

SUPPLEMENTAL MATERIAL

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Supplemental Table 1. Predicting canning quality traits through hyperspectral (HYP) imaging and near-infrared spectroscopy (NIRs).

Trait	Imaging	Wavelength	Method	Avg. Fact.	\bar{R}_{cal}	\overline{SEC}	\bar{R}_{pred}	\overline{SEP}
Texture	NIRs	100 best ratios	Raw	20	0.984	1.4	0.950	2.5
Texture	Fusion	100 best ratios	Raw	11	0.963	2.1	0.920	3.1
Texture	NIRs	100 best ratios	CWT	25	0.976	1.7	0.918	3.2
Color	NIRs	100 best ratios	CWT	25	0.956	0.2	0.890	0.3
Texture	Fusion	200 best bands	CWT	11	0.920	3.0	0.883	3.7
Color	Fusion	100 best ratios	Raw	24	0.985	0.1	0.881	0.3
Texture	NIRs	100 best bands	Raw	25	0.956	2.3	0.880	3.7
Texture	Fusion	200 best bands	Raw	25	0.949	2.4	0.872	3.9
Color	HYP	100 best ratios	Raw	19	0.944	0.2	0.866	0.3
Color	NIRs	100 best ratios	Raw	20	0.949	0.2	0.860	0.4
Texture	HYP	100 best ratios	Raw	20	0.950	2.4	0.860	4.1
Appearance	NIRs	100 best ratios	CWT	25	0.955	0.1	0.850	0.3
Texture	Fusion	100 best ratios	CWT	25	0.982	1.5	0.839	4.4
Color	Fusion	100 best ratios	CWT	7	0.902	0.3	0.833	0.4
Appearance	NIRs	100 best ratios	Raw	20	0.936	0.2	0.824	0.3
Color	HYP	100 best ratios	CWT	11	0.882	0.3	0.823	0.4
Appearance	HYP	100 best ratios	Raw	20	0.923	0.2	0.808	0.3

RILs from both populations grown in 2016 (n=295) were scanned in the summer of 2017. A series of post-processing image analyses were performed using variable wavelengths and factors to generate predictive models for black bean quality traits. The best performing models ($\bar{R}_{pred} > .80$) are shown.

Fusion: Combination of hyperspectral imaging and near-infrared spectroscopy

CWT: Continuous wavelength transformation

Avg. Fact.: average number of features required for the partial least square regression model after optimization

\bar{R}_{cal} and \bar{R}_{pred} : average correlation coefficients of calibration and prediction, respectively, over four calculations

\overline{SEC} and \overline{SEP} : average standard error for calibration and prediction, respectively, over four calculations

Supplemental Table 2. List of *Phaseolus vulgaris* genes within the physical interval of QTL for post-processing color retention on Pv11.

