A GENOMEWIDE ANALYSIS OF THE USDA SOYBEAN ISOLINE COLLECTION

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DEDICATIONS

To my parents, Jim and Caroline Gilbert, and my sister, Aisha Gilbert.

ABSTRACT

The USDA Soybean Isoline Collection was analyzed by combining historical phenotype and pedigree data with recently collected and publicly released SoySNP50K data. This collection was created and released over the course of nearly 20 years in order to isolate intervals associated with contemporarily significant qualitative traits (Bernard, 1991). With the release of the SoySNP50K genotyping array and the subsequent genotyping of the USDA germplasm, it is possible to bring higher resolution analysis of this historical collection. Publically available genotyping data for 277 near isogenic lines (NILs) and their associated parents were downloaded from Soybase.org. These data were combined with pedigree and phenotyping records to characterize this population in terms of pedigree type and content, parent/offspring identity, and donor parent introgressions. Here we present results regarding the characterization of this collection in terms of content and NIL isogenicity, and also use the NIL data for trait mapping. Forty-one traits were mapped here, with 33 improving upon previous mapping data and 8 newly mapped traits.

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CHAPTER 1

Introduction

The rich history of soybean qualitative trait mapping goes back to the early twentieth century and continues today. The leguminous plant was brought to the United States from Southeast Asia in the early 1800s, but it wasn't until 1908 that cultivation experiments began for this crop (Bowdidge, 1935). The first mention of qualitative trait behavior in soybeans in western literature was in reference to the Mendelian inheritance of pubescence color (Piper and Morse, 1910). The late 1920's saw three major literature reviews released in Genetics that summarized qualitative genes (then known only as factors) associated with soybean in categories of interest to research and industry such as pigmentation, pubescence, maturity, and linkage (Owen, 1927a, 1927b, 1928). These three reviews highlighted relationships significant to early breeders developing forage soybeans from Chinese varieties (Owen, 1927a, 1927b, 1928; Piper and Morse, 1910). The first discussed multiple factors associated with cotyledon color and their respective inheritance patterns (Owen, 1927a). This study was also important in showing that some major traits used to distinguish between varieties (in this case, cotyledon color) could be affected by multiple factors or genes. Using previous work on the *D* genes, it was put for that there were at least two factors affecting cotyledon color (Owen, 1927a; Woodworth, 1921). These factors were named D_1 and D_2, and were later mapped and cloned in the

21^{st} century (Fang, 2014). The second and third papers in this series expanded into the nature of linkage relations in soybean (Owen, 1927b, 1928).

For the soybean community as a whole, qualitative traits also played a major role in standardizing nomenclature. In 1955, the Soybean Genetics Committee was formed in order to, among other tasks, establish guidelines for gene symbols in soybean and review qualitative genetic interpretation and gene symbols in manuscripts (Palmer, 2004). It has since moved on to establishing similar standards for quantitative trait loci (QTL), with its qualitative rules serving as a base. By 1963, sixty-seven qualitative traits, referred to as "simply inherited characters", had been reported (Johnson and Bernard, 1963). Most of these new traits were observed in the so-named "T" (for "Type") lines which had been added to the USDA collection from outside sources (Palmer, 2004). These traits expanded on the categories in the original three literature reviews of soybean traits important to breeders (Owen, 1927a, 1927b, 1928). In 1974, the Soybean Genetic Newsletter began circulating in order to showcase articles reviewed by the Soybean Genetics Committee, including additions to the USDA Soybean Genetic Type Collection. In this newsletter, the phenotyping and pedigree data for the collection addressed in the current study was published (Bernard et al., 1991).

The USDA Soybean Isoline Collection of near-isogenic lines (NILs) is a collection of lines that were created in order to view the effect of a gene or allele in a common genetic background (Bernard *et al.*, 1991). These types of lines are popular in plant molecular studies, and have been used in studies of other crop species such as oat, wheat, and maize

(Moerschbacher *et al.,* 1988; Pumphrey *et al.*, 2006; Poerschmann *et al.*, 2005). Introgression of a gene from source to target can be achieved using a backcross scheme in which the donor parent (DP) carrying the allele of interest is first crossed to a parent which does not confer this allele (also called the recurrent parent) (Bernard, 1991). Progeny are then backcrossed to the recurrent parent (RP) and phenotypic selection for the trait allele of interest is performed each generation. Ultimately, the resulting line will have a genome comprised mostly of the recurrent parent genome with small introgressions of the donor parent genome containing the gene for the trait of interest. In soybean, NILs have been used to confirm the gene action of resistance genes by eliminating confounding effects of the genetic background from which the gene came (Glover, 2004) . Maturity, another consideration for growers and breeders often seen as multifactorial, was explored through photoperiod sensitive NILs (Cober *et al.*, 1996). Studies need not be limited to chromosomal DNA with NILs either: RNAseq analysis of NILs allowed expression data to be utilized in a study on soybean bacterial leaf pustule (Kim et al., 2011).

In the USDA Soybean Isoline collection, over 100 nuclear alleles representing 81 unique traits were sampled, each falling into one of ten categories (disease resistance, nutrient response, stem growth, maturity time, leaf form, pubescence type, pigmentation, other, miscellaneous, combinations transferred together (linked genes), and miscellaneous combinations (genes deliberately selected together)) for the purpose of genetic studies and assessing potential for commercial use (Bernard et al., 1991). Many of these genes originated from the lines in the USDA Soybean Genetic Type Collection, or "T" lines (Palmer, 2004). These traits were introgressed into the backgrounds composed of the varieties Clark, Harosoy, Williams, or another appropriate line (Supplementary Table 1). This was achieved through the use of backcrossing schemes, usually five backcross generations. In some cases, NILs of the same background were crossed together in order to combine traits (Bernard, 1991). The development of this collection stretched over two decades, with the first release in 1972, the second in 1975 (coinciding with the first Soybean Genetics Newsletter publication), and the last in 1991 (Bernard, 1991).

Molecular and physiological characterization of many such genes in soybean have helped to illuminate many more aspects of plant biology and development since the formation of the Soybean Genetics Committee. The first soybean linkage maps were based around markers associated with qualitative traits, and made locating genetic locations of traits possible (Tanksley & McCouch, 1997). Because of the binary nature of single gene qualitative traits and the relative lack of molecular markers for cytoplasmic genes, RFLP markers were used to create these resources (Keim, 1990). RFLP markers had also been shown as useful tools for mapping quantitative trait loci (Young *et al.* 1988; Young and Tanksley, 1989). Shortly after the release of the Isoline collection, RFLP markers were used to map specific qualitative genes in NILs (Muehlbauer et al., 1991). This led to 15 traits being newly mapped. Since its release, the USDA Soybean Isoline collection has been referenced in over 100 publications to include scientific articles, textbooks, and newsletters covering topics from maturity (Watanabe *et al.*, 2009), disease resistance (Yu, 1996), and even yield (Guzman *et al.*, 2007).

Though this collection has been available for over a quarter of a century, a single easily accessible reference which summarizes the collection in terms of pedigree, traits isolated, the extent to which the NILs are isogenic, or the status of gene discovery and validation for these traits does not exist. The objectives of this study were to combine historic phenotypic data collected by Bernard *et al.* and modern genotyping data from the SoySNP50K BeadChip to first characterize the collection as an isoline resource for soybean researchers, and second to map genetic intervals for traits isolated in this collection to confirm and improve upon previously reported results.

Methods

Plant materials and genotype data

Pedigree information for all 611 NILs in the USDA Soybean Isoline Collection were acquired from Dr. Randy Nelson (University of Illinois). This information was checked for accuracy against the original collection release information reported by Bernard *et al.* (1991). All 611 lines were used in a basic analysis of population descriptors. Pedigree shorthand was tabulated and lines were sorted to find NILs with at least one nuclear trait for use in this study. The pedigree structure nearly half (251) NILs in this collection is primarily a backcross five (BC_5) type derived from a RP(6)xDP crossing scheme. Of these

NILs, 238 are ones in which the DP is a NIL. The remaining lines in this collection are either NILS with varying number of backcross generations from 2 to 20 (23 lines), biparental crosses between NILS (320 lines), or mutations discovered in established lines (17 lines).

Genotype data on the NILs collected using the SoySNP50K BeadChip was made available as part of the genotyping of the entire USDA Soybean Germplasm Collection by Song *et al.* (2015). NILs for which genotype data were not available, or in which genotype data were not available for the donor parent (DP) or recurrent parent (RP) used to create that NIL, were removed from all genetic analyses. This left 277 NILs representing 114 unique DPs in combination with the three major RPs that were used in analyses described below.

Isogenicity of Lines within the Collection

For all NILs for which parental genotype data were available, the genetic contribution of the RP was calculated as

$$Contribution\ of\ RP\ to\ NIL = \frac{S_{RP/NIL} - (S_{RP/DP} \times S_{DP/NIL})}{1 - (S_{RP/NIL})^2}$$

(Bernardo, 2010)

where $S_{RP/DP}$ is the marker identity between the RP and DP, $S_{RP/NIL}$ is the marker identity between the RP and NIL, and $S_{DP/NIL}$ is the marker identity between the DP and NIL. NILs for which multiple traits were donated from various donor parents were analyzed with all donors and the mean contribution of the recurrent parent was taken. Cases where genotype data on the DP or RP were not available were not considered in this analysis.

Number and size of DP introgressions for each NIL were determined and summarized. Introgressed DP SNP alleles were those loci polymorphic between DP and RP in the NIL that matched the DP. Introgressed DP SNP alleles separated by 1Mb or less were combined to define a DP introgression. The size of the introgression was defined as the physical length between the start and end SNP locus.

Trait Mapping

Mapping of each trait was carried out by combining SoySNP50K BeadChip data with pedigree and trait information on the Collection (Bernard *et al*, 1991). To start, NILs sharing a common trait were selected and introgressions were compared across NILs by scoring RP markers and DP markers, then comparing the proportions of scores across NILs. The fact that different RP and DP pairs are polymorphic for different loci leads to a situation in which NILs comprising a trait set may not be completely overlapping for RP/DP scores. In order to prevent excessive loss of data for use in the calculation of probability described below, we carried out a simple interpolation scheme where missing scores were interpolated using flanking marker scores. If flanking markers had the same score, all intervening missing scores were given this same score. If the flanking marker scores were different, then the scores were left as missing data.

The next step in the mapping process involved calculating the probability each SNP was subjected to selection versus inherited by chance alone. To do this, we used the binomial probability function and assigned the probability of each allele according to the number of backcrosses used to create each NIL.

$$P = \binom{n}{x} \theta^{x} (1 - \theta)^{n-x}$$

Where n is the total number of NILs for the trait in question, *x* is the number of DP scores, and theta is the expected probability of a DP allele, which was set based on the pedigree (i.e., number of backcrosses). Pedigrees of NILs in this collection ranged from straight forward backcross NILs to simple crosses between NILs of identical background. (Supplementary Table 1). When sets of NILs for a given trait included NILs with differing pedigree structures, *P* was calculated for each case. These probabilities were multiplied together to obtain a single probability for the DP allele at a locus. DP allele probabilities were transformed using a $-\log_{10}$ transformation in order to easily visualize the results on Manhattan-style plots (e.g.,Supplementary Figures 1). A significance threshold of $-\log(P) = 4$ was used to identify putative linked loci.

In order to quickly select a genetic interval from these significant SNPs, a simple algorithm used the highest scoring significant locus as reference for the center and chose interval boundaries based on the closest upstream and downstream RP scores. This analysis returned one significant introgression for 76% of the traits. For the remaining traits where our analysis returned more than one significant introgression, the introgression with at least three consecutive introgressed SNPs displaying the highest level of significance was chosen. These results were printed in tab delimited format (Supplementary Text Files), Manhattan plot format (Supplementary Figures 1) and heat map format (Supplementary Figures 2) for visual analysis. This required visual evaluation of potential introgressions and eliminating those that showed errors. One such example would be choosing between two introgressions, one which has all loci across all NILs as introgressed, and the other which has all loci introgressed except for in one NIL. In both cases, the loci would be significant (-log(*P*)>4), but one is a more likely candidate. Essentially, it was easy for the human eye to detect 2-dimensional introgression patterns, but computational analysis was necessary to narrow down regions of interest.

No major effect was seen on interval mapping from the trait type, but combining alleles aided in producing intervals for traits which had too few NILs or for which all NILs for that trait had a high level of introgressed polymorphic markers. As the case of the former, the Ps-s allele for sparse pubescence could not be used in mapping because the donor parent showed both sparse and dense pubescence phenotyping, and could not be considered a reliable donor. Fortunately, the Ps allele donor provided 3 NILs, and the trait interval could be correctly mapped to chromosome 12. Had only Ps-s NILs been in the collection, this trait could not have been mapped. For the latter, both *I* and *R* traits, responsible for various seed coat pigmentation patterns, had high levels of introgressed polymorphic markers and all loci were above the significant threshold. Though these traits can be easy to phenotype, pedigree information suggests this trait was often combined with other pigmentation traits, which could have led to some mis-phenotyping. The solution to this was to combine NILs with different alleles of *R* (*r*, *r-m*, etc.) and *I* (*I*, *i*, *i-i*) and perform mapping. The combined allele mapping approach was used for three traits as a last resort in these two seed coat pigmentation traits (*R* and *I*), and also as a check in the other 7 traits with available alternate alleles (Supplementary Table 1).

Like Ps-s, four other traits had uncertainty of whether the donor parent carries the trait of interest. *K1*, a saddle pigmentation gene, and *ms2*, a male sterility gene, had no significant introgressed loci, and therefore could not be mapped. This came as no surprise, as the validity of their respective donors were called into question prior to mapping. For the two remaining traits, *Rsv2*, a gene conferring resistance to soybean mosaic virus, and *ln*, a narrow leaf gene, showed a donor parent error, mapping with many low confidence NILs yielded an interval concurrent with previous results.

Results obtained here were checked against literature searches and information available through on Soybase.org. Supplementary Table 1 contains current information on the status of each trait. For many of the traits with only genetic locations, flanking markers were aligned to the Williams 82 genome via BLAST and those physical locations are listed.

