

GENOME DATABASE FOR ROSACEAE



Resources for Rosaceae Research Discovery and Crop Improvement

April 2022

Welcome to the April 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 **8 whole genome assemblies of Malus, Prunus, Pyrus, Rosa 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.

- [Malus prunifolia Fupingqiuzi](#)
- [Prunus persica Zhongyoutao 14](#)
- [Prunus persica 124 Pan](#)
- [Prunus avium Big Star](#)
- [Prunus mume Tortuosa](#)
- [Pyrus pyrifolia Cuiguan](#)
- [Rosa wichuraiana Basye's Thornless](#)
- [Rubus idaeus Anitra](#)

New Search Ortholog and Paralog

[Retrieve orthologs/paralogs](#) that are detected using MCSScanX. You can choose a genome or upload a subset of genes and then choose another genome to compare to. You can also use this tool to generate a list of matching genes (and true paralogs) between two genome assemblies of the same species.

Search Orthologs and Paralogs

Retrieve orthologs/paralogs that are detected using MCSScanX (Wang et al. 2012) using default settings. Sequences in ortholog/paralog columns between different assemblies/annotations of the same species represents potentially the same genes. In most cases, mRNA transcripts were used in the analysis and genes were used only when mRNAs are not available. The result table provides associated gene names as well.

Genome:

Chromosome/Scaffold:

Gene/Transcript Name: No file chosen

Compare to:

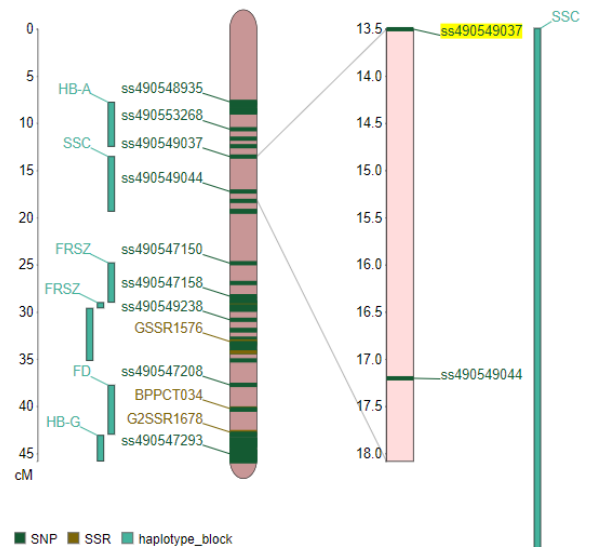
Chromosome/Scaffold:

763 records were returned

#	Genome1	Chromosome/Scaffold1	Ortholog/Paralog1	Genome2	Chromosome/Scaffold2	Ortholog/Paralog2	Associated Gene
1	Malus x domestica GDDH13 v1.1 Whole Genome Assembly & Annotation	Chr01	MD01G1025300	Malus x domestica Genome v1.0 NCBI annotation	NC_024239.1	XM_008368969.2	LOC103430537

New QTL, marker, map, and haplotype data available

[New marker, map, QTL and haplotype data](#) available for apple, apricot, plum, pear, rose, strawberry and sweet cherry. View data in [QTL Search](#), [Haplotype Block Search](#) (choose Sweet_Cherry-Cai-Haplotype-2017 under Dataset), and in [MapViewer](#).



Chr02 of map Sweet Cherry-QTL-HotSpot-Chr2-2017

New filter in Search Nearby Marker

In [Search Nearby Markers](#), you can retrieve a list of all loci that are within a specified distance of the locus on any genetic map. You can now restrict the data by marker type (e.g., SSR).

More tutorial videos are available

[How to use MapViewer](#) and [How to use Marker](#) 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

Marker Search in MegaSearch

Did you know? You can retrieve customized information on markers in MegaSearch. Choose 'Marker' data type in [MegaSearch](#).

The MegaSearch interface includes a 'Query' section with dropdowns for Marker Type, Marker Name, SNP Array Name, Organism, Mapped in Organism, and Developed in Organism. It also has input fields for Genome location (Genome, Chromosome/Scaffold, Start, Stop) and Genetic location (Map, Linkage Group, Start, Stop). A 'Downloadable Fields' section on the right allows users to select fields like Unique Name, Marker Name, Organism, etc. Checkboxes at the bottom indicate 'Has Marker Primer' and 'Has Marker Sequence'.

You can filter the markers and choose what you want to download such as genome positions and primer sequences.

1290 records were returned

#	Unique Name	Genome	Landmark	Genome Position (Start)	Primers
1	BPPCT016	Prunus persica Whole Genome Assembly v2.0 & Annotation v2.1 (v2.0.a1)	Pp01	37047997	Reverse primer:GAGGATTCATGATTTGTGGR primer:GAGGATTCATGATTTGTGCF primer:GATTGAGAGATTGGGCTGCJForward primer:GATTGAGAGATTGGGCTGC
2	BPPCT020	Prunus persica Whole Genome Assembly v2.0 & Annotation v2.1 (v2.0.a1)	Pp01	34255110	R primer:ATTGACGCTGGACTACAGGTQJF primer:CGTGGATGTCAGGATGC
3	BPPCT027	Prunus persica Whole Genome Assembly v2.0 & Annotation v2.1 (v2.0.a1)	Pp01	34014917	Forward primer:CTCTCAAGCATCATGGGCR primer:TGTTGCCCGGTTGTAATATCJReverse primer:TGTTGCCCGGTTGTAATATCJF primer:CTCTCAAGCATCATGGGC
4	BPPCT028	Prunus persica Whole Genome Assembly v2.0 & Annotation v2.1 (v2.0.a1)	Pp01	44130041	R primer:GAGCTTGGCTATGAGAAGCCJF primer:TCAAGTACGCTGAAGATCGCReverse primer:GAGCTTGGCTATGAGAAGCCJForward primer:TCAAGTACGCTGAAGATCGC

View the result in the page or download a file

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Retrieve sequences around Markers

Did you know? You can retrieve sequences around markers in [Marker Search](#)

The Marker Search interface includes dropdowns for Marker Name, Marker Type, Marker Mapped in Species, and Marker Developed from Species. It also has input fields for Genome, Chr/Scaffold, Map, Linkage Group, and Trait Name. A 'Sequence retrieval' section at the bottom has checkboxes for Upstream bases and Downstream bases. A warning message states: 'Warning: this may take hours if too many sequences are being downloaded. Please do not start too sequence retrieval jobs at the same time. To create a job, specify upstream and downstream bases to include with the sequences. The job won't be started until the Download "Sequence Retrieval" link is clicked. (Limit for job creation: 5000 records)'. Search and Reset buttons are at the bottom.

Filter the markers or upload a file with marker names

Search Nearby Markers

Did you know? In [Search Nearby Markers](#), you can retrieve a list of all loci that are within a specified distance of the locus on any genetic map. Type in a marker or upload a file with marker names.

The Search Nearby Markers interface includes dropdowns for Marker Name, Locus, Marker Type, and Distance. It has input fields for Locus and Distance. A 'Search' and 'Reset' button are at the bottom. A warning message states: 'Warning: this may take hours if too many sequences are being downloaded. Please do not start too sequence retrieval jobs at the same time. To create a job, specify upstream and downstream bases to include with the sequences. The job won't be started until the Download "Sequence Retrieval" link is clicked. (Limit for job creation: 5000 records)'. Search and Reset buttons are at the bottom.

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