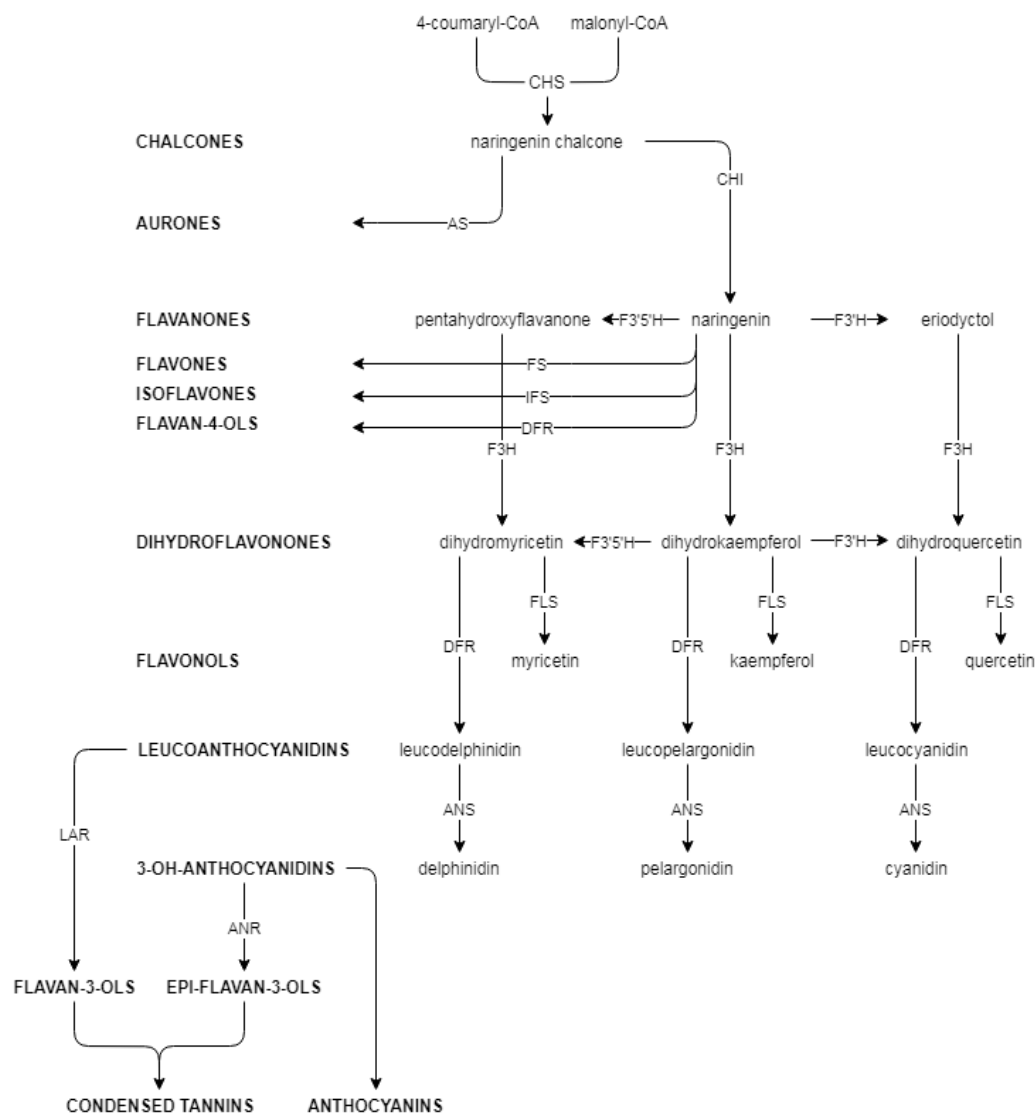
Phvul Gene ID	Orthology Term	Description	Start (bp).	End (bp)
Phvul.011G206500	K07047	uncharacterized protein (K07047)	52,411,332	52,421,199
Phvul.011G206500	K07047	UNCHARACTERIZED PROTEIN (K07047)	52,411,332	52,421,199
Phvul.011G206400	PTHR31604:SF2	PROTEIN SHI RELATED SEQUENCE 6	52,434,964	52,440,240
Phvul.011G206400	PTHR31604:SF2	PROTEIN SHI RELATED SEQUENCE 6	52,434,964	52,440,240
Phvul.011G206300	PTHR23086:SF29	PHOSPHATIDYLINOSITOL 4-PHOSPHATE 5-KINASE 6	52,442,526	52,447,566
Phvul.011G206300	PTHR23086:SF29	PHOSPHATIDYLINOSITOL 4-PHOSPHATE 5-KINASE 6	52,442,526	52,447,566
Phvul.011G206200		FAMILY NOT NAMED	52,485,285	52,489,990
Phvul.011G206100	PTHR13683:SF258	ASPARTYL PROTEASE FAMILY PROTEIN-RELATED	52,498,725	52,500,499
Phvul.011G207400	K15542	POLYADENYLATION FACTOR SUBUNIT 2 (PFS2)	52,536,582	52,547,537
Phvul.011G207500	PTHR11783//PTHR11783:SF89	SULFOTRANSFERASE SULT // SUBFAMILY NOT NAMED	52,550,711	52,551,694
Phvul.011G207600	PTHR10168//PTHR10168:SF84	GLUTAREDOXIN // SUBFAMILY NOT NAMED	52,593,279	52,595,263
Phvul.011G207700	PTHR23180:SF249	ADP-RIBOSYLATION FACTOR GTPASE-ACTIVATING PROTEIN AGD11-RELATED	52,600,434	52,605,733
Phvul.011G207800	2.4.2.10	OROTATE PHOSPHORIBOSYLTRANSFERASE / OROTIDYLIC ACID PHOSPHORYLASE	52,608,333	52,612,347
Phvul.011G207900	PTHR10315//PTHR10315:SF29	SEVEN IN ABSENTIA HOMOLOG // SUBFAMILY NOT NAMED	52,612,952	52,618,001
Phvul.011G210200		FAMILY NOT NAMED	52,723,304	52,728,358
Phvul.011G210100		FAMILY NOT NAMED	52,736,445	52,739,134
Phvul.011G210000	PTHR24078:SF219	DNAJ HEAT SHOCK N-TERMINAL DOMAIN-CONTAINING PROTEIN	52,747,036	52,754,695
Phvul.011G209900	PTHR13683:SF298	ASPARTYL PROTEASE FAMILY PROTEIN-RELATED	52,760,184	52,761,685
Phvul.011G209800	PRICHEXTENSIN	PROLINE RICH EXTENSIN SIGNATURE	52,764,327	52,765,437
Phvul.011G209700		FAMILY NOT NAMED	52,766,583	52,767,630
Phvul.011G209600	PTHR22979	ZINC FINGER PROTEIN-RELATED	52,770,861	52,773,922
Phvul.011G209500	PTHR10502:SF99	ANNEXIN D3	52,778,448	52,782,342
Phvul.011G209400	PTHR10502:SF104	ANNEXIN D4	52,788,550	52,791,464
Phvul.011G209300	PTHR10502//PTHR10502:SF113	ANNEXIN // SUBFAMILY NOT NAMED	52,795,513	52,798,483
Phvul.011G209200	K17099	ANNEXIN A13 (ANXA13)	52,803,665	52,806,589

Supplemental Table 2. (cont'd)

Phvul Gene ID	Orthology Term	Description	Start (bp).	End (bp)
Phvul.011G209100		FAMILY NOT NAMED	52,814,777	52,824,388
Phvul.011G209000	PTHR13683:SF298	ASPARTYL PROTEASE FAMILY PROTEIN-RELATED	52,829,610	52,831,021
Phvul.011G208900	PTHR13683:SF298	ASPARTYL PROTEASE FAMILY PROTEIN-RELATED	52,837,327	52,838,607
Phvul.011G208800	PTHR13683:SF298	ASPARTYL PROTEASE FAMILY PROTEIN-RELATED	52,841,304	52,842,636
Phvul.011G208700	PTHR13683:SF298	ASPARTYL PROTEASE FAMILY PROTEIN-RELATED	52,844,268	52,845,584
Phvul.011G208400	PTHR13683:SF298	ASPARTYL PROTEASE FAMILY PROTEIN-RELATED	52,859,820	52,861,124