Results

Population Characteristics

Collection Composition

The 611 NILs in the USDA soybean genetic collection were developed using one of four different recurrent parent types. The three most commonly used recurrent parents were Clark (MG IV), Harosoy (MG II) and Williams (MG III) or disease resistant isolines of these varieties (e.g., Williams 82) (Bernard, 1991). Over half of the NILs (58%) have a Clark genetic background, while 24% of the NILs have a Harosoy background and 13% of the NILs have a Williams genetic background (Figure 1). The subset of this collection (277 lines) which is genotyped fully has nearly identical proportions of recurrent parent groups, and therefore serves as a good sample. The “other” category (5%) refers to lines with recurrent parents which are not Clark, Harosoy, or Williams. Most of the lines in this category are isolines for which the donor is Clark, Harosoy, or Williams, and other lines, such as Chippewa and Corsoy, serve as recurrent parents. Seven of sixty-six lines in the “other” group have one or two disease resistance genes while the rest are NILs of a leaf, pigmentation, stem growth, or nodulation trait. In total, 81 different traits, representing over 100 different alleles, were isolated onto the Clark, Harosoy, or Williams backgrounds in this collection (Supplementary Table 2).

Though all traits in this collection are controlled by a single locus and are qualitatively inherited, they vary widely in type. The NILs comprising this collection can be categorized into one of seventeen different classes according to the type of trait that has been introgressed, or if they carry more than one trait (Figure 2). Many of these classes have been subdivided from those originally published in the Soybean Genetics Newsletter (Bernard et al., 1991). Of these seventeen, the largest group is comprised of NILs in which a combination of two or more traits of different types had been isolated together (e.g. PI547437 carries the alleles Dt2, a stem growth gene, and e2, a maturity gene). NILs not in the "combination" category can also carry multiple traits but they would be of the same type (e.g. PI547406 carries the two resistance alleles Rps1 and rxp). In total, 61% of the NILs in this collection, and 52% of lines used in this study, have at least two traits introgressed into the RP background.

Isogenicity of Lines within the Collection

The SoySNP50K BeadChip profiles for each NIL in the collection were used to determine the isogenicity of NILs by calculating the marker similarity between the NIL and its RP (Clark, Harosoy, or Williams). The majority of NILs showed at least 90% contribution from the RP (Figure 3). The largest group was that near the predicted incorporation percentage (97.5%) for recurrent parents in the BC_5 scheme, from which the majority of lines are derived. Introgressed polymorphic markers were indicators of the regions responsible for the traits selected for each NIL. These data provide an approximate indication of the isogenicity of lines, and can be used to estimate the number of introgressed loci available to probe for candidate gene regions.

Introgressed SNPs within a NIL are relatively few and clustered together. The majority of lines in this collection have fewer than 1000 introgressed SNPs in their genome inherited from the DP (Figure 4A), most within 100kb of another introgressed locus (Figure 4B). Exact figures for introgressed loci in each NIL are listed in Supplementary Table . Higher levels of introgressed loci are seen in the root fluorescence and nodulation trait categories (Figure 5). These loci were grouped to form introgressions, and so NILs in these categories also contained the highest introgression count.

In this study, introgressed markers less than 1Mb apart were combined into introgressions. The number of introgressions per NIL varied with changing this parameter, but stabilized between 1 and 2 Mb. Therefore, introgression lengths were calculated for 1Mb analysis are dependent on this threshold, and are displayed in Figure 6. The majority of introgressions were below 10Mb in length, with the largest group being introgressions less than 1 Mb. Some introgressions are the length of chromosome arms, and few are represented by SNPs spread across areas up to one chromosome in length.

Mapping

Over half of the traits contained in this collection could be mapped. These included only those traits controlled by nuclear genes. The major limiting factor was the number of NILs for each trait with available genotypic information for the NIL, DP, and RP. Only traits represented by a minimum of three genotyped NILs and for which the parents were genotyped parents could be used. Of the 41 successfully mapped traits all but two produced single candidate intervals after mapping analysis followed by visual verification (Figure 7). The two traits that could not be mapped to a single interval were *Y7* and *Y8*, which only appeared in this collection together in the same NILs and thus the two intervals predicted for these traits could not be attributed to either.

Thirty-three of the traits mapped here have been cloned or mapped previously. Genes for thirteen traits have been previously cloned, while twenty traits have been previously mapped at varying levels of resolution ranging from 1.3kb to over 7 Mbp. Eight of the traits mapped in our analysis had never been mapped before. Details of all traits mapped are presented in Supplementary Table 4. As a validation of our mapping algorithm, we compared our mapping results to previously reported mapping results. We mapped 32 of 33 (97%) previously mapped genes to their previously reported location (Figure 7). Of the thirteen cloned genes, all fell within our predicted intervals. In nearly all cases in which the gene had not been previously cloned, the previously reported interval length was shortened by our analysis of the NIL collection. When observing the overlap between previously mapped intervals and intervals mapped in this study, these intervals were reduced 1.8Mbp on average. Fourteen of the mapped traits had intervals smaller than 2Mbp. Some or complete overlap with previously published results. The largest interval was close to 9Mbp and represented the previously unmapped I_m trait, which is discussed below.

Because of the large number of genes mapped in this study, a gene-by-gene discussion is not included, but rather we included information on the mapped genes in Table 1, Supplementary Table 4, Supplementary Figures 1, Supplementary Figures 2, and the electronic supplementary files. A short description of two interesting cases is provided below, as well as a summary of traits newly mapped in this study.

The *pa1* Locus Moves from Chromosome 11 to Chromosome 12

A pubescence/trichome appression locus, *pa1*, was mapped to chromosome 12 in this study (Supplementary Table 4). This differs from previous results in which *pa1* was mapped to linkage group B1 (Lee, 1999), corresponding to chromosome 11 (Figure 7). No significant loci are detected on chromosome 11, and significant scores can only be seen on chromosome 12 and 13. *Pa2*, a paralog of *pa1*, was concurrently isolated with *pa1* in this collection, and *pa2* has been mapped to chromosome 13 with results from this study and linkage group study. Therefore, the significant markers on chromosome 13 are attributed to *pa2*.

An analysis of genes and gene order in and around the *pa1* (chr12) and *pa2* (chr13) intervals showed many homologous genes between the two genomic regions. Glyma.12G213900 was selected as a candidate gene for *pa1* based on a previously performed GWAS study (Bandillo *et al.*, 2017) and its homolog in *Arabidopsis* (AT3G01140.1) responsible for trichome formation. Furthermore, a potential paralog of Glyma.12G213900, Glyma.13g287700, occurs on chromosome 13 just downstream of the interval mapped here for *pa2*.

The I_m Locus Shows Evidence of Increasing Difficulty in Selection Over Time

Initial mapping results for the I_m trait, which is responsible for preventing seed coat mottling under infection by soybean mosaic virus, showed a very strong peak of significant SNPs on chromosome 9, but a single interval could not be selected by the mapping algorithm used. Further investigation found that NILs created around 1991 may not carry the I_m trait as they were noted as no longer mottling (Bernard et al., 1991). When allelic states within the putative interval were viewed alongside the year of release, it became clear that lines released later (and presumably developed later) carry RP alleles at the candidate interval (Figure 9). Removing questionable lines (reducing the NIL pool from 13 to 8) allowed identification of a clear, single interval.

The distribution of introgressed markers across the genome also highlights differences between the lines released in 1972, 1975, and 1989 (Figure 10). A visualization of the introgressions within the lines released in 1972 show a strong clustering of introgressions at a single genomic region on chromosome 9. Near isogenic lines released between 1975 and 1989, however, show introgressions from the DP appearing on all twenty chromosomes.

Mapping Previously Unmapped Traits

Eight traits that have not been previously mapped were mapped successfully in this study (Table 1). Three of these traits are chlorophyll traits. *Y3* was mapped to chromosome 3. *Y7* and *y8* were selected in tandem and so the intervals on chromosomes 3 and 19 cannot be attributed to one or the other. Two pigmentation traits were mapped.

The I_m seed coat mottling trait is discussed above. The tawny pubescence gene, *td*, has been mapped to chromosome 3. The two unrelated non-color traits newly mapped were placed on chromosome 13; the *S* gene confers short interned length and *Rsv2* confers resistance to Soybean Mosaic Virus (SMV).

Discussion

Here we have collected and organized current available data on the soybean isoline collection into a comprehensive set containing NIL categories, trait types, trait descriptions, mapped intervals, and cloned genes. The overarching goal of this study is to revitalize this collection for the use of soybean researchers through two objectives: characterize the collection in terms of content/ isogenicity and present new and improved mapping results for 41 qualitative traits isolated in this collection. Two small case studies and a discussion on newly mapped traits are also described to highlight these objectives.

Collection Overview

The lines in this collection are primarily of the Clark, Harosoy, or Williams genetic background. These contemporary commercial varieties were suitable recurrent parents for multiple reasons. First, their elite commercial status in the mid twentieth century ensured they were true breeding and could provide a reliable clean slate onto which traits could be incorporated and judged for commercial use. Second, these lines were members of the three closest maturity groups to Urbana, Illinois, where this collection was being developed. As for relevance to today's research, all three of these lines are common in variety development and soybean genetic studies. GRIN identifies hundreds of lines in the Clark, Harosoy, and Williams sub collections, and many more lines in the USDA Soybean collection have at least one of those three in their direct genetic background (ars-grin.gov). These lines were ideal for isolating traits for future genetic studies.

Though all traits in this collection are single locus and qualitative, they vary widely in type. Bernard identified nine categories in the 1991 Soybean Genetic Newsletter, but some were subdivided here in order to give a clearer idea of the range of traits available in the collection. For example, *ms1*, a male sterility gene, had been put into the "other" category by Bernard, which included other traits such as the seed trait *n* (abnormal hilum abscission) and a multitude of cytoplasmic genes. In the end, 17 categories were more appropriate.

The largest category, "combination", highlights a key feature of this collection: most isolines in this collection had two or more traits introgressed onto their recurrent parent background. "Combination" NILs were developed with traits from at least two different categories. Many of these combinations were predicted to be linked genes, while others were targeted combinations of traits such as stem growth and maturity (Bernard et al., 1991). Lines outside of the "combination" category could also contain at least two traits, but all are from the same category. These lines were useful in this study because they could be utilized in mapping multiple traits because more of their introgressions were informative.

NILs in this collection could have anywhere between 0 and ~4500 introgressed loci. Loci within 1Mb of each other were combined into introgressions, 70% of which are under 10Mbp in length. Given the majority of NILs carry at least two traits, and recombination was unrestricted outside of the regions for these traits, the number and length of off target introgressions is inconsequential to this study. Though most NILs carried at least two traits, the number of traits selected for during development had no effect on the number of extraneous introgressed loci seen in each NIL. Instead, the trait type had a significant effect, indicating phenotyping quality may have played a major role in the proportion of introgressed markers across the chromosomes. Additionally, though not likely, these traits could have other polygenic factors, leading to more loci being introgressed across the genome.

In general, a very high marker introgression percentage indicates a decreased ability to accurately select for the target trait (see I_m case study below for an in-depth example). The four trait types with the highest mean introgression count per NIL (seed composition, root fluorescence, male sterility, and nodulation) all require more in-depth phenotyping procedures than a visual scan of plant rows at crossing time. Seed composition is determined by wet lab techniques, root fluorescence and nodulation require destructive assays, and male sterility genes introduce multiple considerations for the maintenance of a line. The lines with the largest introgressions were selected for the *ab* (delayed leaf abscission) and *Rj1* (non-nodulation). Both *Ab* and *Rj1* are traits for which phenotyping procedures may have been more complex: *Ab* requires making crosses before leaf abscission can occur, most likely relying on culling in the next generation for selection, while *Rj1* requires a destructive assay of the roots. High polymorphic marker introgression can be a strong indicator for insights to the development of NILs in this collection.

Low marker introgression can also be a source of inference. The most obvious example of this would be the few NILs with one or a few small introgressions in their genome. In this case, trait selection was fairly easy. A NIL with no polymorphic introgressions tells a different story. Four lines showed no introgressed polymorphic markers. However, none of these lines were isolines derived from point mutations in one of the common recurrent parents. This indicates one of two possibilities: the line was mis-phenotyped and does not carry the target gene allele or the SoySNP50K BeadChip did not have the resolution to capture the mutation.

Trait Mapping

Thirty-nine traits plus two tandem traits, a totally of 41, were successfully mapped using the methods in this study with a mean interval length of 2.35Mbp and a median interval length of 1.54Mb. All traits with cloned genes or established physical locations were mapped to the same location by this method (except *pa1*, see below). Therefore, newly mapped traits have a high probability of having a candidate gene in their respective intervals mapped here. Eight mappable traits in this collection have yet to be mapped in other studies, and intervals have been mapped for all of them (Table 1). The mean interval size for the newly mapped traits is 2.56 Mb, and the median size is 1.18 Mb.

For traits with previous information on their location in the soybean genome, results here contributed to reducing the genomic interval size for fourteen which do not already have a cloned gene. These traits have been previously mapped with other markers, such as SSRs or RFLPs, have overlapping or completely encompassed these previously reported regions.

Traits selected in tandem added a different layer to interval mapping. The primary example for this was the *Y7* and *Y8* pair. Both of these genes confer homozygous lethal chlorophyll deficiencies. However, when they are present together and heterozygous, lethality is eliminated in favor of a yellow color in new leaves (Williams, 1950). Therefore, these genes were isolated together and neither are individually present in any of the collection's NILs. In mapping both, intervals appear concurrently on chromosomes 19 and 3. However, because neither gene is completely isolated from the other, the intervals cannot be attributes to either *Y7* or *Y8*. In some cases, tandem selection could confirm mapping results, as with *pa1* and *pa2* (discussed below). It can also help narrow candidate intervals to a single one by eliminating peaks which can be attributed to other traits present in the NILs according to pedigrees.

Case studies and Newly Mapped Traits

Two case studies have been observed to show the flexibility of the data associated with this collection. In the first, a trait which has been previously mapped to one chromosome is shown to reside on a different chromosome. In the second, meta-analysis of the mapping of an outdated resistance gene gleans new knowledge on the change in ability to select for a trait over time. Additionally, the traits newly mapped in this study have been highlighted.

The pa1 Locus Moves from Chromosome 11 to Chromosome 12

The *pa1* trait, responsible for pubescence appression, is the only trait which was mapped confidently to a different chromosome than previous literature indicated (Figure 7). *Pa1* had been mapped to Linkage group B1 (Lee et al., 1999). *Pa1* and *pa2*, another pubescence density gene, were seen as potential paralogs resulting from the most recent soybean genome duplication. They were historically located on chromosomes 11 and 13 respectively, and these chromosomes were assumed ancient duplicates. In the USDA Soybean isoline collection, most *pa1* isolines were also selected for *pa2*, so two significant regions were expected from mapping. For both traits, mapping results showed significant introgressions on chromosome 12 and 13, but none on chromosome 11. The chromosome 13 interval was confidently associated with *pa2*, but there was still the question of whether *pa1* had been mistakenly placed on chromosome 11 previously.

