

Supplemental figures for:

Zhao, D., Sapkota, M., Glaubitz, J., Bassil, N., Mengist, M. F., Iorizzo, M., Heller-Uszynska, K., Mollinari, M., Beil, C. T., Sheehan, M. J. (2024). A public mid-density genotyping platform for cultivated blueberry (*Vaccinium* spp.). *Genetic Resources* 5 (9), 36–44. doi: [10.46265/genresj.WQZS1824](https://doi.org/10.46265/genresj.WQZS1824).

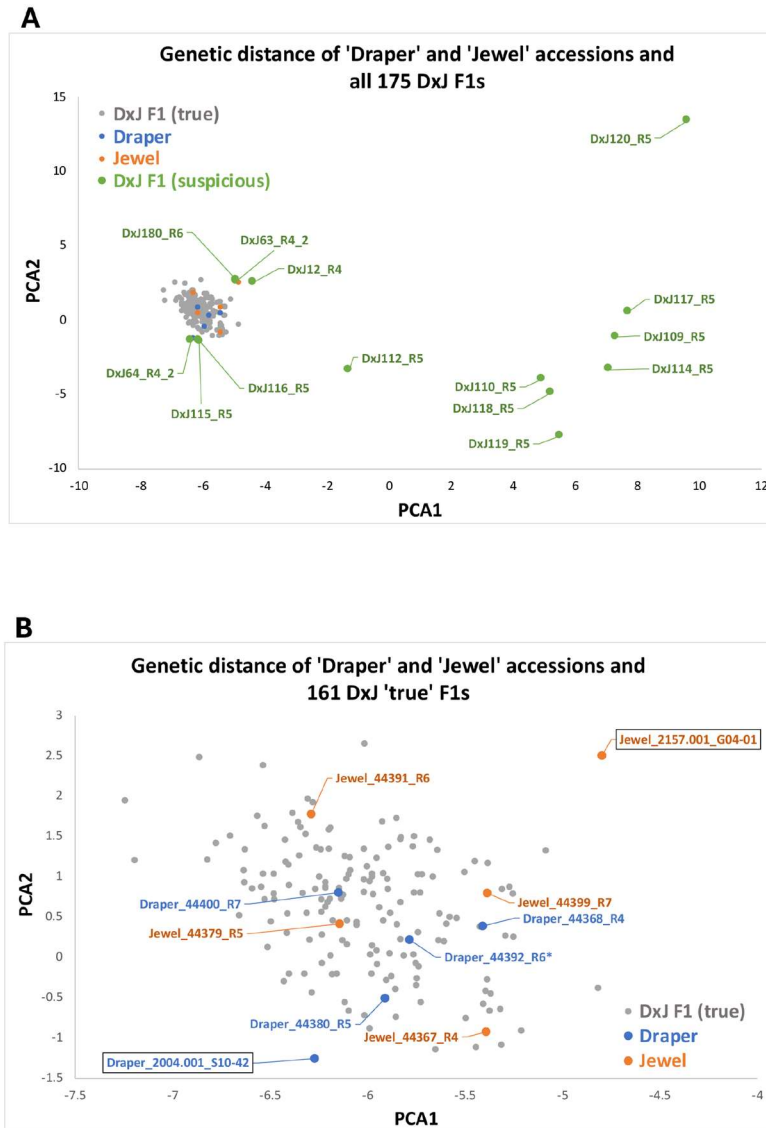
Contents

Supplemental Figure 1. Principle Component Analysis (PCA) plots of the ‘Draper’ x ‘Jewel’ F₁ population.