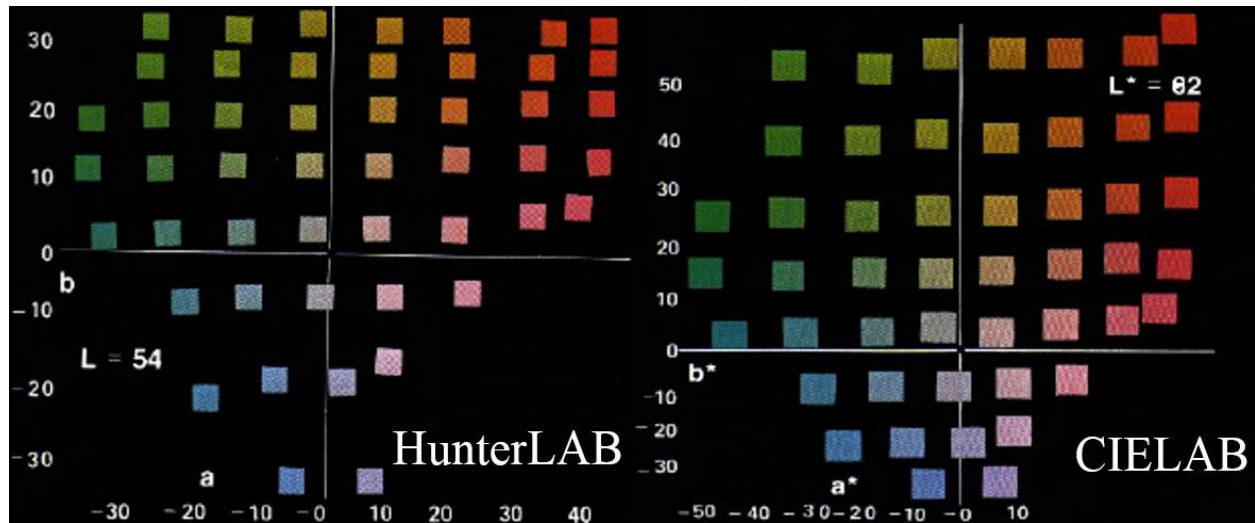
The physical interval from 52.47-52.84 Mb was shared among COL11.1⁷⁶ and COL11.1⁸⁶. The list was compiled using PhytoMine (DOE-JGI and USDA-NIFA, <https://phytozome.jgi.doe.gov/phytomine/begin.do>). Highlighted gene families are mentioned in the discussion section

Supplemental Figure 1. Flavonoid biosynthetic pathway.



Anthocyanins and condensed tannins influencing black bean seed coat coloration are part of a complex pathway.

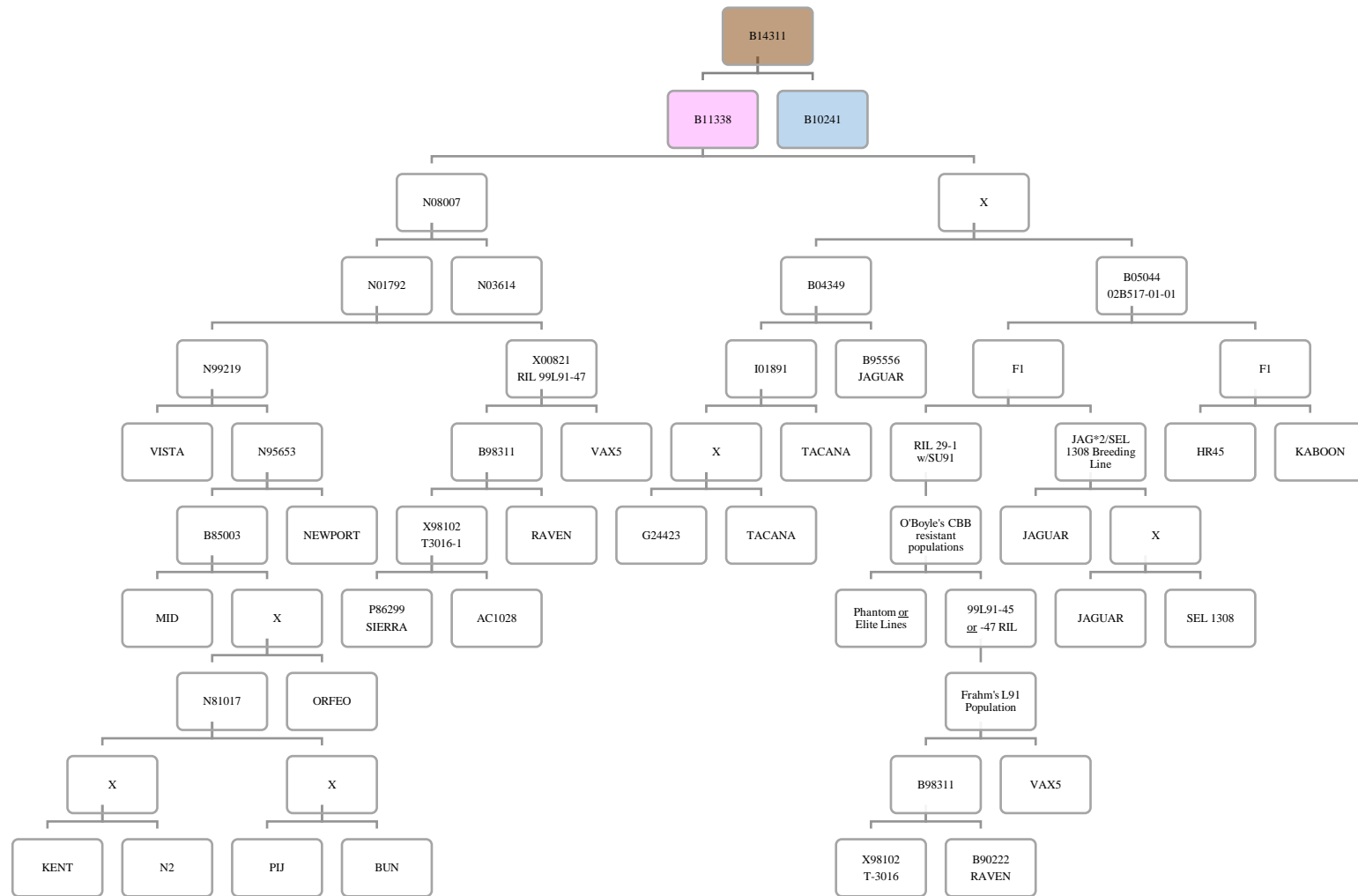
Supplemental Figure 2. Comparison of HunterLAB and CIELAB color spaces.