To support the hypothesis stating the *pa1* gene resides in an interval on chromosome 12, we looked to other literature sources. An association study in which *pa1* was placed on chromosome 12 provided not only support for our results, but a significant SNP revealed a candidate gene, Glyma.12G213900 (Bandillo *et al.*, 2017). This gene has yet to be annotated in soybean, but is homologous to an MYB gene responsible for leaf trichome branching in Arabidopsis. This gene serves as a likely candidate for *pa1*, a pubescence density gene, as leaf trichomes and pubescence share similar structure. Further genetic analysis is required to confirm its function in soybean. If this gene is to serve as a candidate, then it was safe to assume its paralog on chromosome 13 would be the candidate gene for *pa2*.

The chromosome 13 paralog to Glyma.12G213900 lies downstream of the interval mapped for *pa2*, not within it. Referencing the Bandillo study again, significant loci for *pa2* lie directly upstream of our candidate interval, and nowhere near this paralog. Taking a closer look, many genes associated with the same pathways are located in and surrounding both *pa1* and *pa2* intervals, and gene order is generally conserved. This calls into question previously reported results yet again. If *pa1* and *pa2* are paralogs, there should be evidence of highly significant loci in or around two paralogous genes. Instead, we see highly significant loci in duplicated chromosomal regions. These results indicate *pa1* and *pa2* may not be paralogous genes. They are instead genes from same pathway affecting pubescence development.

The I_m Locus Shows Evidence of Increasing Difficulty in Selection Over Time

Mapping the I_m trait, responsible for preventing seed coat mottling under infection by Soybean Mosaic Virus (SMV), provided a different view of the decreased ability to phenotype. Unlike other traits discussed, where phenotyping procedures can prevent efficient selection, this is an example in which a trait became more difficult to phenotype over time. The first I_m isolines for this collection were released in 1972. More were released in the second wave of lines in 1975, and a final set was released in 1991. With the 1991 release, Bernard left a note in the I_m description in the Soybean Genetic Newsletter: “In recent years at Urbana lines with this genotype have mottled”(Bernard et al., 1991). Sometime between 1972 and 1991, the I_m isolines lost the ability to resist mottling under SMV pressure, even with selection.

A look at the I_m NILs grouped by year reveals this pattern to be true. These lines can be divided into three categories by year entered into GRIN (1972, 1975, and 1989). The genetic interval for the I_m trait was clearly outlined by introgressed polymorphic loci in 1972. As time went on, phenotyping became less compact. This is seen in the 1975 lines, where fewer introgressed markers are at the I_m site and more introgressed markers are on other chromosomes. With introgressed markers becoming less focused at the target locus, it can be inferred that selecting the trait was hindered. By 1989, the interval has all but disappeared, selection was problematic, and the interval could not be successfully isolated in those lines.

The reasons for this increase in selection difficulty are not clear. One possibility is the disease was overcoming the trait, and Bernard was encapsulating its progress by releasing isolines as the process went on. This, however, cannot be confirmed without first eliminating other likely causes, such as crossing too many confounding traits together or seed mix-ups with susceptible lines. Unfortunately, the I_m trait can no longer be probed molecularly to confirm the genetic interval mapped here as it was shown to be ineffectual against SMV infection (Hobbs et al., 2003). One thing is for certain, isolation of the *Im* trait became impossible near the end of the 1980's (Orf, 2017). Though it is no longer a viable trait for researchers today, this case study provides a solid example of using historical collections and notes to track ability to select a trait over time.

Mapping Previously Unmapped Traits

Eight traits have been mapped in this study, but further studies will be needed to select candidate genes. Three chlorophyll genes were newly mapped. *Y3* was mapped to chromosome 3 using 5 NILs. As discussed above, the tandem selection of *y7* and *y8* prevents a discernment regarding which interval is which gene. If subsequent studies to definitively map these genes cannot use other lines with these alleles, more advanced molecular techniques must be considered. Two pigmentation traits were mapped: the I_m seed coat mottling trait is discussed above. The tawny pubescence gene, *td*, has been mapped to chromosome 3.

The two unrelated non-color traits newly mapped were placed on chromosome 13; the *S* gene confers short internode length and *Rsv2* confers resistance to Soybean Mosaic Virus (SMV). The *S* trait, combined with the *Dt1* allele, creates short internodes in the soybean plant resulting in a shorter plant (Lewers, 1998). Though the plant is shorter, it does not significantly affect yield. Therefore, this allele could be useful in breeding for production. Rsv2 was mapped to chromosome 13. Studies published after the release of this collection have indicated that *Rsv2* is nothing more than an allele of the *Rsv1* gene (Wang et al., 1998; Buss et al., 1995). Our analysis indicates that the *Rsv2* interval lies just under 1Mb from the predicted interval of the Rsv1 gene on Soybase.org. This supports the multiple gene theory of SMV resistance (Zhang, 2012). Further analysis of the *Rsv2* interval here could give rise to more knowledge of the resistance genes region on chromosome 13.

Conclusions

In this study, we have demonstrated the organization and expansion of data and information available for the USDA Soybean Isoline Collection. In the first part, the collection underwent characterization in terms of content and isogenicity. It was shown that isogenicity varies across the collection according to trait type, and it was hypothesized that phenotyping protocols had an effect on the ability to select. In the second part, highly confident intervals have been mapped for 41 of the traits isolated by Bernard in this collection. From these, candidate genes have been selected for two traits, *pa1* and *pa2*, which will require further validation studies. Another use of this data has been demonstrated by the temporal analysis of I_m. Additionally, further studies will be necessary to select candidate genes for the eight previously unmapped genes discussed here. Most of the traits mapped here produced smaller intervals than what has been previously published. The information provided in this study is a sufficient starting off point for gene cloning studies for many traits. This study has shown a simple method to revitalize a historical resource by mining public datasets and using more recent technology to fill gaps rather than creating all new, redundant, datasets.

ILLUSTRATIONS

Table 1 Newly mapped traits from this study.

Trait	Other Alleles	Description	Type	Chr	Start	End	Size (Mb)
ab	Ab	Delayed leaf abcission	Leaf Form	13	30086805	34775605	4.68
lm		Non-mottling (Non-mottling under SMV infection)	Pigmentation	9	12809350	21080454	8.27
Rsv2		Resistant to Soybean Mosaic potyvirus Infection	Disease Resistance	13	29761581	32459471	2.69
S	s-t	Short internode length	Stem Growth	13	38027686	39207273	1.17
td		Light tawny to near-grey pubescence with T	Pigmentation	3	43513124	45643162	2.13
y3		Leaves turn rusty yellow with g	Chlorophyll	11	2175770	6565408	4.38
y7/y8		New leaves very light green in cool weather with y8	Chlorophyll	3	561263	2315408	1.75
y7/y8		New leaves very light green in cool weather with y7	Chlorophyll	19	36161480	40236466	4.07

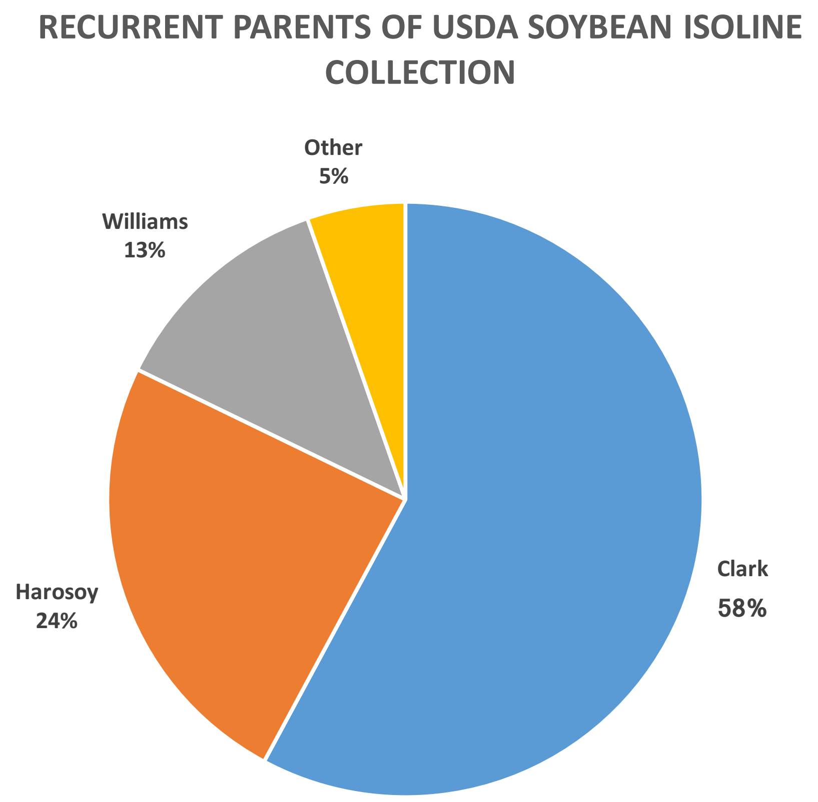


Figure 1 Proportion of NILs derived from each recurrent parent type in the USDA Soybean Isoline Collection (611 lines in all).

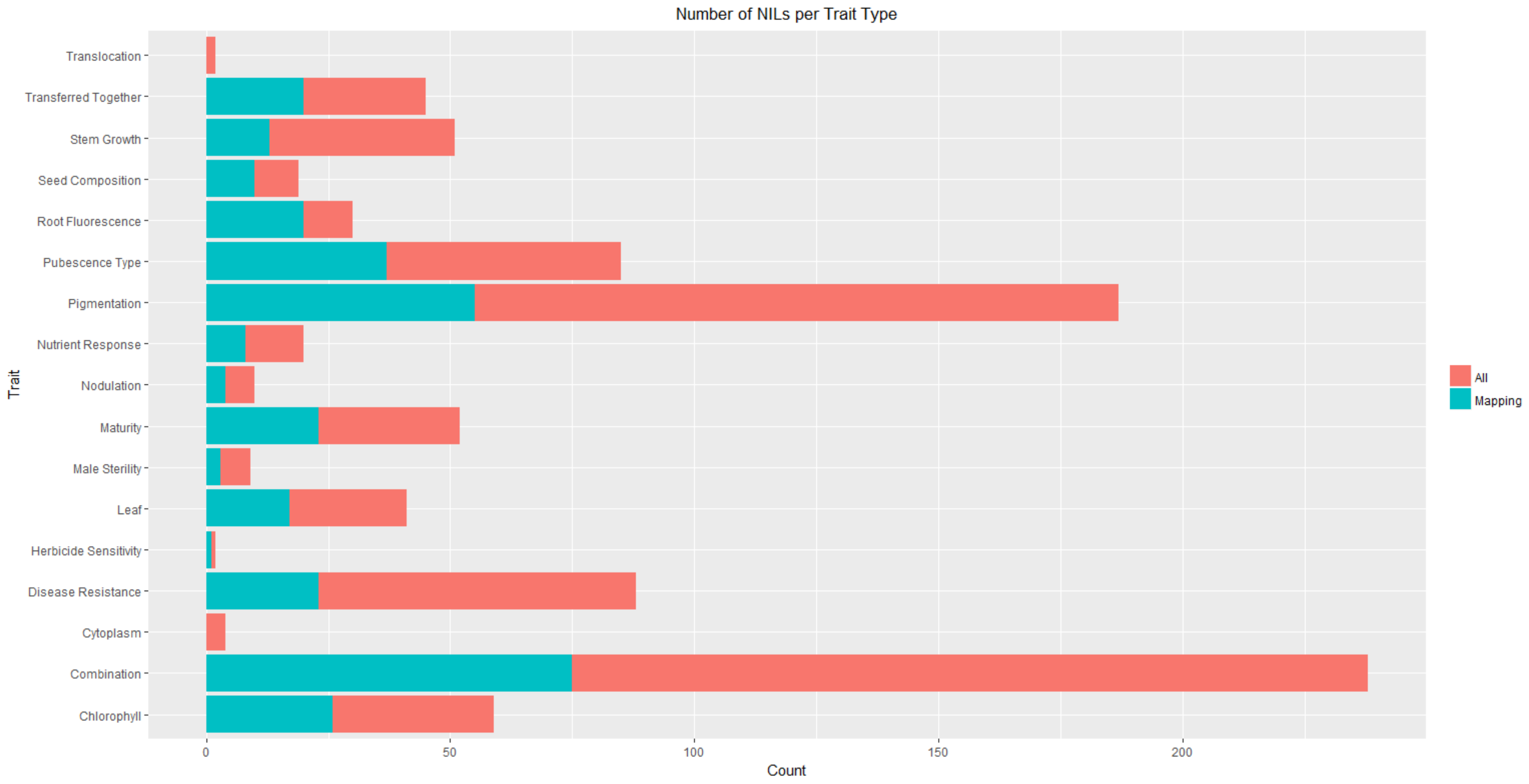


Figure 2 Number of NILs distributed for each category. Colored bars indicate the proportions of these lines that were genotyped and had genotyped parents (blue) These line were used in parent contribution and trait mapping analyses (277 lines). The pink indicates the proportion of lines with incomplete genotypic profiles (not genotyped or one or both parents not genotyped).

