



GENOME DATABASE FOR VACCINIUM

Genomics, genetics, and breeding resources for blueberry, cranberry, bilberry, and lingonberry research

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What is GDV?

GDV is a centralized database for genomics, genetics, and breeding data and analysis tools for *Vaccinium* sp. Genome sequences are available to view and search and there is also information about genetic maps, molecular markers, and QTL. If you are a breeder who needs to manage a private breeding program data, access to the Breeding Information Management System (BIMS) can be requested through GDV. Visit us at www.vaccinium.org to see everything that is available. Each issue of the newsletter will focus on a different type of data and what features are available.

Updates to Genetic Data Resources

There have been a few improvements to the search interfaces for genetic data and MapViewer over the last few months.

Improved [Map Search](#) – Previously the map search was more of a filtering interface with only genus and species as the option, but now that we are using a MegaSearch interface users have numerous options on how to configure the search. Organism is still an option and the following have been added: map name, mapping population name, maternal parent name, paternal parent name, QTL labels, QTL traits, publication citation, and number of map LG and loci.

Data Type

38 Map. Note: actual rows in downloaded file depend on the selected fields.

Map Search Interface

Query

Organism

Map Name

Mapping population

Population

Maternal Parent

Paternal Parent

QTL

Publication

Size

Downloadable Fields

All Fields

Map Name

Description

Unit Type

Organism

Population

Maternal Parent

Paternal Parent

Number of LG

Number of Loci

Number of QTL

Publication

Expandable option fields

Select what is viewed/downloaded


Improved MapViewer Features


We have made it easier to download corresponding marker information and compare maps. From the 'Tools' menu, select 'MapViewer'. And then click on the 'View Correspondence Matrix and browse correspondences between genetic maps'. Two sets of pull-down menus appear, and you can select maps that have correspondences.

Once you click submit, a Correspondence Matrix appears with numbers that correspond to the number of corresponding markers between linkage groups. Clicking on the number opens the maps of the linkage groups so you can view them and download information on the corresponding markers and view a dot plot graph.

MapViewer Quick Start

MapViewer is a graphical tool for viewing and comparing genetic maps. It includes dynamically scrollable maps, correspondence matrices, dot plots, links to details about map features, and exporting functionality. It was developed by the MainLab at Washington State University and is available for download for use in other Tripal databases.

 Select a map and start using MapViewer


 View the Correspondence Matrix and browse correspondences between genetic maps

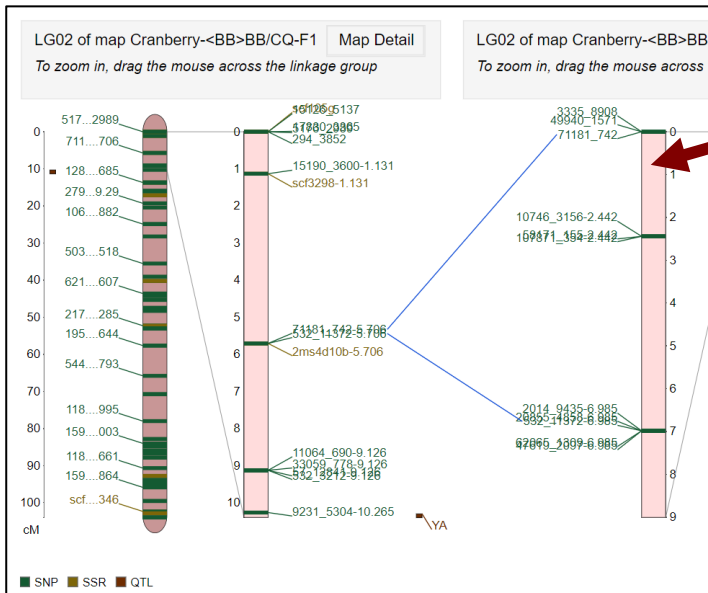
When the Submit button is clicked, a new correspondence matrix page will appear to allow browsing correspondence between two genetic maps or between all genetic maps in a species and one genetic map.

Species Map

Compare To
Species Map

Submit

 View the Correspondence Matrix and browse correspondences between whole genomes and



Cranberry-<BB>BB/US893-F1

	LG01	LG02	LG03	LG04	LG05	LG06	LG07	LG08	LG09	LG10	LG11	LG12
LG01	33	0	0	0	0	0	0	0	0	0	0	0
LG02	0	22	0	0	0	0	0	0	0	0	0	0
LG03	0	0	23	0	0	0	0	0	0	0	0	0
LG04	0	0	0	27	0	0	0	0	0	0	0	0
LG05	0	0	0	0	25	0	0	0	0	0	0	0
LG06	0	0	0	0	0	24	0	0	0	0	0	0
LG07	0	0	0	0	0	0	37	0	0	0	0	0
LG08	0	0	0	0	0	0	0	31	0	0	0	0
LG09	0	0	0	0	0	0	0	0	35	0	0	0
LG10	0	0	0	0	0	0	0	0	0	36	0	0
LG11	0	0	0	0	0	0	0	0	0	0	23	0
LG12	0	0	0	0	0	0	0	0	0	0	0	29

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