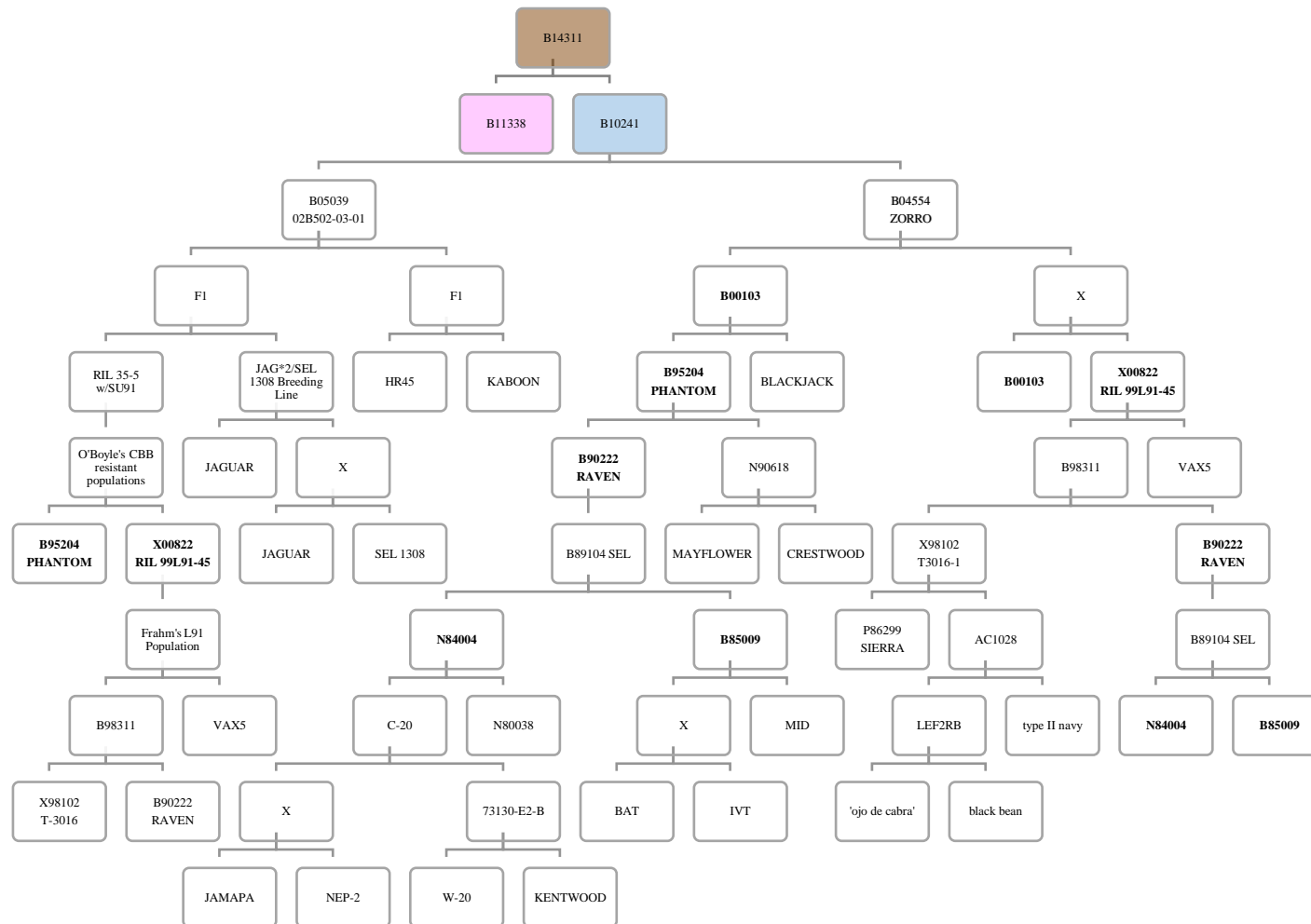
The same color swatches are used in both photographs, but their spatial distribution differs depending on color space. CIELAB color space is an improvement on HunterLAB color space because colors are more evenly-distributed and better represent darker regions. Image source: HunterLab (2008).