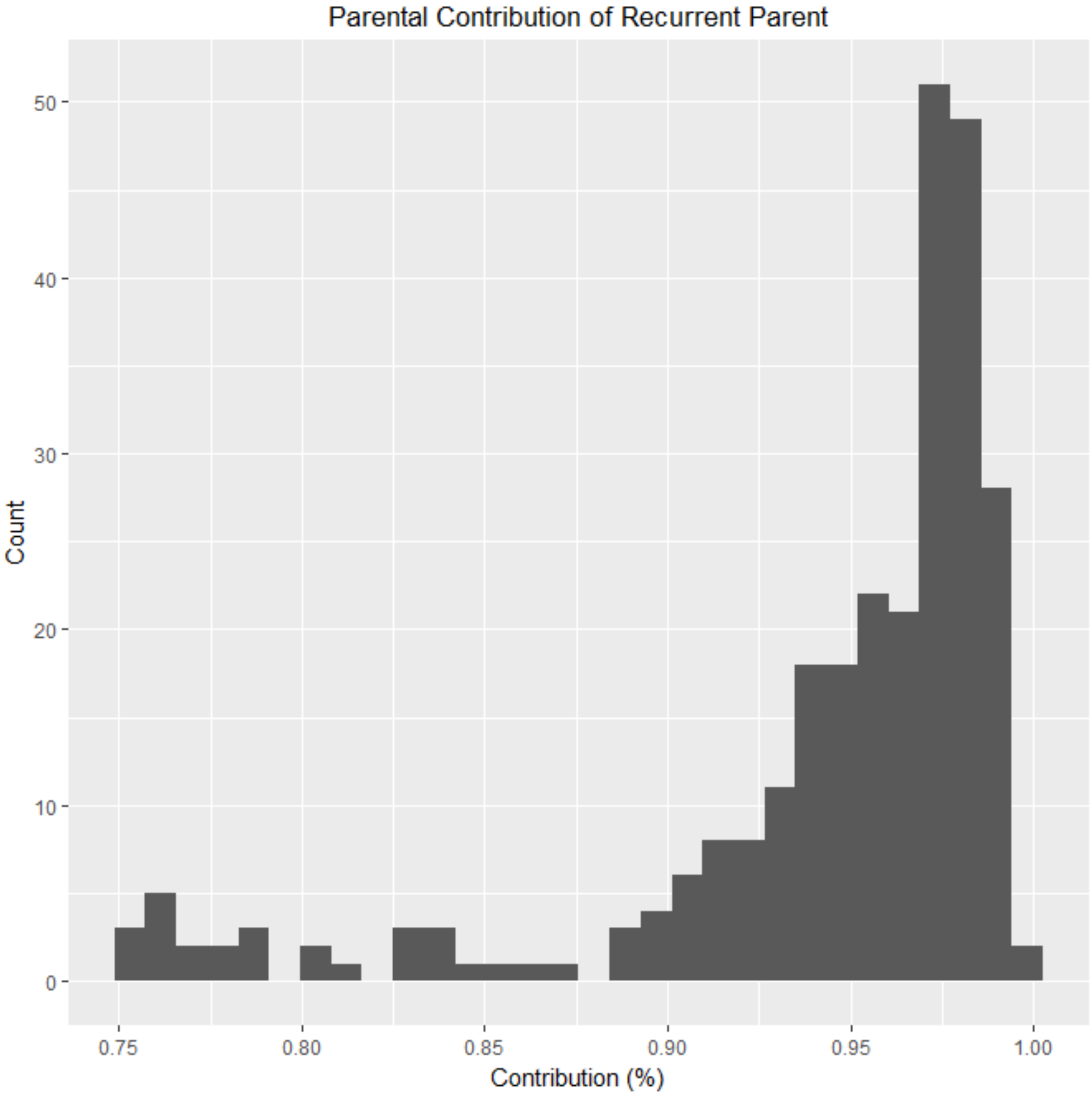


Figure 3 Histogram displaying the distribution of NILs with varying levels of genetic contribution from their respective recurrent parents.

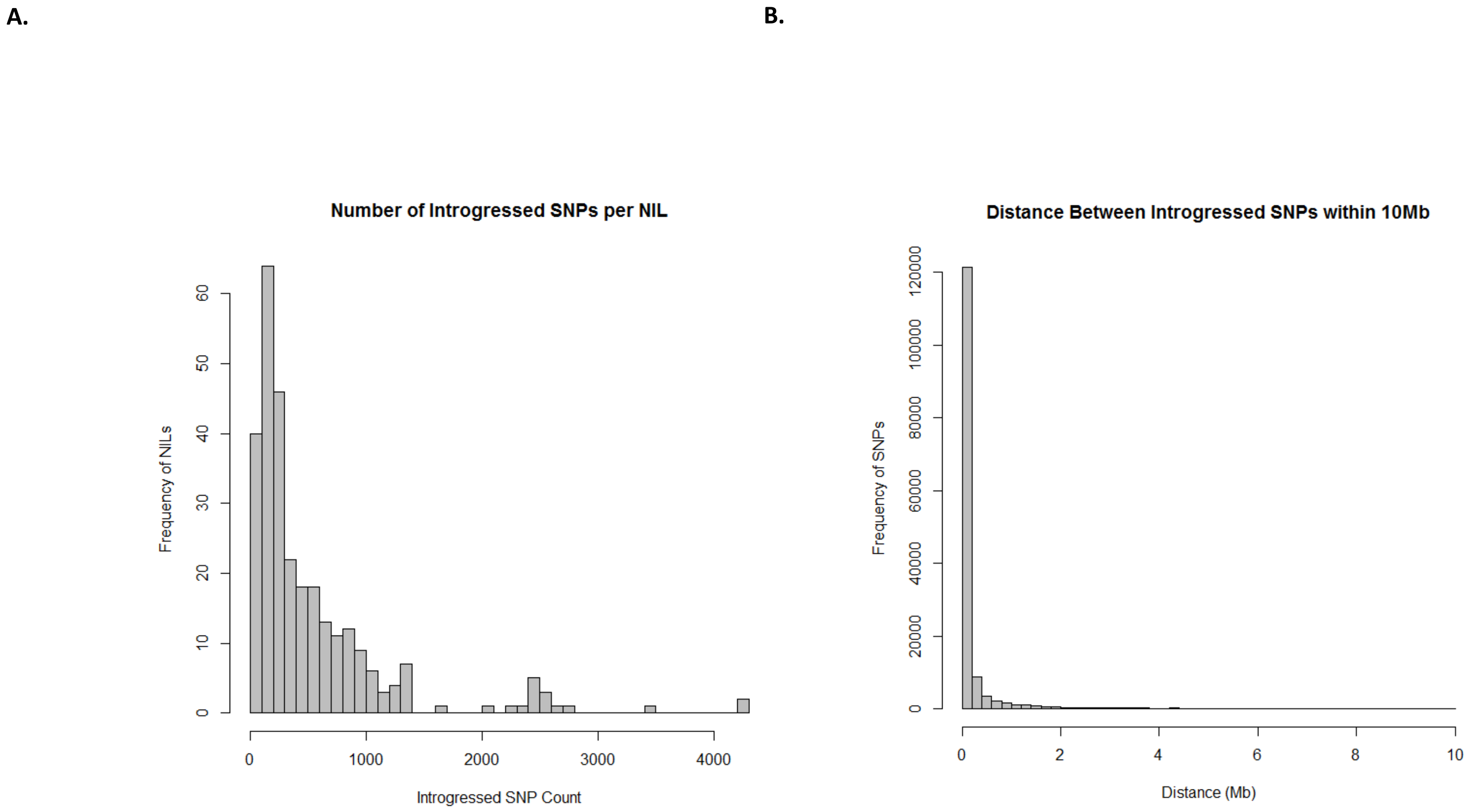


Figure 4 Number and distribution of introgressed SNPs across the NIL genomes. A) Histogram showing the distribution of NILs with varying number of introgressed loci. B) Histogram showing the distribution of distances between introgressed SNPs in the same NIL on the same chromosome.

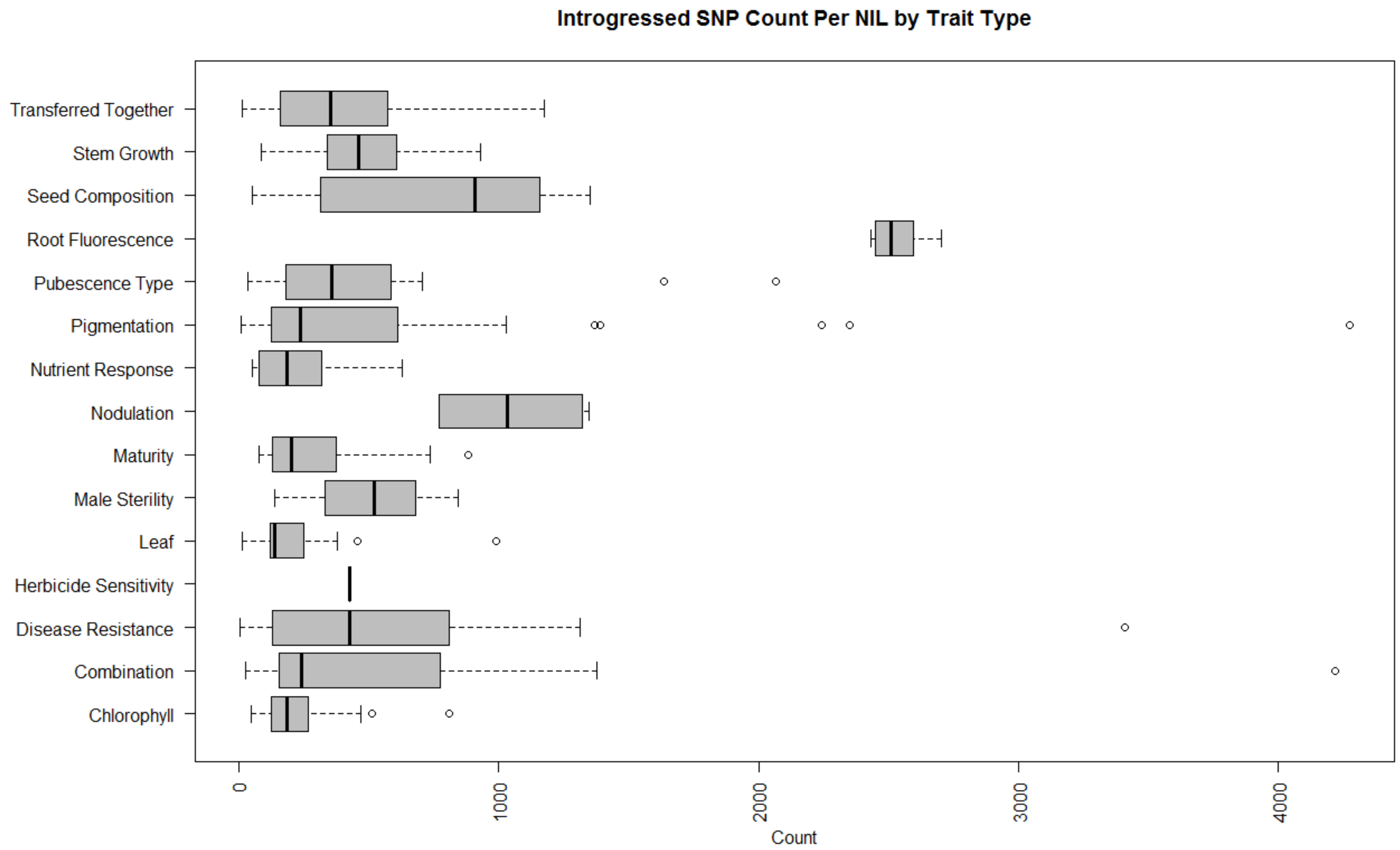


Figure 5 Boxplot displaying the number of introgressed SNPs per NIL divided by trait type.

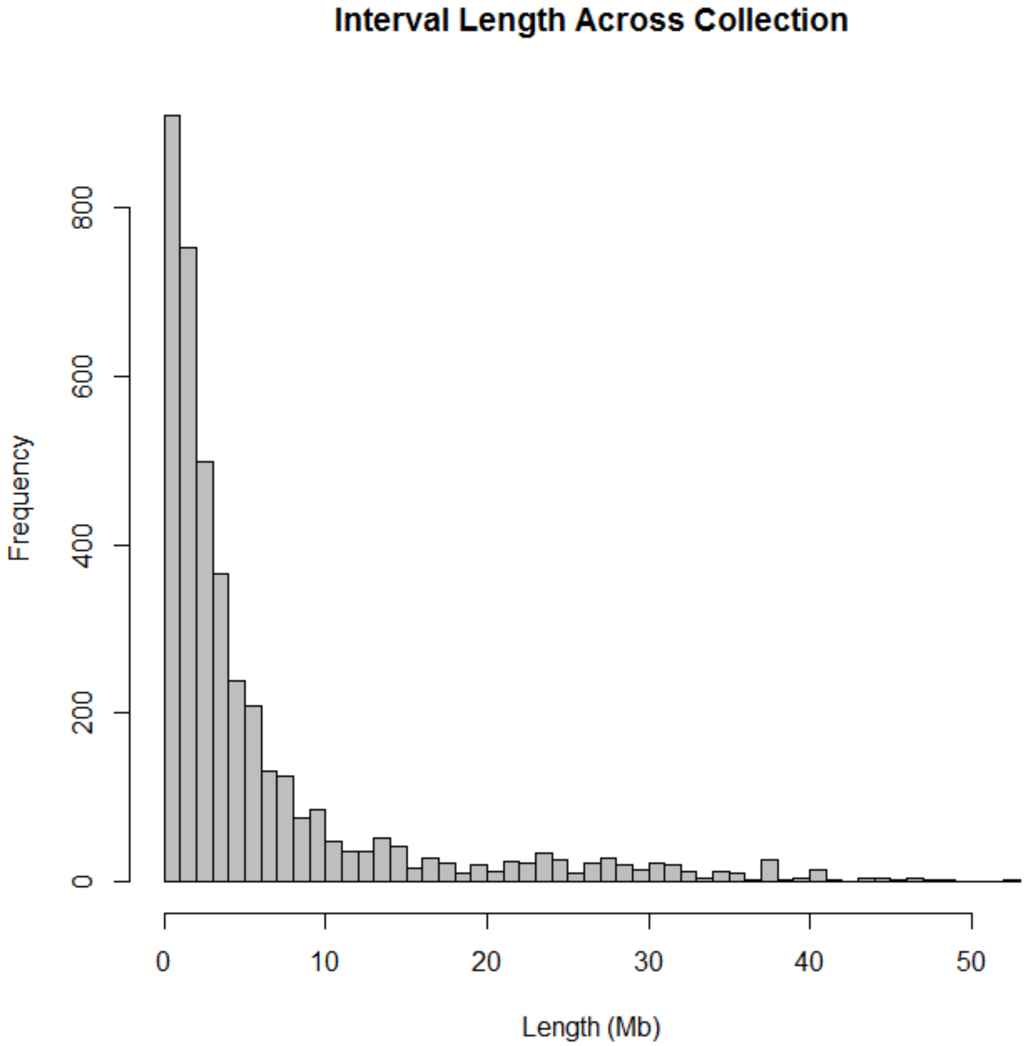


Figure 6 Histogram of lengths of all introgressions found in lines with complete genotypic information. These introgressions were generated by groupins introgressed loci within 1Mb of each other.