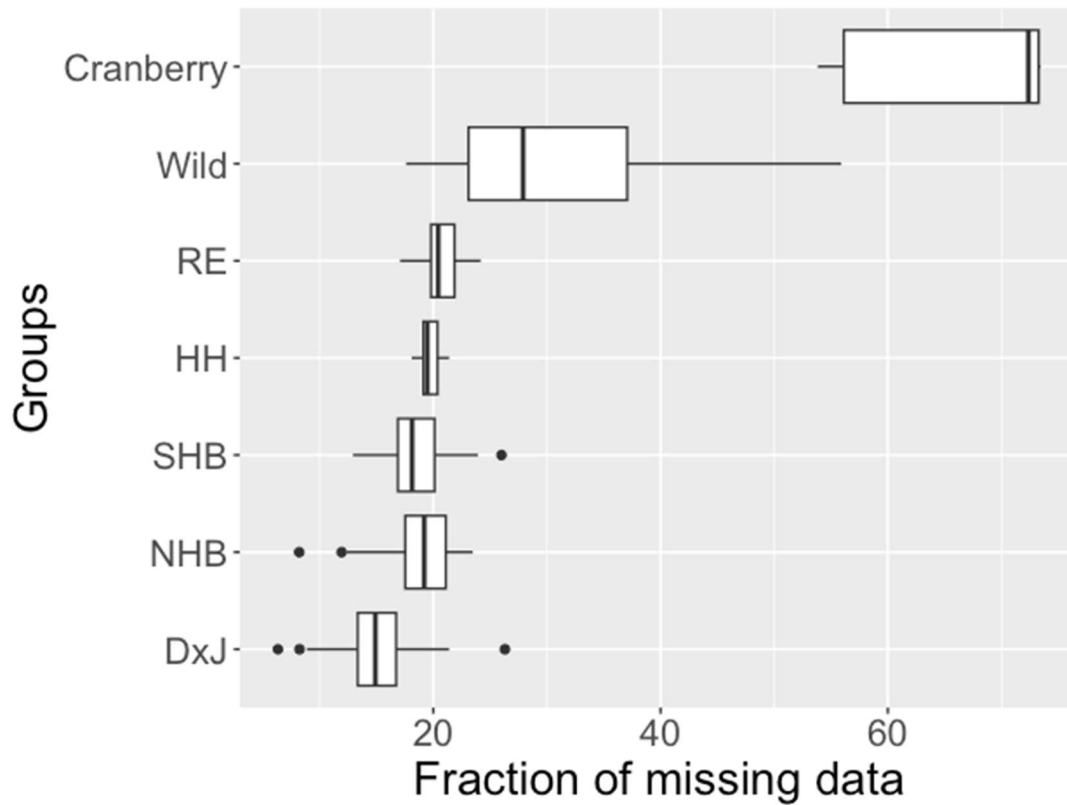
Supplemental Figure 2. Missing data rates for different grouped subsets of genetic material.

Supplemental Figure 3. Blueberry Genetic map construction for the F₁ population.

Supplemental Figure 1. Principle Component Analysis (PCA) plots of the ‘Draper’ x ‘Jewel’ F_1 population. A) PCA of all designated 175 F_1 s plus 5 ‘Draper’ accessions and 5 ‘Jewel’ accessions. Labeled individuals do not appear to be true F_1 s or part of the population and were removed in plot B. B) PCA plot of 161 F_1 used for linkage map construction with all ‘Draper’ and ‘Jewel’ accessions labeled. The closest ‘Draper’ accession and the closest ‘Jewel’ accession to the true ‘Draper’ and ‘Jewel’ parents, respectively, are indicated with black bounding boxes.



Supplemental Figure 2. Missing data rates for different grouped subsets of genetic material. SHB: southern highbush, RE: Rabbiteye, NHB: northern highbush, HH: half high blueberry, DxJ: ‘Draper’ X ‘Jewel’ F₁ population, Wild: *V. stamineum*, *V. fuscatum*, *V. elliotii*, *V. tenellum*, *V. ovatum*, *V. angustifolium*, *V. fuscatum* x *V. darrowii*, *V. corymbodendron*, *V. myrtilloides*, *V. pallidum*, *V. vitis-idaea*, *V. constable*



Supplemental Figure 3. Blueberry Genetic map construction for the F₁ population. A) Pipeline workflow for genetic map construction. B) Summary of the final map with 1,301 unique (1,487 total) markers. C) Example haplotype reconstructions from MAPpoly2 for two individuals from the F₁ population (DxJ002 and DxJ003). The x-axis represents genetic map position and y-axis represents the probability of 0 to 1 within each of the four homologs shown as labels (0, 1, 2, 3, and 4) from Draper (D) and Jewel (J) parent across all linkage groups. The inversions in the probability of magnitudes between homologous from the same parent (different colors) represent possible regions of crossover occurrence.