Supplemental Figure 3. Pedigree for B14311.

A: Maternal pedigree for B14311



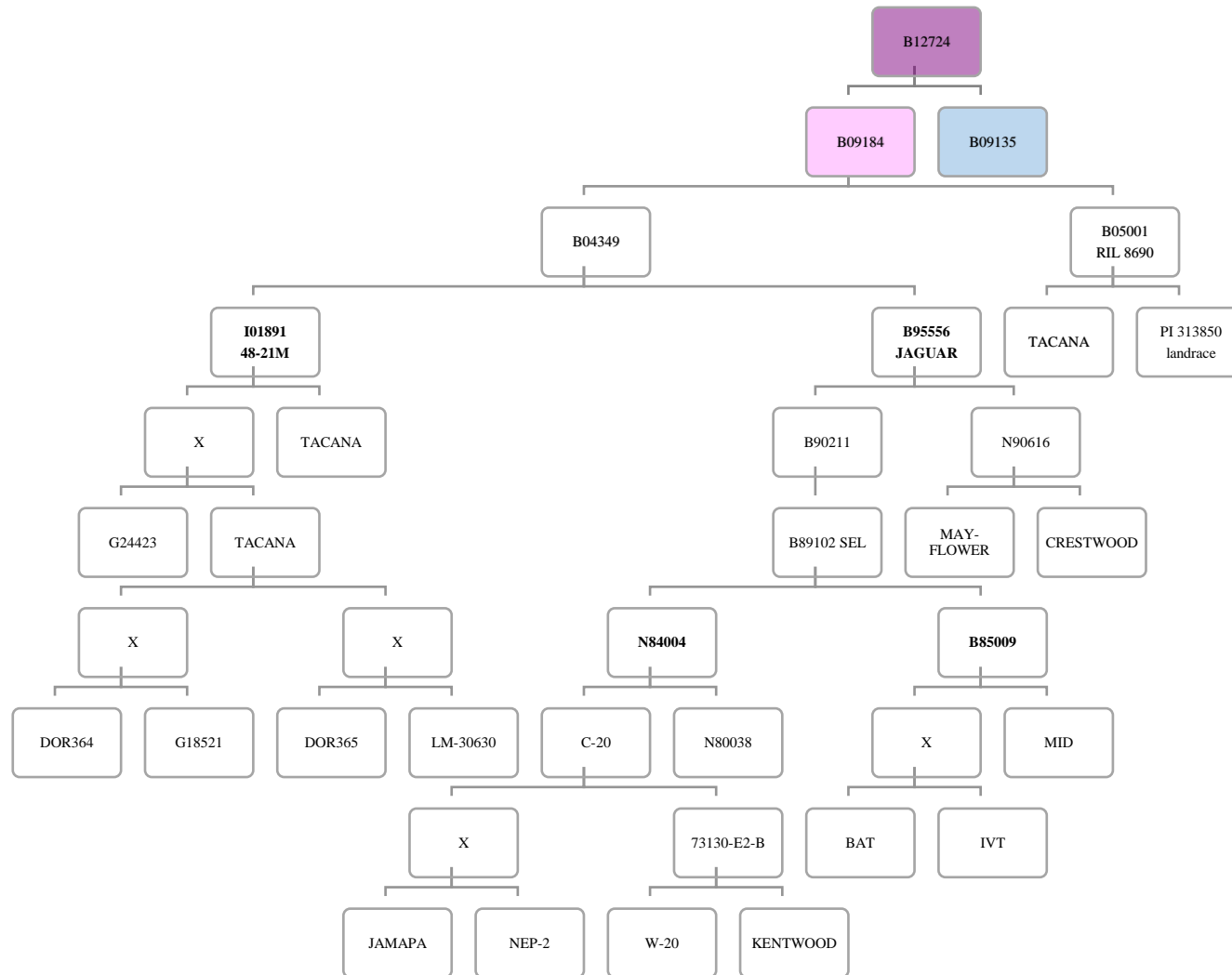
B: Paternal pedigree for B14311



Pedigree information was gathered from MSU dry bean breeding accession files, previous graduate students' theses, and variety release reports. The female parent is always on the left side of a cross. X's represent placeholder genotypes for F₁s. Bolded genotypes occur multiple times throughout the pedigree.

