



GENOME DATABASE FOR VACCINIUM

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

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What's new in GDV?

New Training Videos

- [Marker search by trait and viewing genome position](#) (2:41 mins)
- [Cross-searching with gene or mRNA names](#) (1:41 mins)

New Data and Outreach

- 3,117 new QTL added from Maule et al. 2024. *Frontiers in Plant Science*. 15:1294570
- GDV and BIMS Workshop at 13th International Vaccinium Symposium

GDV and BIMS Training Workshop

We hosted a GDV and BIMS training workshop at the 13th International Vaccinium Symposium in August. Thanks to the 40 attendees who came and asked some great questions and learned how to use both these resources.

If you could not make it, the [workshop materials are available on GDV](#). On that webpage you will find the slides for both the GDV and BIMS sessions as well as the data files needed to work along with the GDV hands-on exercises.

If you want to learn more about how to use GDV and BIMS, please visit our [YouTube channel](#) and check out the [BIMS User Guide](#) and [GDV User Guide](#). If your program would like in-person or virtual training on these resources, that can also be arranged by [contacting us](#).

Also watch for updates to the GDV User Guide in the coming year. We will be making it more example driven. If there is any task or search process you want included, please let us know. We would like to tailor the guide to address the needs of our users with video examples of commonly used tasks.

QTL for Berry Quality and Yield

Last quarter more data from the [VacCAP project](#) became available on GDV. To read all the details, please see Maule et al., 2024, [Of Buds and Bits: A metaQTL Study Identifies Stable QTL for Berry Quality and Yield Traits in Cranberry Mapping Populations \(*Vaccinium macrocarpon* Ait.\)](#).

This study identified 22 meta-QTL for traits involved with berry shape, weight, yield, and color. In addition to these mQTL being stored in GDV, the other QTL identified in this massive study are also available to search in GDV.

These QTL also have positions on the [Cranberry Composite Map](#) and can be viewed with MapViewer. And as with all QTL, the data for the QTL and the map positions can be queried and retrieved using the [QTL/GWAS Search](#) and [Map Search](#).

The 3,117 QTL from this new study can also be visualized on the Cranberry Composite Map along with QTL from two previous studies. A previous study about [anthocyanin and chemical traits](#) yielded 113 QTL and another about [fruit shape and size](#) had 206 QTL.

New option in Gene and Transcript Search

Do you have gene names for a genome, but need the mRNA names? Or do you have mRNA names and need the gene names? We have a solution for you!

In the [Gene and Transcript Search](#), you can now cross-search using the gene or mRNA and retrieve data on the other. Let's say you have a list of differentially expressed genes and want to retrieve the functional annotations (which are associated with the mRNA in GDV), you can now search with the list of gene names and no longer need to convert the gene names to mRNA names.

Data Type: Gene/Transcript [Reset]

7,264,912 Gene/Transcript. Note: actual rows in downloaded file depend on the selected fields.

Query

Sequence Type: Any [Clear] [Refresh Count]

Genome

Genome Name: Any
Vaccinium caesariense clone W85-20 P0 v2.0 genome sequence
Vaccinium caesariense clone W85-20 P1 v2.0 genome sequence
Vaccinium corymbosum cv. Brigitta Blue v1.0 genome

Chromosome/Scaffold: Any

Start: > []

Stop: < []

Transcriptome/Other Dataset

Gene/Transcript name

Name: contains []

File Upload: Choose File No file chosen

Provide names in a file. Separate each name by a new line.

Also search associated mRNA/gene if the name in uploaded file matches a gene/mRNA

Functional Annotation

Downloadable Fields

View FASTA CSV TSV

Sequence retrieval

- All Fields
- Name
- Unique Name
- Organism
- Type
- Genome/Transcriptome
- Chromosome/Scaffold
- Start position
- Stop position
- Location
- BLAST
- InterPro
- GO Term
- GO Accession
- GenBank Keyword

Simply type the gene or mRNA in the box under the Gene/Transcript name section or upload a file of names and check the box. Then select the data you want to view or download in the right-hand box. You can also download a FASTA file of the sequences using the 'Sequence retrieval' option. You can watch our [video tutorial](#) on YouTube for more details.

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