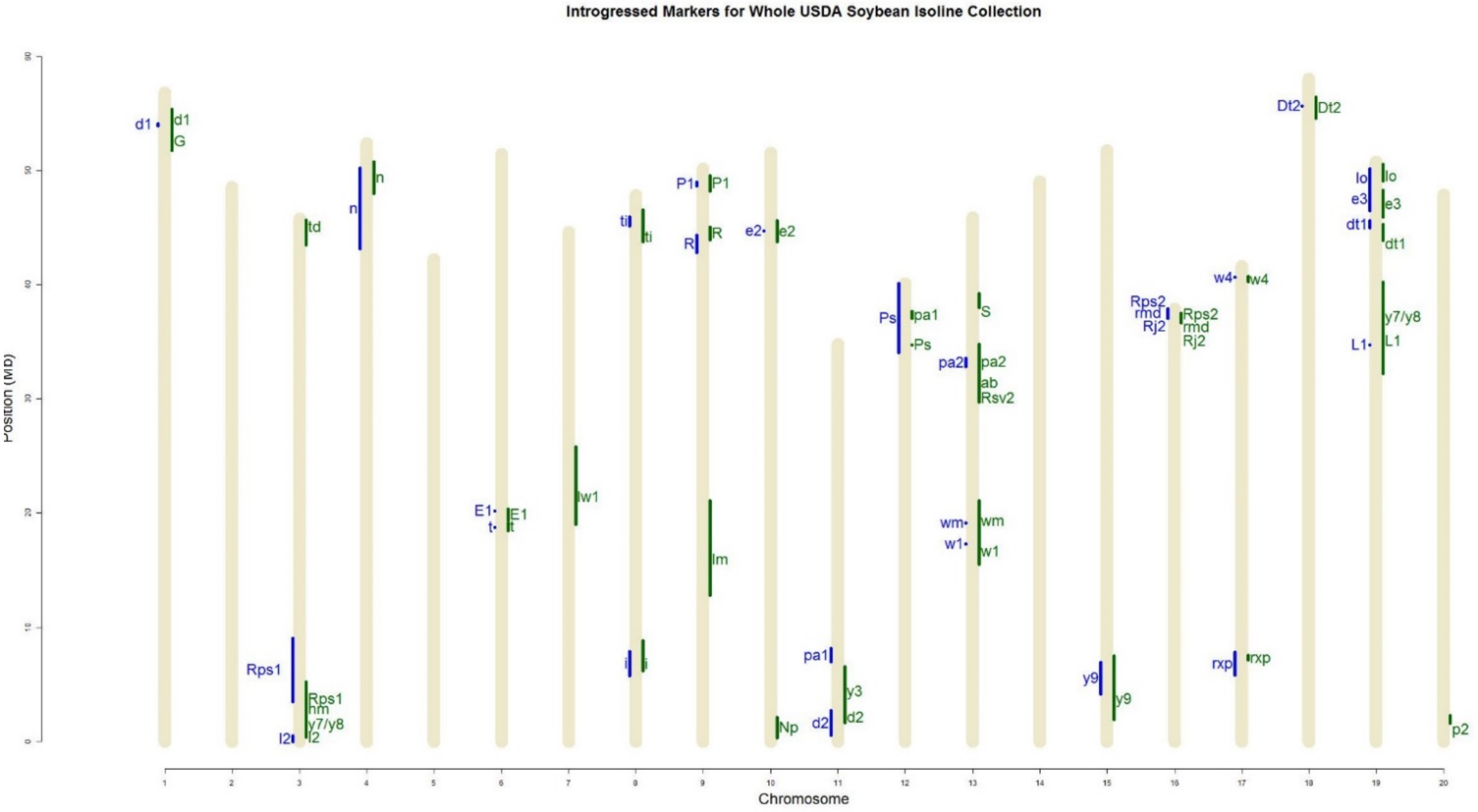


Figure 7 Physical map of the soybean genome diplaying position of genes mapped in this study. Blue lines and labels indicate the previously reported gene location. Blue points and labels indicate cloned genes. Green lines and labels indicate the interval mapped in this study for each gene.

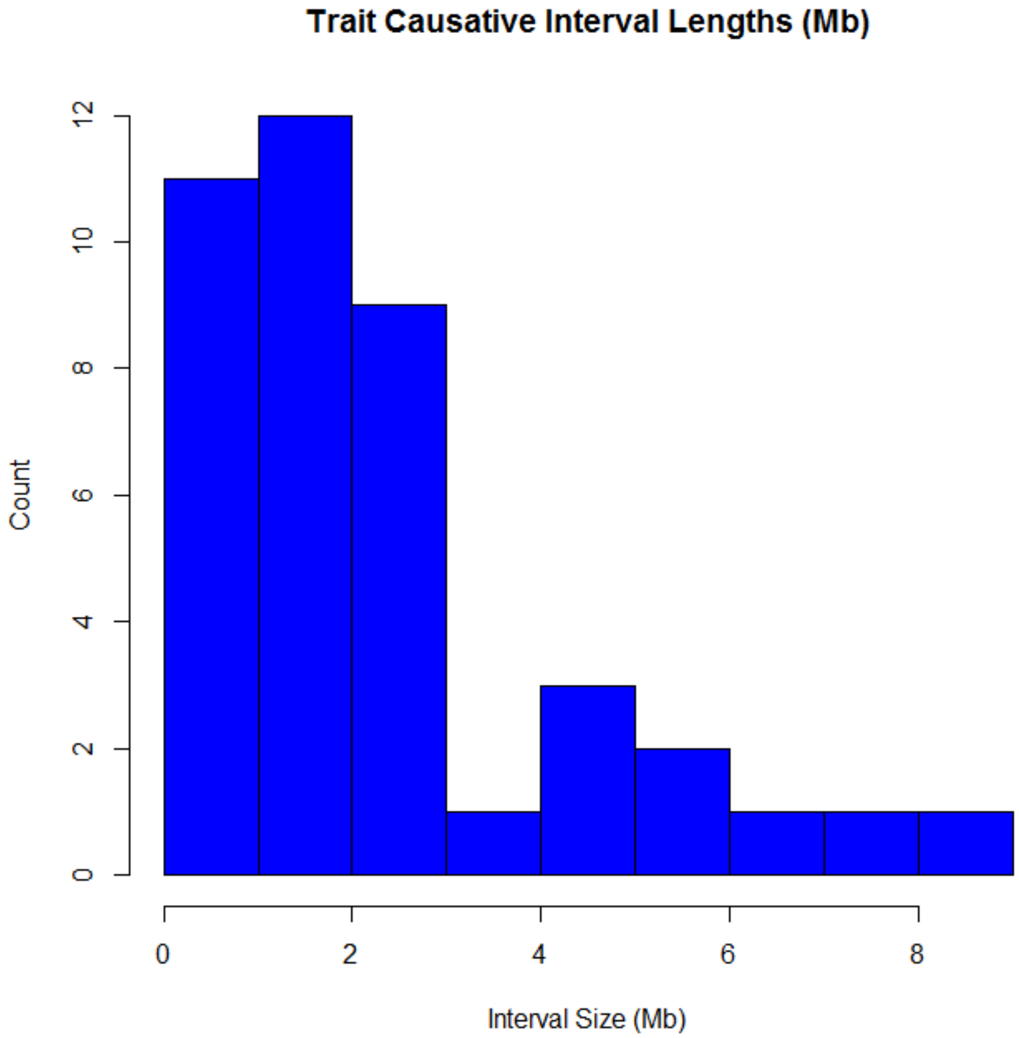
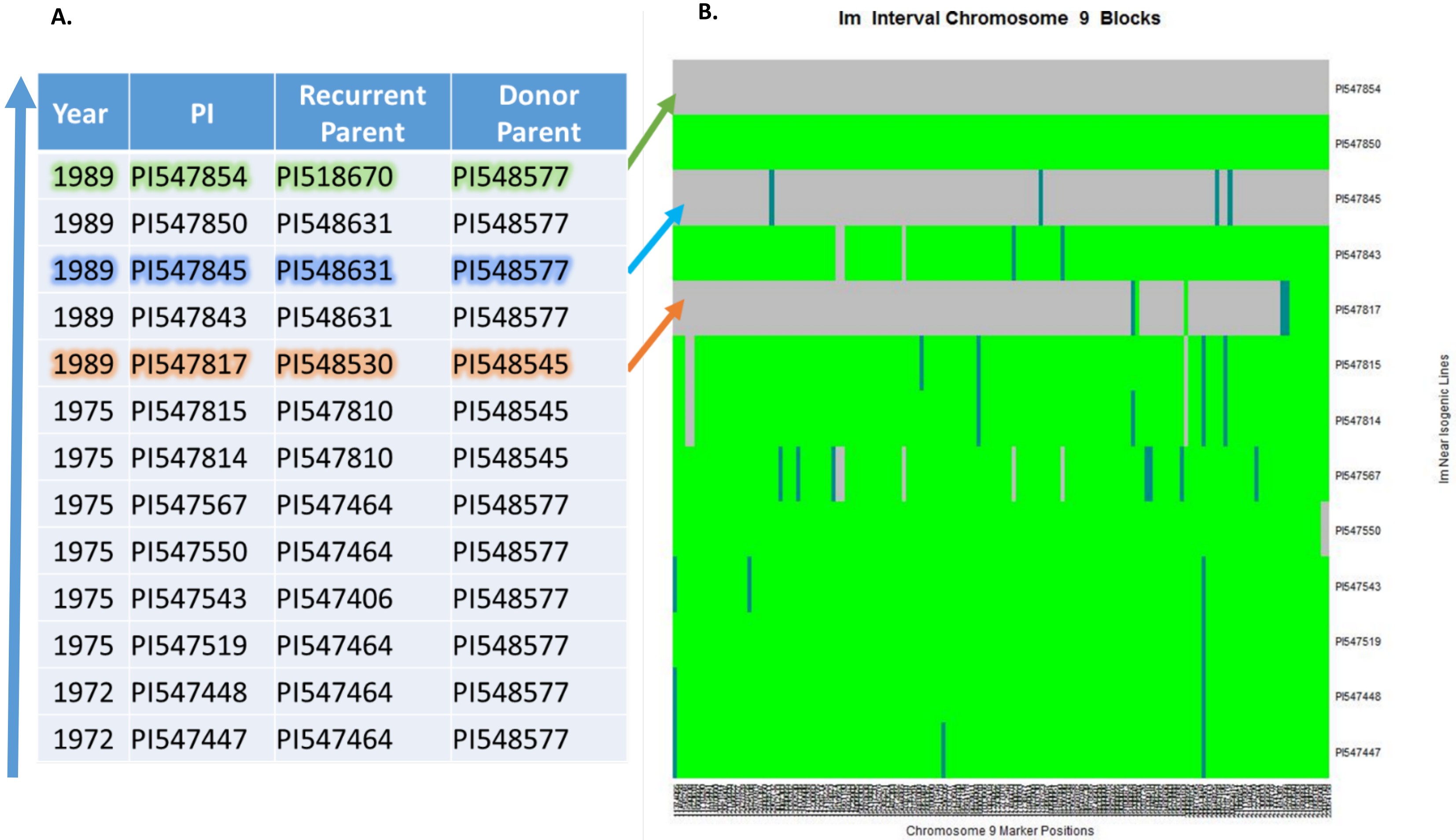
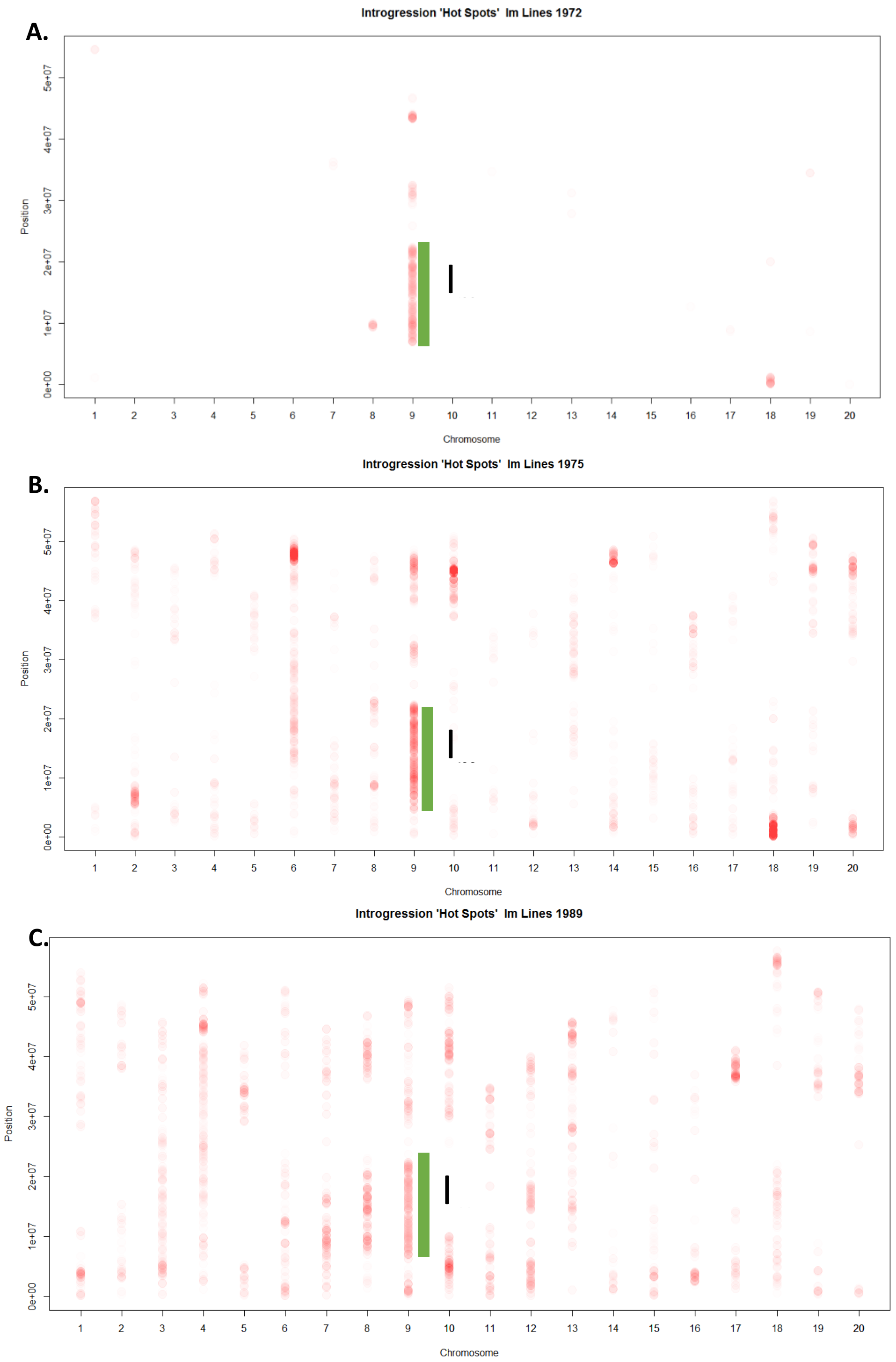


Figure 8 Distribution of interval sizes in megabases for all 41 traits mapped.