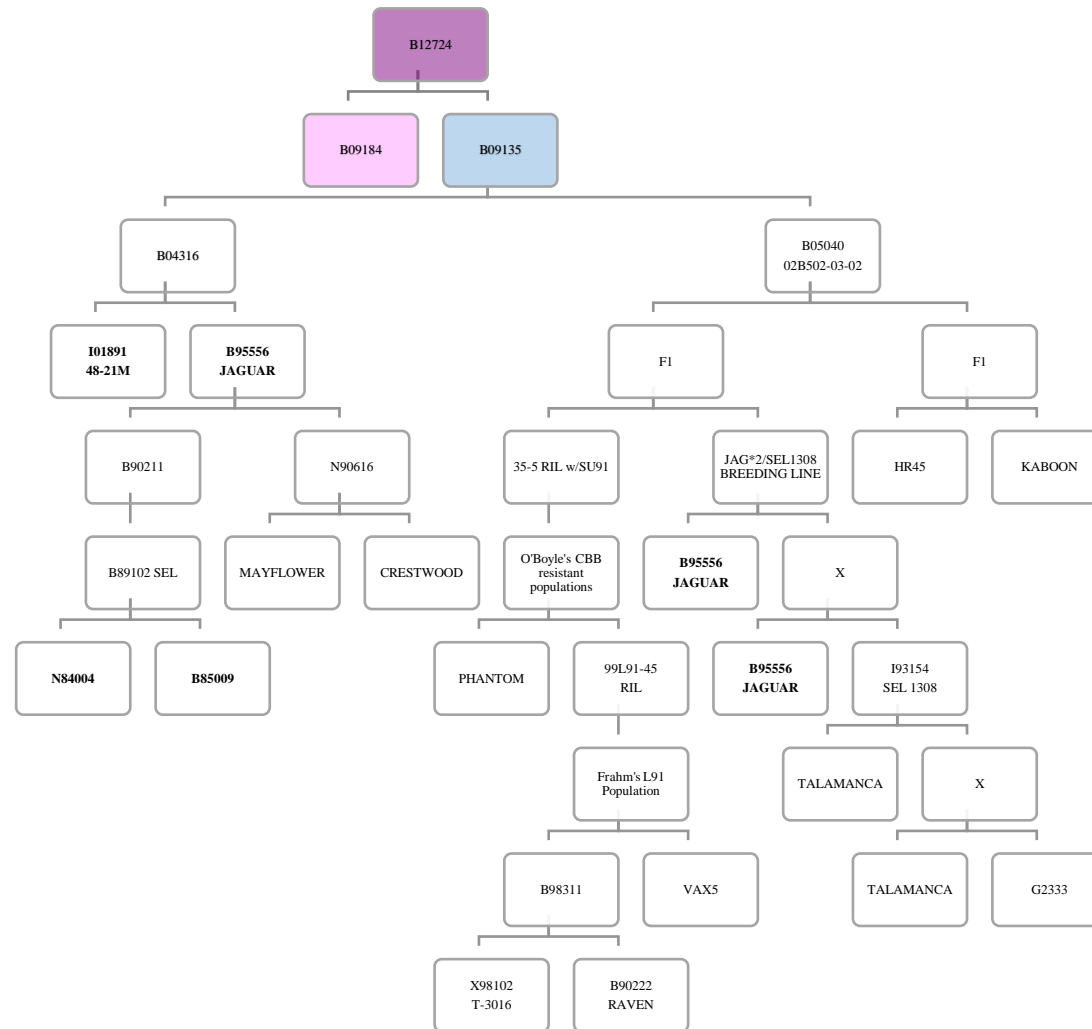
Supplemental Figure 4. Pedigree for B12724.

A: Maternal pedigree for B12724



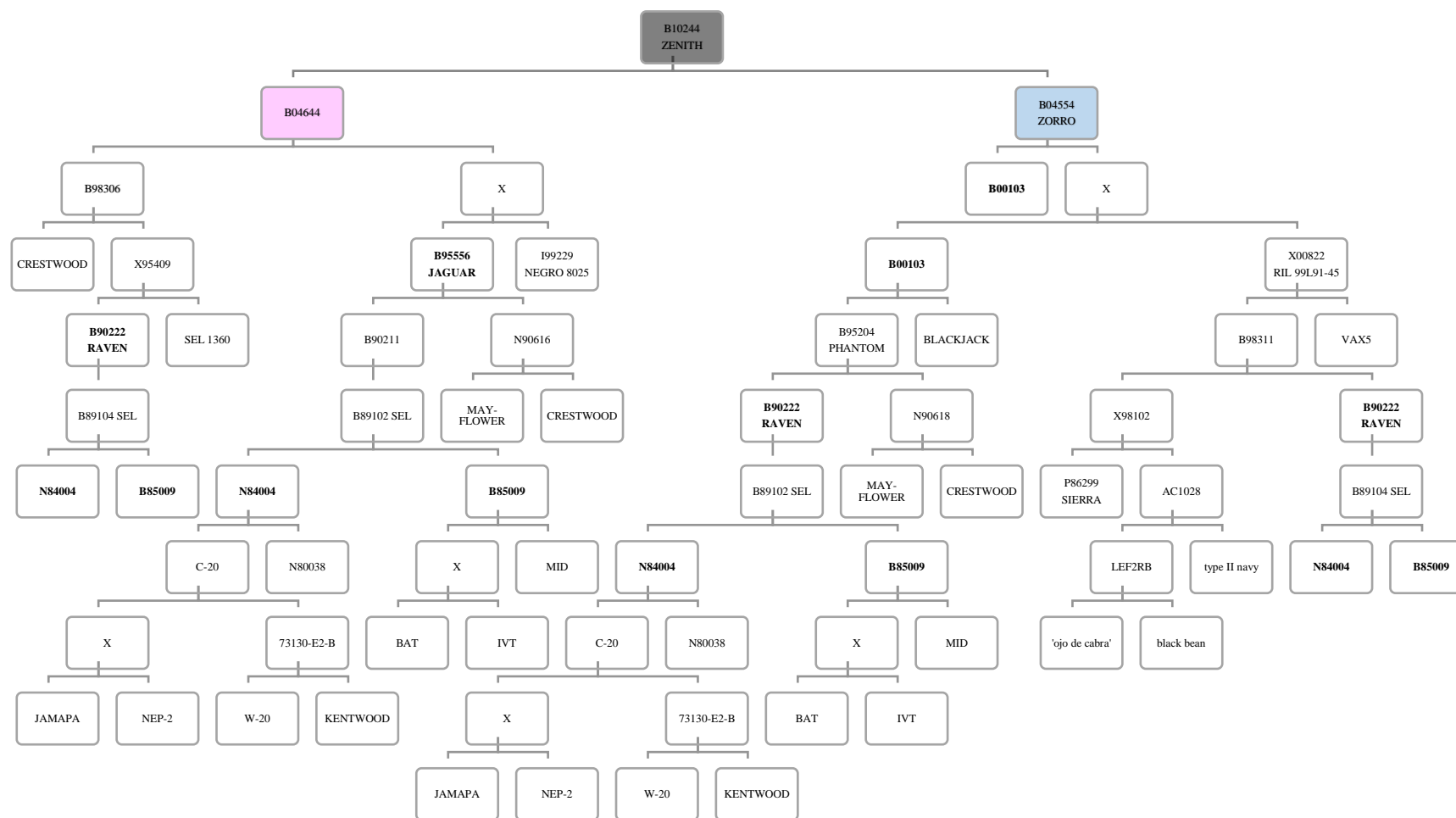
Supplemental Figure 4. (cont'd)

