness&Dimension-Wunsch-2020	View

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## Featured Data and Tools

### Ortholog/Paralog Search

#### Did you know?

You can retrieve customized information on

[Orthologs/paralogs in MegaSearch](#). So now you can choose data fields to view and download.

Data Type:

8,344 Ortholog/Paralog. Note: actual rows in downloaded file depend on the selected fields.

Query

Genome:

Chromosome/Scaffold:

Start:

Stop:

Gene/Transcript Name:

No file chosen

Compare to:

Chromosome/Scaffold:

Downloadable Fields

- All Fields
- Genome1
- Chromosome1
- Location1
- Ortholog1
- Genome2
- Chromosome2
- Location2
- Ortholog2
- Associated Gene

#### Did you know?

You can also use this tool to generate a list of matching genes (and true paralogs) between two genome assemblies of the same species.

Genome1	B	C	Ortholog1	D	Genome2	E	F	G	H
Malus x domestica GDDH13 v1.1	Chr01	MD01G1011600	Ortholog1	MD01G1011700	Malus x domestica Genome v1.0 NCBI annotation	NC_024252.1	XM_017937379.1	LOC103454238	
Malus x domestica GDDH13 v1.1	Chr01	MD01G1011800	Ortholog1	MD01G1012000	Malus x domestica Genome v1.0 NCBI annotation	NC_024252.1	XM_008393790.2	LOC103454197	
Malus x domestica GDDH13 v1.1	Chr01	MD01G1012100	Ortholog1	MD01G1012300	Malus x domestica Genome v1.0 NCBI annotation	NC_024252.1	XM_008393791.2	LOC103454199	
Malus x domestica GDDH13 v1.1	Chr01	MD01G1012400	Ortholog1	MD01G1012600	Malus x domestica Genome v1.0 NCBI annotation	NC_024252.1	XM_017322456.1	LOC103454201	
Malus x domestica GDDH13 v1.1	Chr01	MD01G1012700	Ortholog1	MD01G1012900	Malus x domestica Genome v1.0 NCBI annotation	NC_024252.1	XM_017322453.1	LOC103454241	
Malus x domestica GDDH13 v1.1	Chr01	MD01G1013000	Ortholog1	MD01G1013200	Malus x domestica Genome v1.0 NCBI annotation	NC_024252.1	XM_008393795.2	LOC103454203	
Malus x domestica GDDH13 v1.1	Chr01	MD01G1013400	Ortholog1	MD01G1013600	Malus x domestica Genome v1.0 NCBI annotation	NC_024252.1	XM_008393796.2	LOC103454204	
Malus x domestica GDDH13 v1.1	Chr01	MD01G1013700	Ortholog1	MD01G1013900	Malus x domestica Genome v1.0 NCBI annotation	NC_024252.1	XM_008393797.2	LOC103454205	
Malus x domestica GDDH13 v1.1	Chr01	MD01G1014000	Ortholog1	MD01G1014200	Malus x domestica Genome v1.0 NCBI annotation	NC_024252.1	XM_008393798.2	LOC103454206	

Downloaded file of GDDH13 genes and corresponding NCBI annotated M. x domestica v1.0 gene names

**Did you know?** Orthologs/paralogs in GDR are detected using MCSanX. Visit gene pages to see orthologs/paralogs and syntenic blocks in all other genomes.

Prupe.1G000100.1, Prupe.1G000100.1\_v2.0.a1 (mRNA) Prunus persica

View Edit Reload

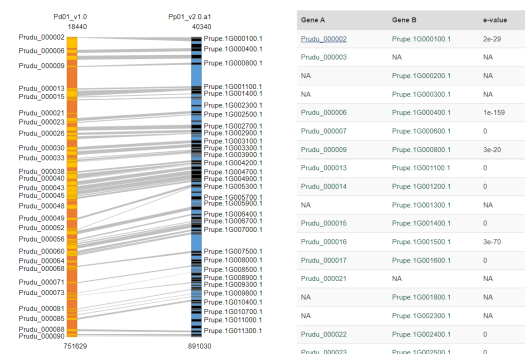
Transcript Overview

- Alignments
- Analyses
- Annotated Terms
- Homology
- InterPro
- Relationships**
- Sequences

Relationships

This mRNA is member of the following **syntenic\_region** feature(s):

Feature Name	Unique Name	Species	Type
fmappR302	fmappR302	Prunus persica	syntenic_region
mdppR456	mdppR456	Prunus persica	syntenic_region
fvppR165	fvppR165	Prunus persica	syntenic_region
pprol038	pprol038	Prunus persica	syntenic_region
pappR002	pappR002	Prunus persica	syntenic_region



#### Did you know?

Now checkbox is available in the result table so that you can choose the results to download.

