

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).

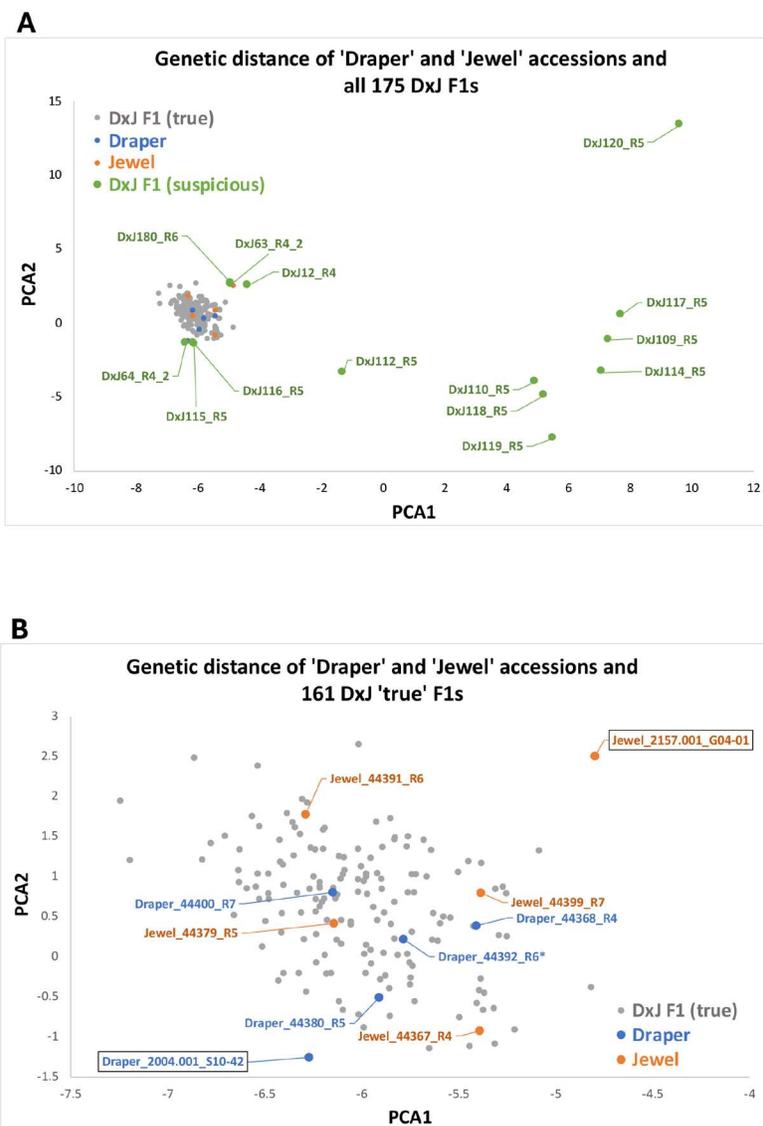
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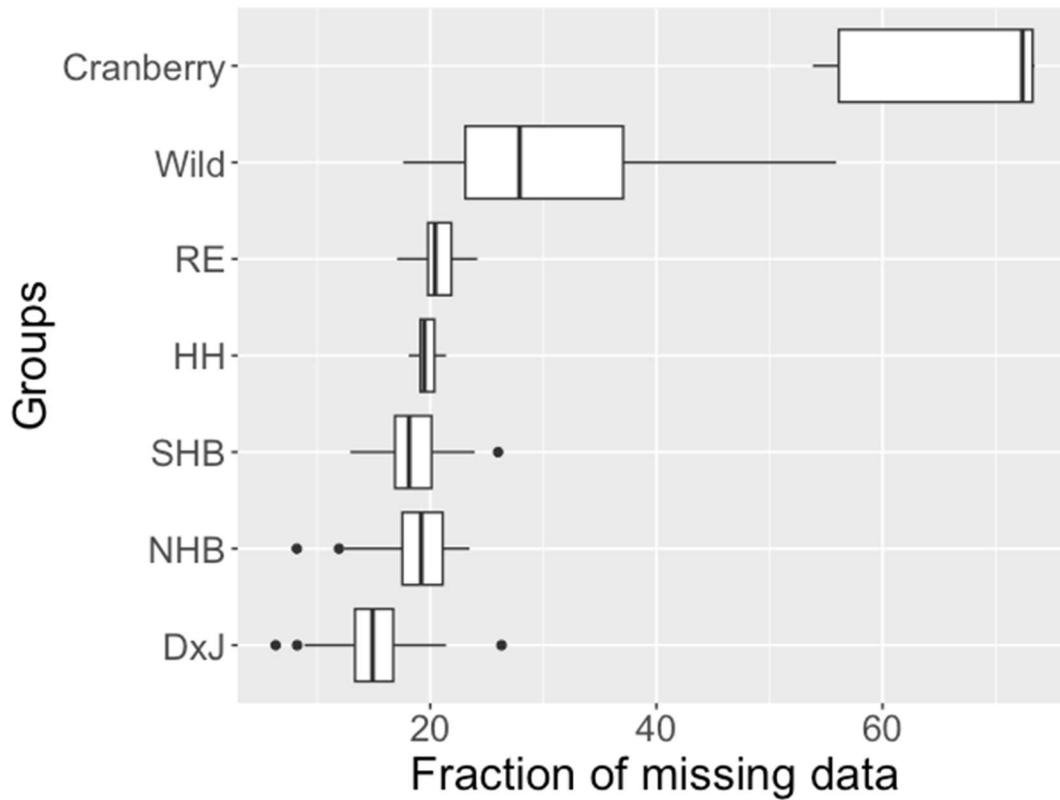
Supplemental Figure 2. Missing data rates for different grouped subsets of genetic material.

