



GENOME DATABASE FOR VACCINIUM

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

Issue 11 | April 2024

What's new in GDV?

New Training Videos

- [Finding a marker associated with a trait](#) (2:30 mins)
- [Downloading markers from a map region](#) (2:12 mins)

New Data and Functionality

- 12 genetic markers, 12 GWAS and 3 expression datasets added in last quarter
- Wild blueberry genome added
- Additional permission levels added to BIMS

Data added in first quarter of 2024

Below is the list of new data added to GDV in the last quarter. These data can be searched in the database and are available in the tools on GDV.

New GWAS data:

- da Silva et al. [Genome-wide association study and transcriptome analysis reveal candidate genes for off-season flowering in blueberry.](#)

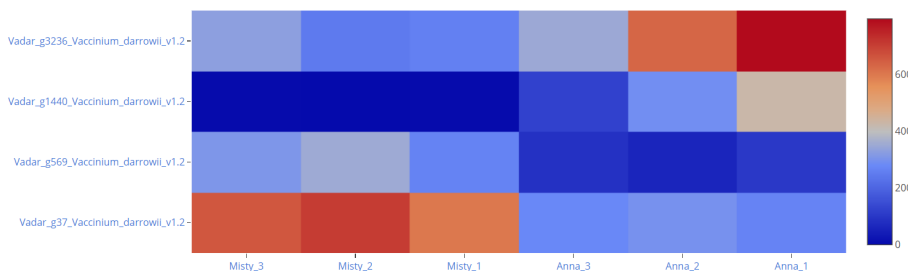
New genome and expression dataset:

- Zeng et al. [The telomere-to-telomere gap-free reference genome of wild blueberry \(*Vaccinium duclouxii*\) provides its high soluble sugar and anthocyanin accumulation.](#)

New expression datasets

- Aligned to *V. vitis-idaea* cv. Red Candy genome
 - Hirabayashi et al. [Unveiling the evolutionary history of lingonberry \(*Vaccinium vitis-idaea* L.\) through genome sequencing and assembly of European and North American subspecies.](#)
- Aligned to *V. darrowii* clone NJ8810/NJ8807 genome
 - Yang et al. [Transcriptomic and Metabolomic Profiling Reveals the Variations in Carbohydrate Metabolism between Two Blueberry Cultivars.](#)

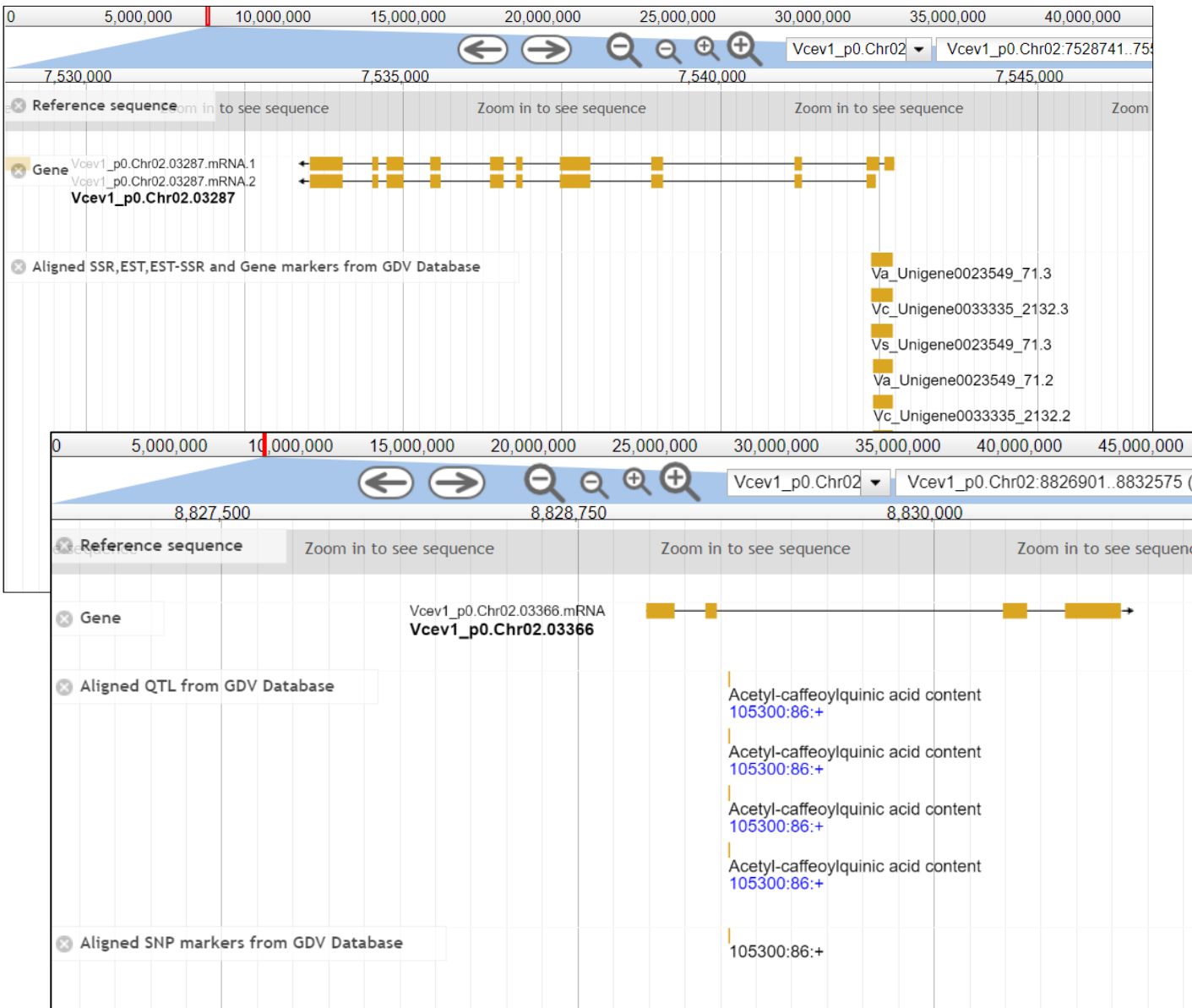
Expression: Carbohydrate metabolism in blueberry fruit Expression



Aligned markers and new JBrowse tracks

GDV is always looking for ways to take existing data and make it more useful for researchers. Using primer sequences from PCR-based markers (SSR, EST, etc.) in the database, and a short sequence BLAST analysis along with filtering, we have aligned the marker primers to representative genomes of each species. The aligned positions are stored under the marker record. We have then mapped QTLs which are associated with aligned markers to genomes.

We have also added three new JBrowse tracks. One track is SNPs mapped to the genome (GWAS are associated with SNPs). The second track is the aligned markers with PCR primers. And the last track is aligned QTL either from provided genome positions or based on aligned markers associated with the QTL.



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Funded by: USDA-SAES NRSP10, SCRI-NIFA Award 2019-51181-30015 (VacCAP), SCRI-NIFA Award 2022-51181-38449