#	Genome1	Chromosome1	Ortholog1	Genome2	Chromosome2	Ortholog2	Associated Gene
1	<input checked="" type="checkbox"/> Fragaria vesca Whole Genome v4.0 a1 Assembly & Annotation	Fvb1_v4.0.a1	FvH4_1g00010.11	Fragaria x ananassa Camarosa Genome Assembly v1.0 & Annotation v1.0 a1	Fvb1-1	maker-Fvb1-1-augustus-gene-274.109-mRNA-1	maker-Fvb1-1-augustus-gene-274.109
2	<input checked="" type="checkbox"/> Fragaria vesca Whole Genome v4.0 a1 Assembly & Annotation	Fvb1_v4.0.a1	FvH4_1g00020.112	Fragaria x ananassa Camarosa Genome Assembly v1.0 & Annotation v1.0 a1	Fvb1-1	maker-Fvb1-1-snap-gene-274.162-mRNA-1	maker-Fvb1-1-snap-gene-274.162
3	<input checked="" type="checkbox"/> Fragaria vesca Whole Genome v4.0 a1 Assembly & Annotation	Fvb1_v4.0.a1	FvH4_1g00020.112	Fragaria x ananassa Camarosa Genome Assembly v1.0 & Annotation v1.0 a1	Fvb1-3	maker-Fvb1-3-augustus-gene-2.40-mRNA-1	maker-Fvb1-3-augustus-gene-2.40
4	<input checked="" type="checkbox"/> Fragaria vesca Whole Genome v4.0 a1 Assembly & Annotation	Fvb1_v4.0.a1	FvH4_1g00030.02	Fragaria x ananassa Camarosa Genome Assembly v1.0 & Annotation v1.0 a1	Fvb1-1	maker-Fvb1-1-augustus-gene-274.124-mRNA-1	maker-Fvb1-1-augustus-gene-274.124
5	<input checked="" type="checkbox"/> Fragaria vesca Whole Genome v4.0 a1 Assembly & Annotation	Fvb1_v4.0.a1	FvH4_1g00030.02	Fragaria x ananassa Camarosa Genome Assembly v1.0 & Annotation v1.0 a1	Fvb1-3	maker-Fvb1-3-augustus-gene-2.41-mRNA-1	maker-Fvb1-3-augustus-gene-2.41
6	<input checked="" type="checkbox"/> Fragaria vesca Whole Genome v4.0 a1 Assembly & Annotation	Fvb1_v4.0.a1	FvH4_1g00040.11	Fragaria x ananassa Camarosa Genome Assembly v1.0 & Annotation v1.0 a1	Fvb1-1	maker-Fvb1-1-augustus-gene-274.108-mRNA-1	maker-Fvb1-1-augustus-gene-274.108
7	<input checked="" type="checkbox"/> Fragaria vesca Whole Genome v4.0 a1 Assembly & Annotation	Fvb1_v4.0.a1	FvH4_1g00040.11	Fragaria x ananassa Camarosa Genome Assembly v1.0 & Annotation v1.0 a1	Fvb1-3	maker-Fvb1-3-augustus-gene-2.47-mRNA-1	maker-Fvb1-3-augustus-gene-2.47
8	<input type="checkbox"/> Fragaria vesca Whole Genome v4.0 a1 Assembly & Annotation	Fvb1_v4.0.a1	FvH4_1g00050.11	Fragaria x ananassa Camarosa Genome Assembly v1.0 & Annotation v1.0 a1	Fvb1-1	maker-Fvb1-1-augustus-gene-274.107-mRNA-1	maker-Fvb1-1-augustus-gene-274.107

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USDA SCRI and NRSP10 (National Research Project)

Very interesting information was shared at the U.S. RosEXEC meeting in October. Here's a quick overview!

## Administrative

- As a way to quickly inform our community of the happenings in RosEXEC, these summarized updates will be added to the GDR quarterly newsletter. So, here we go!
- Per McCord from WSU was elected Secretary of RosEXEC, and he joined us in June. Welcome!
- New elections for RosEXEC membership will be held in Fall 2023, are you running?
- The next RosEXEC quarterly meeting will be during PAG in January 2023! Stay tuned for more information in the GDR mailing list!
- Talking about the GDR mailing list, please join so you receive fresh information on all the developments in GDR and RosEXEC! To do so, click [here](#). We will stay in touch!

## GDR insights

- Several new resources including tutorials, updated interfaces, and 7 genomes(!) have recently been posted in GDR. Take a [look](#) and enjoy the bounty!

## Future plans

- RosEXEC will facilitate the coordination of taskforces and subcommittees to encourage community participation, collaboration, and improved access to resources. We will provide information about these opportunities through these communications and GDR. Stay tuned!

## Announcements for specific crops: choose your favorite!

- Genome databases received [support from SCRI](#), including GDR! [Dorrie Main](#) & [Sook Jung](#) can provide you with the latest info on it!
- Saving roses! New SCRI funded project on diseases in rose. Learn more about it [here](#).
- Strawberries gained some love too! SCRI has funded a project (PI: Steve Knapp) tackling disease resistance, breeding, and management.
- Interested in the genomic composition of NPGS apples representing wild species? This [paper](#) is going to be of interest to you. [Gayle](#) will look forward to telling you more about it!
- Not only the [nuclear genome, but plastids](#) also have a say on the origin of apples.
- Looking for some pear? The [d'Anjou pear genome is in GDR!](#) Contact [Loren Honaas](#) if you need more information.

## Engagement with the Rosaceae community (What you can do? / How to get involved?)

- Interested in visualizing large/complex gene expression datasets in JBrowse and other visualization tools on GDR? [Loren Honaas](#), [Chris Gottschalk](#) and [Sook Jung](#) too! Do not hesitate to contact them if you want to be part of this task force!
- Do you have ideas or interests that benefit the Rosaceae community? Do not hesitate to get involved with RosEXEC and GDR and form a task force. You can contact [Gayle Volk](#), current Chair of RosEXEC, [Jonathan Fresnedo Ramirez](#), current vice-chair, or [Per McCord](#), current secretary. We are looking forward to hearing from you!