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

Supplemental Figure 1. Principle Component Analysis (PCA) plots of the ‘Draper’ x ‘Jewel’ F₁ population. A) PCA of all designated 175 F₁s plus 5 ‘Draper’ accessions and 5 ‘Jewel’ accessions. Labeled individuals do not appear to be true F₁s or part of the population and were removed in plot B. B) PCA plot of 161 F₁ 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.

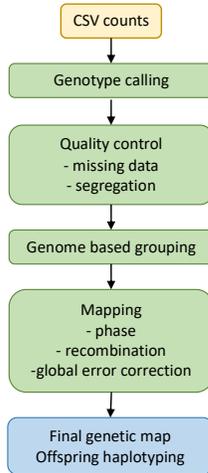


Supplemental Figure 2. Missing data rates for different grouped subsets of genetic material. SHB: southern highbush, RE: Rabbiteye, NHB: northern highbush, HH: half high blueberry, DxJ: ‘Draper’ X ‘Jewel’ F₁ population, Wild: *V. stamineum*, *V. fuscatum*, *V. elliotii*, *V. tenellum*, *V. ovatum*, *V.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

A.



B.

Chrom	Linkage Group	Genomic sequence	Map length (cM)	Markers/cM	Simplex Draper	Simplex Jewel	Double-simplex	Multiplex	Total unique	Max gap
Chr01	lg9	VaccDscaff1	111	1.045	44	29	27	16	116	7.1
Chr02	lg6	VaccDscaff2	148.3	1.133	46	50	31	41	168	13.8
Chr03	lg2	VaccDscaff4	116	1.034	44	38	16	22	120	9.4
Chr04	lg3	VaccDscaff6	110.4	0.906	23	24	14	39	100	18.3
Chr05	lg8	VaccDscaff7	122.3	0.638	23	35	8	12	78	12.5
Chr06	lg4	VaccDscaff11	92.7	1.273	33	36	31	18	118	10
Chr07	lg1	VaccDscaff12	97.4	0.862	21	31	13	19	84	9.3
Chr08	lg10	VaccDscaff13	106.8	1.067	40	25	21	28	114	6.7
Chr09	lg12	VaccDscaff17	129	0.791	26	30	23	23	102	10.1
Chr10	lg5	VaccDscaff20	133.9	0.597	13	34	18	15	80	20.9
Chr11	lg11	VaccDscaff21	90.5	1.116	32	23	21	25	101	8.2
Chr12	lg7	VaccDscaff22	110.3	1.088	38	28	21	33	120	7.8
Total			1368.6	0.962	383	383	244	291	1301	

C.