B: Paternal pedigree for B12724



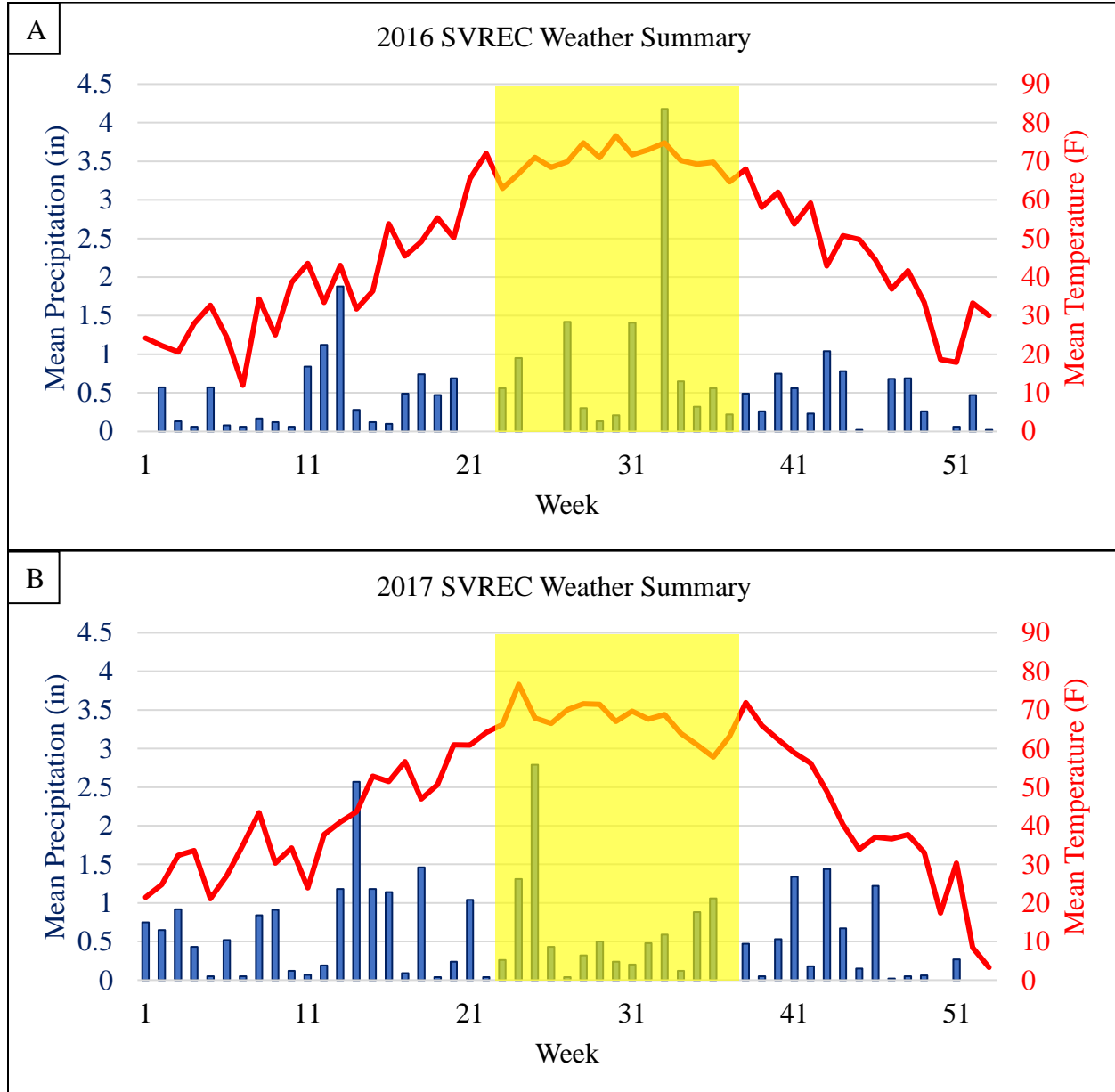
Pedigree information was gathered from MSU dry bean breeding accession files, previous graduate students' theses, and variety release reports. The female parent is always on the left side of a cross. X's represent placeholder genotypes for F₁s. Bolded genotypes occur multiple times throughout the pedigree.