Year	PI	Recurrent Parent	Donor Parent
1989	PI547854	PI518670	PI548577
1989	PI547850	PI548631	PI548577
1989	PI547845	PI548631	PI548577
1989	PI547843	PI548631	PI548577
1989	PI547817	PI548530	PI548545
1975	PI547815	PI547810	PI548545
1975	PI547814	PI547810	PI548545
1975	PI547567	PI547464	PI548577
1975	PI547550	PI547464	PI548577
1975	PI547543	PI547406	PI548577
1975	PI547519	PI547464	PI548577
1972	PI547448	PI547464	PI548577
1972	PI547447	PI547464	PI548577

Figure 9 Visualization of recurrent parent allele contamination over time in Im isolines on. A. Lines with their parents are listed by year they are released. B. Heat map of lines colored according to locus allele on chromosome 9 between positions 12809350 and 21080454. Green represents a donor allele while grey represents a recurrent allele. Lines are stacked in the same order as in A.


Introgression 'Hot Spots' Im Lines 1972

Introgression 'Hot Spots' Im Lines 1975

Introgression 'Hot Spots' Im Lines 1989

Figure 10 Spread of introgressed markers over the genome in lines that were developed at different times (A. 1972, B. 1975, C. 1989) .The predicted interval for Im is indicated with a green bar.

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APPENDICES

Supplementary Methods

NIL Scoring

Each NIL SNP allele was compared to its corresponding read in both DP and RP and scored. Loci at which the DP and RP were monomorphic or the NIL allele was undefined "U" were given a null. Loci in which all NILs had null scores were removed from analysis to save computation time. Each locus where the NIL matched the DP only and the NIL s known to carry the trait was scored as 1. Where the NIL matched the RP only, it was scored as a 0. In the special case where the NIL was carrying an alternative allele (A) than the target allele (a), these 1 and 0 scores were reversed. This inversion of scores depending on the wildtype/mutant status of the NIL allowed mapping with the maximum number of lines per NIL. This increased the mapping power for 9 traits by allowing NILs with different alleles of the same trait to be combined. SNPs with a heterozygous (H) score in the NIL were scored as 0.5. When these lines were genotyped, samples from multiple individuals representing each line were bulked and then genotyped. Therefore, if either DP or RP had a heterozygous read, it was scored with a "*" to indicate that it is unknown whether the locus is truly heterozygous or if the bulked samples were heterogeneous. SNPs at which either of the parents had a "U", or undefined, read were also given a "*" for the purpose of removing them from calculation but indicating their presence in visual verification. If the NIL had a "U" call, it was given a "-" null score.

Supplementary Table 1

Supplementary Table 1 This table summarizes each line in the full USDA soybean isoline collection. The PI number, traits isolated in the line, pedigree, trait class, and subcollection. Credit to R. Nelson for cataloging this data.

acid	entry	genes	parentage	trait	MG	Subcoll-ection
PI597653	A93-213	fr1	Hark	root fluorescence	I	Other
PI597654	A93-214	fr2	Hark	root fluorescence	I	Other
PI597655	A93-215	Fr3	Hark	root fluorescence	I	Other
PI597656	A93-216	fr4	Hark	root fluorescence	I	Other
PI597660	A95-FR-10	fr1 Fr3	Hark	root fluorescence	I	Other
PI597661	A95-FR-11	fr2 Fr3	Hark	root fluorescence	I	Other
PI597662	A95-FR-12	Fr3 fr4	Hark	root fluorescence	I	Other
PI597657	A95-FR-7	fr1 fr4	Hark	root fluorescence	I	Other
PI597658	A95-FR-8	fr1 fr2	Hark	root fluorescence	I	Other
PI597659	A95-FR-9	fr2 fr4	Hark	root fluorescence	I	Other
PI547895	BARC-2	Rj4 *	Clark 63(9) x Hill	Nutrient Response	IV	Clark
PI509547	BARC-4	Rj2 Rps2 *	Clark 63(9) x Hardee	combination	IV	Clark
PI548531	Chippewa 64	Rps1	Ch(8) x Blackhawk	disease resistance	I	Modern
PI518669	Corsoy 79	Rps1-c	Corsoy(6) x Lee 68	Disease Resistance	II	Modern
PI542044	Kunitz	ti Rps1-k	Wm 82(6) x PI 157.440	Seed composision	III	Modern
PI547402	L58-231		Lincoln(2) x Richland	typical subline of Clark	IV	Clark
PI547676	L58-266		Mandarin (Ottawa)(2) x AK (Harrow)	typical subline of Harosoy	II	Harosoy
PI547677	L59-731	Rps1	H(8) x Blackhawk	Disease Resistance	II	Harosoy
PI547403	L60-246	Rps1 rxp	(C(7) x CNS)rxp x (C(6) x Blackhawk)Rps1	Disease Resistance	IV	Clark
PI547678	L61-4094	rxp	H(6) x S54-1207	Disease Resistance	II	Harosoy
PI547404	L61-4180	rxp	C(8) x CNS	Disease Resistance	IV	Clark

PI547405	L61-4222	Rps1	C(8) x Blackhawk	Disease Resistance	IV	Clark
PI547679	L61-5047	Rps1 rxp	Harosoy 63 x L3,rxp	Disease Resistance	II	Harosoy
PI547406	L61-5448	Rps1 rxp	L8,rxp x L7,Rps1	Disease Resistance	IV	Clark
PI547407	L62-1027	cyt-G	Medium Green x C(7)	Chlorophyll	IV	Clark
PI547408	L62-1058	I	C(6) x T201	Pigmentation	IV	Clark
PI547409	L62-1251	Dt2	C(6) x T117	Stem Growth	IV	Clark
PI547410	L62-1377	P1 r	C(6) x T145	transferred together	IV	Clark
PI547411	L62-1383	r	C(6) x T145	Pigmentation	IV	Clark
PI547412	L62-1385	P1	C(6) x T145	Pubescence Type	IV	Clark
PI547451	L62-1568	ln t	C(6) x T204	transferred together	IV	Clark
PI547413	L62-1579	ln	C(6) x T204	leaf	IV	Clark
PI547414	L62-1615	lo	C(6) x T204	leaf	IV	Clark
PI547415	L62-1686	Pd1	C(6) x PI 80.837	Pubescence Type	IV	Clark
PI547680	L62-17	cyt-G	Medium Green x H(7)	Chlorophyll	II	Harosoy
PI547416	L62-1932	e2	C(6) x PI 86.024	Maturity	II	Clark
PI547681	L62-364	Dt2	H(6) x T117	Stem Growth	II	Harosoy
PI547714	L62-542	l2	H(6) x T145	Pigmentation	II	Harosoy
PI547715	L62-558	l2 P1	H(6) x T145	Transferred together	II	Harosoy
PI547682	L62-561	P1	H(6) x T145	Pubescence Type	III	Harosoy
PI547716	L62-667	e3	H(6) x T204	Maturity	II	Harosoy
PI547683	L62-801	Pd1	H(6) x PI 80.837	Pubescence Type	II	Harosoy
PI547763	L62-812	Dt2 E5	H(6) x PI 80.837	combination	II	Harosoy
PI547684	L62-880	Ps	H(6) x PI 91.160	Pubescence Type	II	Harosoy
PI547764	L62-904	Rps5 w1	H(6) x PI 91.160	combination	II	Harosoy
PI547685	L62-906	w1	H(6) x PI 91.160	Pigmentation	II	Harosoy
PI547686	L62-956	Lf1	H(6) x PI 86.024	leaf	II	Harosoy
PI547687	L62-973	dt1	H(6) x PI 86.024	Stem Growth	II	Harosoy
PI547688	L63-1016	y3	H(6) x T139	Chlorophyll	II	Harosoy
PI547765	L63-1069	R	H(6) x T139	Pigmentation	II	Harosoy
PI547689	L63-1097	pc Fg3	H(6) x PI 84.987	Pubescence Type	III	Harosoy
PI547690	L63-1212	ln	H(6) x T204	leaf	II	Harosoy
PI547717	L63-1397	Dt2	H(6) x PI 80.837	Stem Growth	II	Harosoy

PI547795	L63-16	Rps1	Ch(10) x Blackhawk	disease resistance	I	Other
PI547718	L63-1612	wm Rps1	Harosoy 63 x [(T235(2) x H(5) x Blackhawk)]	combination	II	Harosoy
PI547417	L63-1677	Np	C(6) x Chief	Nutrient Response	IV	Clark
PI547418	L63-1792	y7 y8	C(6) x T138	Chlorophyll	IV	Clark
PI547419	L63-1889	rj1	C(6) x T201	Nutrient Response	IV	Clark
PI547452	L63-2346	y3	C(6) x T139	Chlorophyll	IV	Clark
PI547420	L63-2373	w1	C(6) x T139	Pigmentation	IV	Clark
PI547453	L63-2404	e3	C(6) x PI 84.987	Maturity	II	Clark
PI547421	L63-2435	pc	C(6) x PI 84.987	Pubescence Type	IV	Clark
PI547588	L63-2441	e3 pc	C(6) x PI 84.987	transferred together	IV	Clark
PI547422	L63-2999	Ps	C(6) x PI 91.160	Pubescence Type	IV	Clark
PI547454	L63-3016	dt1	C(6) x PI 86.024	Stem Growth	IV	Clark
PI547455	L63-3022	dt1 Lf1	C(6) x PI 86.024	transferred together	IV	Clark
PI547423	L63-3117	e2	C(6) x PI 86.024	Maturity	II	Clark
PI547589	L63-3270	dt1 e3	C(6) x PI 84.987	combination	III	Clark
PI547424	L63-3297	dt1	C(6) x PI 84.987	Stem Growth	IV	Clark
PI547796	L63-42	rxp	Ch(8) x (C1128(2) x S54-1207)	disease resistance	I	Other
PI591543	L64-1061	Dt2 ln	(H6 x T117 Dt2) x (H6 x T204 ln)	combination	II	Harosoy
PI591542	L64-1067	Dt2 Lf1	(H6 x T117 Dt2) x (H6 x PI 86.024 Lf1)	combination	II	Harosoy
PI547719	L64-1069	Lf1 ln	(H(6) x PI 86.024)Lf1 x (H(6) x T204)ln	leaf	II	Harosoy
PI547458	L64-1074	Dt2 ln	(C(6) x T117)Dt2 x (C(6) x T204)ln	combination	IV	Clark
PI547459	L64-1081	Dt2 Lf1	(C(6) x T117)Dt2 x (C(6) x PI 86.024)Lf1	combination	IV	Clark
PI547460	L64-1083	Lf1 ln	(C(6) x PI 86.024)Lf1 x (C(6) x T204)ln	leaf	IV	Clark
PI547461	L64-1316	e2 Lf1	C(6) x PI 86.024	transferred together	II	Clark
PI547425	L64-1344	Lf1	C(6) x PI 86.024	leaf	IV	Clark
PI547462	L64-1731	Np s-t	C(6) x Chief	transferred together	IV	Clark
PI547766	L64-2139	w1	H(6) x Peking	Pigmentation	II	Harosoy
PI547463	L64-2191	I r	(C(6) x T201)I x (C(6) x T145)r	Pigmentation	IV	Clark
PI547464	L64-2244	I r *	L6 x L11,I r	Pigmentation	IV	Clark

PI547465	L64-2281	t w1	(C(6) x T139)w1 x (C(6) x T204)t	Pigmentation	IV	Clark
PI547691	L64-2489	G d1 d2	H(6) x Columbia	Chlorophyll	II	Harosoy
PI591545	L64-2511	G1 d1 d2 E1	H6 x Columbia	combination	IV	Harosoy
PI547426	L64-2545	G d1 d2	C(6) x Columbia	Chlorophyll	IV	Clark
PI547427	L64-2584	cyt-G y3	L62-1027,cyt-G x (C(6) x T139)y3	Chlorophyll	IV	Clark
PI547466	L64-2709	Np *	L6 x (C(5) x Chief)	Nutrient Response	IV	Clark
PI547797	L64-2721	Rps1 rxp	(Ch(8) x CNS) x (Ch(10 x Blackhawk	disease resistance	I	Other
PI547456	L64-314	Ps-s	C(6) x Higan	Pubescence Type	IV	Clark
PI547457	L64-326	pa1 Ps-s	C(6) x Higan	Pubescence Type	IV	Clark
PI547767	L64-4103	E1	H(6) x Columbia	Maturity	IV	Harosoy
PI547768	L64-4584	E2	H(6) x T117	Maturity	IV	Harosoy
PI547769	L64-4830	E5	H(6) x PI 80.837	Maturity	IV	Harosoy
PI547771	L65-1053	i-i	H(6) x T117	Pigmentation	II	Harosoy
PI547725	L65-1058	Dt2 i-i	H(6) x T117	Transferred together	II	Harosoy
PI547592	L65-1068	r	C(6) x Higan	Pigmentation	IV	Clark
PI547593	L65-1077	w1	C(6) x PI 83.945-4	Pigmentation	IV	Clark
PI547430	L65-1255	fe	C(6) x PI 54.619	Nutrient Response	IV	Clark
PI547695	L65-1274	rj1	H(6) x T201	Nutrient Response	II	Harosoy
PI547473	L65-1914	r *	L6 x L11,I r	Pigmentation	IV	Clark
PI547723	L65-237	p1 Ps-s	H(6) x Higan	Pubescence Type	II	Harosoy
PI547720	L65-25	pc Pd1	(H(6) x PI 84.987)pc x (H(6) x PI 80.837)Pd1	Pubescence Type	II	Harosoy
PI547431	L65-3366	E1 t	C(6) x T175	Maturity	IV	Clark
PI547721	L65-34	pc Ps	(H(6) x PI 84.987)pc x (H(6) x PI 91.160)Ps	Pubescence Type	II	Harosoy
PI547692	L65-372	lo	H(6) x T205	leaf	II	Harosoy
PI547798	L65-4059	Rps1	W(6) x Clark 63	disease resistance	III	Other
PI547467	L65-44	pc Pd1	(C(6) x PI 84.987)pc x (C(6) x PI 80.837)Pd1	Pubescence Type	IV	Clark
PI547724	L65-461	lw1	H(6) x T176	leaf	II	Harosoy
PI547468	L65-52	pc Ps	(C(6) x PI 84.987)pc x (C(6) x PI 91.160)Ps	Pubescence Type	IV	Clark
PI547693	L65-540	R	H(6) x T176	Pigmentation	II	Harosoy
PI547770	L65-556	i-i	H(6) x T176	Pigmentation	II	Harosoy

