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
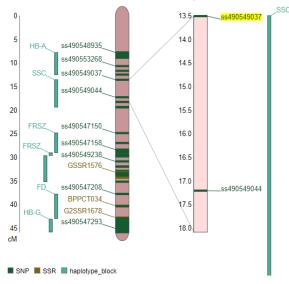- *Rubus idaeus* Anitra

New Search Ortholog and Paralog

Retrieve orthologs/paralogs that are detected using MCScanX. 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.

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.**

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.

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:GAGGATTCTCATGATTTGTGC|R primer:GAGGATTCTCATGATTTGTGC|F primer:GATTGAGAGATTGGGCTGC|Forward primer:GATTGAGAGATTGGGCTGC
2	BPPCT020	Prunus persica Whole Genome Assembly v2.0 & Annotation v2.1 (v2.0.a1)	Pp01	34255110	R primer:ATTGACGTGGACTTACAGGTG|F primer:CGTGGATGGTCAAGATGC
3	BPPCT027	Prunus persica Whole Genome Assembly v2.0 & Annotation v2.1 (v2.0.a1)	Pp01	34014917	Forward primer:CTCTCAAGCATCATGGGC|R primer:TGTTGCCCGGTTGTAATATC|Reverse primer:TGTTGCCCGGTTGTAATATC|F primer:CTCTCAAGCATCATGGGC
4	BPPCT028	Prunus persica Whole Genome Assembly v2.0 & Annotation v2.1 (v2.0.a1)	Pp01	44130041	R primer:GAGCTTGCCTATGAGAAGACC|F primer:TCAAGTTAGCTGAGGATCGC|Reverse primer:GAGCTTGCCTATGAGAAGACC|Forward primer:TCAAGTTAGCTGAGGATCGC

View the result in the page or download a file

Retrieve sequences around Markers

Did you know? You can retrieve sequences around markers in Marker Search.

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.

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