Supplemental Figure 5. Pedigree for Zenith.



Pedigree information was gathered from MSU dry bean breeding accession files, previous graduate students' theses, and variety release reports. The female parent is always on the left side of a cross. X's represent placeholder genotypes for F₁s. Bolded genotypes occur multiple times throughout the pedigree.

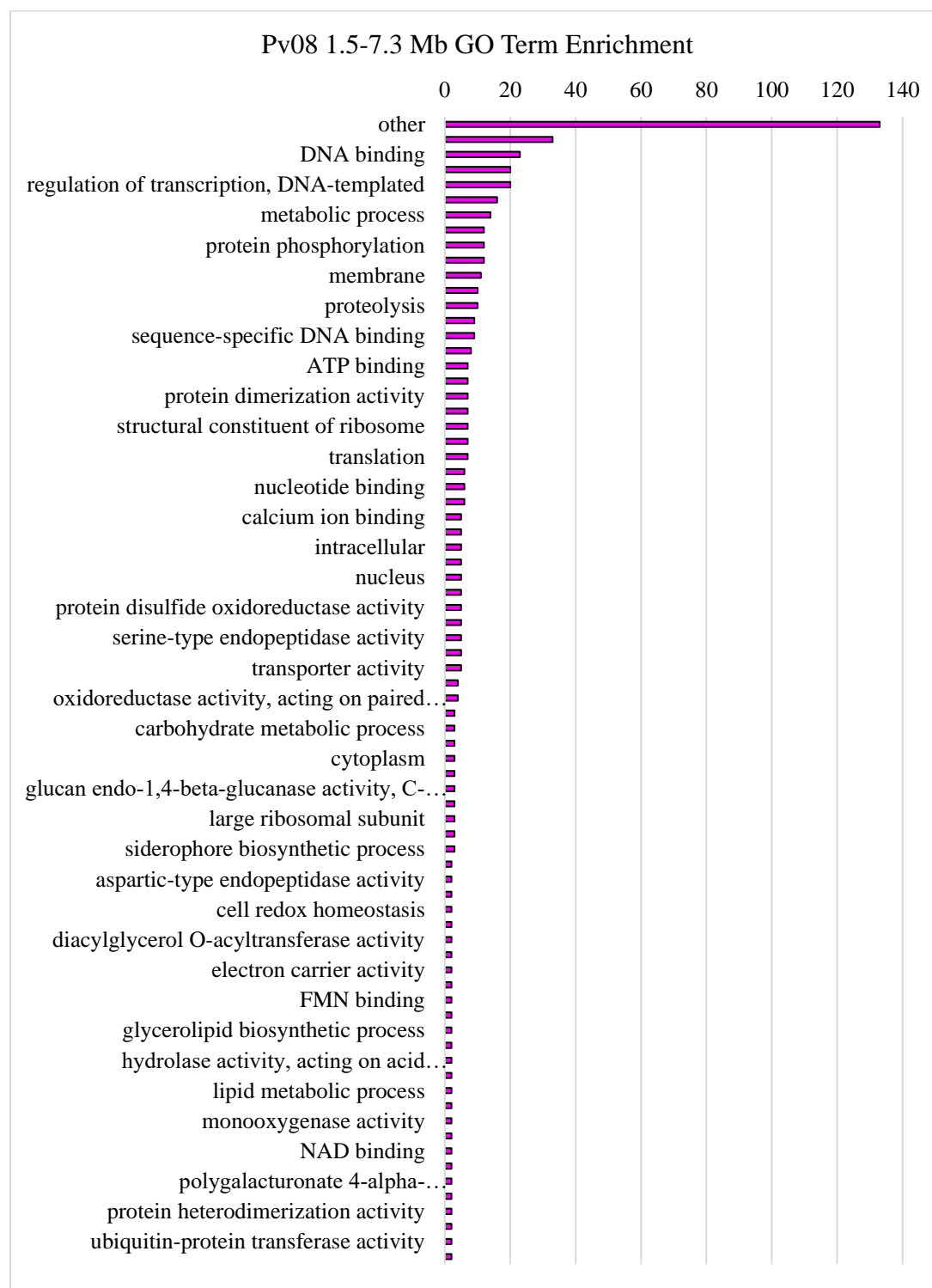
Supplemental Figure 6. Weather summary for SVREC (Richville, MI) from 2016-2017.



A: In 2016, RIL populations were planted on June 3 (week 22) and harvested on September 13 (week 37). It rained 2.76" on August 16, 2016 (week 33).

B: In 2017, RIL populations were planted on June 2 (week 22) and harvested on September 11 (week 37). It rained 1.25" on June 23, 2017 (week 25).

Supplemental Figure 7. GO term enrichment within the physical interval of QTL for post-processing color retention on Pv08.



The physical interval from 1.5-7.3 Mb was shared among COL8.1⁷⁶ and COL8.1⁸⁶. The list of GO terms was compiled using PhytoMine (DOE-JGI and USDA-NIFA, <https://phytozome.jgi.doe.gov/phytomine/begin.do>).

Supplemental Figure 8. Screening parental genotypes for SCAR marker SU91-CG11.



Marker SU91-CG11 is linked to a CBB resistance locus on chromosome Pv08. Presence of the lower band indicates susceptibility and presence of the upper band indicates a level of CBB resistance conferred by the SU91 locus.