PI547722	L65-60	Pd1 Ps	(H(6) x PI 91.160)Ps x (H(6) x PI 80.837)Pd1	Pubescence Type	II	Harosoy
PI547470	L65-600	lw1 t	C(6) x T176	combination	IV	Clark
PI547590	L65-601	t	C(6) x T176	Pigmentation	IV	Clark
PI547471	L65-701	lb1	C(6) x PI 196.166	leaf	IV	Clark
PI547694	L65-756	f	H(6) x PI 83.945-4	Stem Growth	III	Harosoy
PI547428	L65-763	f	C(6) x PI 83.945-4	Stem Growth	IV	Clark
PI547472	L65-774	dt1 e2 Lf1	C(6) x PI 86.024	transferred together	II	Clark
PI547429	L65-778	dt1 e2	C(6) x PI 86.024	combination	II	Clark
PI547591	L65-792	dt1	C(6) x PI 83.945-4	Stem Growth	IV	Clark
PI547469	L65-90	Pd1 Ps	(C(6) x PI 80.837)Pd1 x (C(6) x PI 91.160)Ps	Pubescence Type	IV	Clark
PI547474	L66-14	i *	mutation in Clark 63 received in 1965 from Portageville, MO	Pigmentation	IV	Clark
PI547475	L66-17	i r	i-mutation in L11,I r found in 1965 at Urbana i r *	Pigmentation	IV	Clark
PI547476	L66-180	Rps1	PI 101.404A x C(6)	Disease Resistance	IV	Clark
PI547477	L66-183	wild cytoplasm	PI 101.404A x C(6)	cytoplasm	IV	Clark
PI547478	L66-228	td *	L6(6) x Sooty	Pigmentation	IV	Clark
PI547728	L66-2470	rj1 *	L2 x (H(6) x T201)	Nutrient Response	II	Harosoy
PI547479	L66-260	td	C(6) x PI 91.160	Pigmentation	IV	Clark
PI547432	L66-432	E1 t e2	L62-1932,e2 x L65-3366,E1 t	Maturity	IV	Clark
PI547433	L66-531	dt1 E1 t e2	L64-1477,dt1 e2 x L65-3366,E1 t	combination	IV	Clark
PI547434	L66-546	dt1 E1 t	L64-1477,dt1 e2 x L65-3366,E1 t	combination	IV	Clark
PI547696	L66-704	Np	H(6) x (C(6) x Chief)	Nutrient Response	II	Harosoy
PI547697	L66-707	T	H(6) x Clark	Pigmentation	II	Harosoy
PI547726	L66-713	Np T	H(6) x L9(Clark-Np)	Transferred together	II	Harosoy
PI547727	L66-721	i-i Np	H(6) x L9(Clark-Np)	Transferred together	II	Harosoy
PI547698	L66-731	fe	H(6) x PI 54.619	Nutrient Response	II	Harosoy
PI547799	L66-892	I r *	[L10(6) x (Clark(6) x T201)]I* x [L10(6) x (Clark(6) x T145)]P1 r*	pigmentation	I	Other
PI547800	L66-949	I r	W(5) x L68-2045,Clark-I P1 r	pigmentation	III	Other

PI547484	L67-1189	wild cytoplasm	PI 101.404B x C(6)	cytoplasm	IV	Clark
PI547734	L67-1250	Dt2 *	L2 x (H(6) x T117)	Stem Growth	II	Harosoy
PI547436	L67-1474	E1	C(6) x T175	Maturity	IV	Clark
PI547729	L67-153	dt1	H(6) x Higan	Stem Growth	II	Harosoy
PI547730	L67-166	Ps-s	H(6) x Higan	Pubescence Type	II	Harosoy
PI547735	L67-1687	i-i R lw1	H(6) x T176	Transferred together	II	Harosoy
PI547736	L67-1695	i-i R	H(6) x T176	Pigmentation	II	Harosoy
PI547485	L67-1749	lw1	C(6) x T176	leaf	IV	Clark
PI547731	L67-225	l2 S	H(6) x Higan	Transferred together	II	Harosoy
PI547700	L67-226	l2	H(6) x Higan	Pigmentation	II	Harosoy
PI547702	L67-2324	E1 T	H(6) x PI 196.166	Maturity	IV	Harosoy
PI547732	L67-234	S	H(6) x Higan	Stem Growth	II	Harosoy
PI547733	L67-271	pa1	H(6) x Higan	Pubescence Type	II	Harosoy
PI547737	L67-3099	P1 pc	(H(6) x PI 84.987)pc x L62-561,P1	Pubescence Type	III	Harosoy
PI547738	L67-3101	P1 Pd1	(H(6) x PI 80.837)Pd1 x L62-561,P1	Pubescence Type	II	Harosoy
PI547739	L67-3104	P1 Ps	(H(6) x PI 91.160)Ps x L62-561,P1	Pubescence Type	II	Harosoy
PI547486	L67-3124	P1 pc	(C(6) x PI 84.987)pc x L62-1385,P1	Pubescence Type	IV	Clark
PI547487	L67-3127	P1 Ps	L62-1385,P1 x (C(6) x PI 91.160)Ps	Pubescence Type	IV	Clark
PI547488	L67-3207	dt1 s-t	(C(6) x Chief)s-t x L63-3297,dt1	Stem Growth	IV	Clark
PI547489	L67-3224	Dt2 s-t	(C(6) x Chief)s-t x L62-1251,Dt2	Stem Growth	IV	Clark
PI547437	L67-3232	Dt2 e2	L62-1932,e2 x L62-1251,Dt2	combination	II	Clark
PI547490	L67-3243	e2 s-t	L62-1932,e2 x [L6 x (C(5) x Chief)]s-t	combination	II	Clark
PI547703	L67-3256	dt1 Dt2	(H(6) x T117)Dt2 x L62-973,dt1	Stem Growth	II	Harosoy
PI547740	L67-3298	Dt2 Lf1 ln	[(H(6) x T117)Dt2 x (H(6) x T204)ln] x [(H(6) x T117)Dt2 x (H(6) x PI 86.024)Lf1]	combination	II	Harosoy
PI547704	L67-3388	i	mutation in Harosoy found in 1959 at Urbana	Pigmentation	II	Harosoy
PI547741	L67-3396	i *	mutation in L2 found in 1963 at Shabbona, IL	Pigmentation	II	Harosoy
PI547438	L67-3469	i	mutation in Clark found in 1954 at Urbana	Pigmentation	IV	Clark

PI547491	L67-3472	i *	mutation in Clark 63 found in 1965	Pigmentation	IV	Clark
PI547439	L67-3479	k1	mutation in Clark from Ames, Iowa in 1956	Pigmentation	IV	Clark
PI547492	L67-3480	k1 *	mutation found in 1965 Illinois foundation seeds of Clark 63	Pigmentation	IV	Clark
PI547493	L67-3483	k2	mutation in x-rayed Clark at Columbia, MO	Pigmentation	IV	Clark
PI547494	L67-3484	i r	L66-14,i* x L12,I r*	Pigmentation	IV	Clark
PI547801	L67-3521	I P1 r	W(5) x L68-2045,Clark-I P1 r	combination	III	Other
PI547802	L67-3542	I r Rps1	L15 x (W(4) x L68-2045,Clark-I P1 r)	combination	III	Other
PI547803	L67-3586	I P1 r *	[L10(6) x (Clark(6) x T201)]I* x[L10(6) x (Clark(6) x T145)]P1 r*	combination	I	Other
PI547495	L67-3770	P1 Pd1	L62-1385,P1 x (C(6) x PI 80.837)Pd1	Pubescence Type	IV	Clark
PI547699	L67-38	i-i	H(6) x Clark	Pigmentation	II	Harosoy
PI547435	L67-483	t	C(6) x Higan	Pigmentation	IV	Clark
PI547480	L67-495	pa1 pa2 Ps-s	C(6) x Higan	Pubescence Type	IV	Clark
PI547481	L67-497	pa1 pa2	C(6) x Higan	Pubescence Type	IV	Clark
PI547482	L67-509	pa1 pa2 S	C(6) x Higan	transferred together	IV	Clark
PI547483	L67-592	S	C(6) x Higan	Stem Growth	IV	Clark
PI547772	L67-949	i-i	H(6) x Columbia	Pigmentation	II	Harosoy
PI547701	L67-971	G d2	H(6) x Columbia	Chlorophyll	II	Harosoy
PI547440	L68-1013	l2	C(6) x Higan	Pigmentation	IV	Clark
PI547496	L68-1017	l2 t	C(6) x Higan	Pigmentation	IV	Clark
PI547497	L68-1306	semi-wild cytoplasm	PI 65.388 x C(6)	cytoplasm	IV	Clark
PI547441	L68-1562	L1 *	L6(6) x Seneca	Pigmentation	IV	Clark
PI547498	L68-1774	w4 *	L6(6) x (Laredo x Harosoy)	Pigmentation	IV	Clark
PI547499	L68-1864	pc Ps-s	(C(6) x Higan)Ps-s x L63-2435,pc	Pubescence Type	IV	Clark
PI547500	L68-1874	Pd1 Ps-s	(C(6) x Higan)Ps-s x (C(6) x PI 80.837)Pd1	Pubescence Type	IV	Clark
PI547501	L68-2040	Dt2 Lf1 ln	L64-1074,Dt2 ln x (c(6) x PI 86.024)Lf1	combination	IV	Clark
PI547502	L68-2045	I P1 r	L62-1058,I x (C(6) x T145)P1 r	combination	IV	Clark
PI547810	L69-4180	I r *	L67-3526,I r Rps1 x SL9,Rpm	pigmentation	III	Other
PI547709	L69-4265	G d1	H(6) x Columbia	Chlorophyll	II	Harosoy

PI547710	L69-4266	d2	H(6) x Columbia	Chlorophyll	II	Harosoy
PI547711	L69-4267	d1 d2	H(6) x Columbia	Chlorophyll	II	Harosoy
PI547712	L69-4318	y9 *	L2(6) x T135	Chlorophyll	II	Harosoy
PI547773	L69-4428	L1 *	L2(6) x PI 81.763	Pigmentation	II	Harosoy
PI547442	L69-4544	B1 i	L67-3469,i(6) x Sooty	pigmentation	IV	Clark
PI547514	L69-4607	i-k *	L66-14,i*(6) x Black Eyebrow	Pigmentation	IV	Clark
PI547443	L69-4659	G d1	C(6) x Columbia	Chlorophyll	IV	Clark
PI547444	L69-4662	d2	C(6) x Columbia	Chlorophyll	IV	Clark
PI547445	L69-4663	d1 d2	C(6) x Columbia	Chlorophyll	IV	Clark
PI547515	L69-4667	G d2	C(6) x Columbia	Chlorophyll	IV	Clark
PI547446	L69-4755	y9 *	L6(6) x T135	Chlorophyll	IV	Clark
PI547516	L69-4775	td w1 *	L6(6) x Seneca	Pigmentation	IV	Clark
PI547517	L69-4776	w1 *	L6(6) x Seneca	Pigmentation	IV	Clark
PI547518	L69-4814	l2 w1	C(6) x T204	Pigmentation	IV	Clark
PI547447	L69-5338	Im I r *	L12(6) x Hawkeye	Pigmentation	IV	Clark
PI547448	L69-5343	Im I r *	L12(6) x Hawkeye	Pigmentation	IV	Clark
PI547519	L69-5366	Im r *	L12(6) x Hawkeye	Pigmentation	IV	Clark
PI547742	L69-6095	pa1 pa2	H(6) x Higan	Pubescence Type	II	Harosoy
PI547713	L70-4001	p2 *	L2(6) x T31	Pubescence Type	II	Harosoy
PI547743	L70-4037	d1 d2 p2 *	(L2(5) x T31)p2* x (H(6) x Columbia)	combination	II	Harosoy
PI547449	L70-4049	p2 I r *	L12(6) x T31	Pubescence Type	IV	Clark
PI547744	L70-4112	pa2	H(6) x Higan	Pubescence Type	II	Harosoy
PI547745	L70-4136	ln lo	(H(6) x T204)ln x (H(6) x T204)lo	leaf	II	Harosoy
PI547520	L70-4170	Rpm *	L12 x (Clark 63(5) x Kanrich)	Disease Resistance	IV	Clark
PI547596	L70-4186	r Rpm *	L12 x (Clark 63(5) x Kanrich	combination	IV	Clark
PI547521	L70-4190	I r Rpm *	L12 x (Clark 63(5) x Kanrich)	combination	IV	Clark
PI547450	L70-4204	i-k *	L66-14,i*(6) x Black Eyebrow	Pigmentation	IV	Clark
PI547522	L70-4313	ln lo	(C(6) x T204)ln x L62-1615,lo	leaf	IV	Clark
PI547523	L70-4404	td *	L6(6) x Grant	Pigmentation	IV	Clark
PI547597	L70-4413	L1 *	L6(6) x (Laredo x Harosoy)	Pigmentation	IV	Clark
PI547524	L70-4422	W3 w4 *	L6(6) x (Laredo x Harosoy)	Pigmentation	IV	Clark
PI547525	L70-4478	dt1 E1 t e2 *	L12 x L66-503,dtl E1 t e2	combination	IV	Clark

PI547526	L70-4497	i t w1	L67-3469,i x L64-2281 sib,t wl	Pigmentation	IV	Clark
PI547527	L70-4543	I r t *	L12(6) x Hawkeye	Pigmentation	IV	Clark
PI547528	L70-4558	pa2	C(6) x Higan	Pubescence Type	IV	Clark
PI547529	L70-4566	pa2 Ps-s	C(6) x Higan	Pubescence Type	IV	Clark
PI547530	L70-4611	lo I r *	L12 x L62-1615,lo	combination	IV	Clark
PI547531	L70-4629	ln *	L12 x L62-1579,ln	leaf	IV	Clark
PI547598	L70-9283	heterozygous for translocation	PI 101.404B x C(6)	translocation	IV	Clark
PI547748	L71-1106	E1 T S	L67-234,S x L67-2324,E1 T	combination	IV	Harosoy
PI547749	L71-1116	dt1 E1 T	L67-2324,E1 T x L67-153,dt1	combination	IV	Harosoy
PI547534	L71-1284	Dt2 S	L67-592,S x L62-1251,Dt2	Stem Growth	IV	Clark
PI547535	L71-1363	Dt2 E1 t e2	L62-1251,Dt2 x L66-432,E1 t e2	combination	IV	Clark
PI547536	L71-1374	e2 S	L67-592,S x L66-432,E1 t e2	combination	II	Clark
PI547537	L71-1378	E1 t e2 S	L67-592,S x L66-432,E1 t e2	combination	IV	Clark
PI547538	L71-1388	E1 t S	L67-592,S x L66-432,E1 t e2	combination	IV	Clark
PI547539	L71-1403	dt1 E1 t e2 s-t	L66-531, dt1 E1 t e2 x L67-3246,e2 s-t	combination	IV	Clark
PI547532	L71-149	Ps *	L12 x L63-2999,Ps	Pubescence Type	IV	Clark
PI547746	L71-46	Pd1 *	L2 x L62-801,Pd1	Pubescence Type	II	Harosoy
PI547747	L71-802	E1 T e3	L62-667,e3 x L67-2324,E1 T	Maturity	II	Harosoy
PI547533	L71-920	e2 e3	L63-3117,e2 x L63-2404,e3	Maturity	II	Clark
PI547774	L71L-3004	E1 T E2	L67-2324,E1 T x L64-4584,E2	Maturity	V	Harosoy
PI547775	L71L-3015	E1 T E5	L67-2324,E1 T x L64-4830,E5	Maturity	V	Harosoy
PI547599	L71U-659	dt1 ln	L63-3297,dt1 x L62-1579,ln	combination	IV	Clark
PI547750	L72-1078	W3 w4 *	L2(6) x Laredo	Pigmentation	II	Harosoy
PI547751	L72-1138	w4 *	L2(6) x Laredo	Pigmentation	II	Harosoy
PI547752	L72-1140	n *	L2(6) x Soysota	seed	II	Harosoy
PI547753	L72-1177	dt1 *	L2 x L62-535,dt1(H(6) x T145)	Stem Growth	II	Harosoy
PI547754	L72-1198	S *	L2 x L67-234,S	Stem Growth	II	Harosoy
PI547755	L72-1228	dt1 S	L67-234,S x L67-153,dt1	Stem Growth	II	Harosoy

PI547756	L72-1241	Dt2 S	L67-234,S x L63-1397,Dt2	Stem Growth	II	Harosoy
PI547757	L72-1304	E1 T *	L2 x L67-2324,E1 T	Maturity	IV	Harosoy
PI547811	L72-1369	ln I r *	SL12(6) x (Clark(6) x T204)ln	combination	III	Other
PI547812	L72-1404	e2 I r *	SL12(6) x (Clark(6) x PI 86.024)e2	combination	II	Other
PI547813	L72-1424	I r *	L15,Rps1 x SL12,I r *	pigmentation	III	Other
PI547540	L72-1495	e2 *	L6 x L63-3117,e2	Maturity	II	Clark
PI547541	L72-1566	e2 wm *	L6(6) x T235	transferred together	II	Clark
PI547542	L72-1568	e2 t *	L6(6) x T235	transferred together	II	Clark
PI547543	L72-1582	e2 lm *	L6 x (L12(5) x Hawkeye)	transferred together	II	Clark
PI547544	L72-1630	E1 t *	L6 x L65-3366,E1 t	Maturity	IV	Clark
PI547545	L72-1663	S *	L6 x (C(6)x Higan)	Stem Growth	IV	Clark
PI547546	L72-1727	dt1 L1	(L6(6) x Seneca)L1* x L63-3297,dt1	combination	IV	Clark
PI547547	L72-1737	dt1 *	L6 x L63-3297	Stem Growth	IV	Clark
PI547548	L72-1745	dt1 S	L67-592,S x "	Stem Growth	IV	Clark
PI547549	L72-1832	E1 t e2 s-t	L66-531,dt1 E1 t e2 x L67-3246,e2 s-t	combination	IV	Clark
PI547550	L72-1853	dt1 E1 t e2 lm *	(L12(6) x Hawkeye)lm* x L66-531,dt1 E1 t e2	combination	IV	Clark
PI547551	L72-1879	E1 t e2 Pd1	L66-531,dt1 E1 t e2 x L62-1686,Pd1	combination	IV	Clark
PI547552	L72-1885	dt1 E1 t e2 Pd1	L66-531,dt1 E1 t e2 x L62-1686,Pd1	combination	IV	Clark
PI547553	L72-1893	E1 t s-t	L65-3366,E1 t x L64-1731,s-t Np	combination	IV	Clark
PI547554	L72-1903	dt1 E1 t s-t	L66-531, dt1 E1 t e2 x L67-3207,dt1 s-t	combination	IV	Clark
PI547555	L72-1937	Y11 y11	C(6) x T219H	Chlorophyll	IV	Clark
PI591499	L72-1950	i R* Rps1 rxp	L67-3484 i r Rps1 rxp2 x (L65-1914 r Rps1 rxp4 x T16)	combination	IV	Clark
PI591498	L72-1971	R* Rps1 rxp	L67-3484 i r Rps1 rxp2 x (L65-1914 r Rps1 rxp4 x T16)	combination	IV	Clark
PI547556	L72-1977	n r *	L6(6) x Soysota	transferred together	IV	Clark
PI547557	L72-1987	n *	L6(6) x Soysota	seed	IV	Clark
PI547558	L72-2004	o i r *	L67-3484,i r*(6) x Ogemaw	Pigmentation	IV	Clark
PI547559	L72-2040	i r-m *	L67-3484,i r*(6) x PI 91.073	Pigmentation	IV	Clark
PI547560	L72-2111	ln I r *	L12 x L62-1579,ln	combination	IV	Clark

PI547561	L72-2133	I r rj1 *	L12 x L63-1889,rj1	combination	IV	Clark
PI547562	L72-2157	Lf1 *	L12 x L64-1344,Lf1	leaf	IV	Clark
PI547563	L72-2181	wm *	L6(6) x T235	Pigmentation	IV	Clark
PI547564	L72-2210	wm t *	L6(6) x T235	Pigmentation	IV	Clark
PI547565	L72-2824	d1 d2 p2 *	(L12(5) x T31)p2* x (C(6) x Columbia)d1 d2	combination	IV	Clark
PI547566	L72-2832	d1 d2 p2 I r *	(L12(5) x T31)p2* x (C(6) x Columbia)d1 d2	combination	IV	Clark
PI547817	L72-607	Im Rpm *	SL7 x [L16 x (L10(2) x Merit)]	combination	I	Other
PI547776	L72D-4028	ln Pd1	L63-1212,ln x L62-801,Pd1	combination	II	Harosoy
PI547777	L72D-4029	ln Pd1 Rps1	(L63-1212,ln x Harosoy 63) x L62-801,Pd1	combination	II	Harosoy
PI547778	L72D-4045	ln Rps1	L63-1212,ln x Harosoy 63	combination	II	Harosoy
PI547779	L72D-4110	d1 d2 dt1 ln	L63-1212,ln x L62-535,dt1 (H(6) x T145)	combination	II	Harosoy
PI547780	L72D-4169	dt1 ln Pd1	(L62-535,dt1 x L62-801,Pd1) x (L62-535,dt1 x L63-1212,ln)	combination	II	Harosoy
PI547600	L72U-4191	ln Pd1	L62-1579,ln x L62-1686,Pd1	combination	IV	Clark
PI547601	L72U-4282	dt1 ln Rps1	L62-1579,ln x (L63-3297,dt1 x Clark 63)	combination	IV	Clark
PI547602	L72U-4304	dt1 Pd1	L63-3297,dt1 x L62-1686,Pd1	combination	IV	Clark
PI547603	L72U-4317	dt1 Pd1 *	Clark 63 x (L63-3297,dt1 x L62-1686,Pd1)	combination	IV	Clark
PI547574	L73-1004	Fl i *	L6 x (L67-3472,i*(5) x PI 47.131)	Pigmentation	IV	Clark
PI547575	L73-1018	ab *	L6(6) x Kingwa	leaf	IV	Clark
PI547576	L73-1034	Pb *	L6(6) x Kingwa	Pubescence Type	IV	Clark
PI547577	L73-1046	Pd1 *	L12 x L62-1686,Pd1	Pubescence Type	IV	Clark
PI547761	L73-105	Dt2 S *	(L2 x L67-234)S* x L67-1250,Dt2*	Stem Growth	II	Harosoy
PI547578	L73-1054	r rj1 *	L12 x L63-1889,rj1	combination	IV	Clark
PI547579	L73-1071	t td	L67-483,t x L66-228,td*	Pigmentation	IV	Clark
PI547580	L73-1087	lf2 *	L6(6) x T255	leaf	IV	Clark
PI547581	L73-1101	pa1 pa2 pc	L67-497,pa1 pa2 x L63-2435,pc	Pubescence Type	IV	Clark
PI547582	L73-1118	pa1 pa2 Pd1	L67-497,pa1 pa2 x L62-1686,Pd1	Pubescence Type	IV	Clark
PI547583	L73-1144	pa1 pa2 Ps	L67-497,pa1 pa2 x L63-2999,Ps	Pubescence Type	IV	Clark
PI547814	L73-210	Im I r *	SL12(6) x Merit	pigmentation	III	Other

PI547815	L73-212	Im I r *	SL12(6) x Merit	pigmentation	III	Other
PI547758	L73-54	d1	L69-4268,G d1 x L69-4267,d1 d2	Chlorophyll	II	Harosoy
PI547759	L73-67	ab *	L2(6) x Kingwa	leaf	II	Harosoy
PI547604	L73-671	dt1 i r *	L67-3484,i r*(6) x PI 91.073	combination	IV	Clark
PI547605	L73-681	e2 I r *	L12(6) x Harosoy	combination	II	Clark
PI547606	L73-695	e2 I r *	L12(6) x Chippewa	combination	II	Clark
PI547567	L73-753	e2 I Im r *	L12(6) x Hawkeye,e2 Im*	combination	II	Clark
PI547568	L73-760	e2 I r *	L12(6) x Hawkeye	combination	II	Clark
PI547760	L73-79	Pb *	L2(6) x Kingwa	Pubescence Type	II	Harosoy
PI547569	L73-811	Dt2 *	L6 x L62-1251,Dt2	Stem Growth	IV	Clark
PI547570	L73-879	dt1 Dt2	L62-1251,Dt2 x L63-3016,dt1	Stem Growth	IV	Clark
PI547571	L73-904	dt1 e2 s-t	L66-531, dt1 E1 t e2 x L67-3246,e2 s-t	combination	II	Clark
PI547572	L73-944	dt1 E1 t e2 I r *	(L12(6) x Hawkeye)Im* x L66-531,dt1 E1 t e2	combination	IV	Clark
PI547573	L73-980	Dt2 E1 t	L62-1251,Dt2 x L66-432,E1 t e2	combination	IV	Clark
PI547781	L73D-2733	dt1 Pd1	L62-535,dt1 x L62-801,Pd1	combination	II	Harosoy
PI547782	L73D-2743	dt1 ln Rps1	(L63-1212,ln x Harosoy 63) x (L62-535,dt1 x Harosoy 63)	combination	II	Harosoy
PI547607	L73U-2774	dt1 ln Pd1	(L63-3297,dt1 x L62-1579,ln) x(L63-3297,dt1 x L62-1686,Pd1)	combination	IV	Clark
PI547832	L74-01	ms2	Wm(6) x T259H	male sterility	III	Williams
PI547584	L74-03	ms1 *	L6(6) x T260H	male sterility	IV	Clark
PI591541	L74-102	dt1 E1 T e3	[(H6 x T204 e3) x (H6 x PI 196.166 E1 T)] x [(H6 x PI 196.166 E1 T) x (H6 x Higan dt1)]	combination	II	Harosoy
PI547617	L74-1060	chromosome translocation	PI 101.404B x C(6)	translocation	IV	Clark
PI547585	L74-1089	i-k r o *	L69-4607,i-k* x (L67-3484,i r*(5) x Ogemaw,o)	Pigmentation	IV	Clark
PI547818	L74-142	e2 ln I r *	L72-1369,ln I r * x L72-1392,e2 I r *	combination	III	Other
PI547819	L74-143	e2 ln I r Rps1	L72-1369,ln I r * x L72-1392,e2 I r *	combination	III	Other
PI547833	L74-189	Dt2	Wm(6) x (Clark(6) x T117)	Stem Growth	III	Williams
PI547783	L74-21	E2 T *	L2(6) x Clark	Transferred together	III	Harosoy

PI547835	L74-221	Dt2 ep	Wm(6) x (Clark(6) x T117)	combination	III	Williams
PI547784	L74-27	E2 *	L2(6) x Clark	Maturity	III	Harosoy
PI547608	L74-373	s-t *	L12 x (C(6) x Chief)	Stem Growth	IV	Clark
PI547609	L74-434	e2 s-t *	L6 x L67-3246,e2 s-t	combination	II	Clark
PI547610	L74-441	E1 t e3	L63-2404,e3 x "	Maturity	IV	Clark
PI547762	L74-59	Dt2 E1 T	L67-2324,E1 T x L67-1397,Dt2	combination	IV	Harosoy
PI547785	L74-66	E2 E5	L64-4584,E2 x L64-4830,E5	Maturity	V	Harosoy
PI547611	L74-824	cyt-G y9 **	L62-1027,cyt-G x L69-4755,y9*	Chlorophyll	IV	Clark
PI547612	L74-826	cyt-G Y11 y11	L62-1027, cyt-G x L65-1237,Y11 y11	Chlorophyll	IV	Clark
PI547613	L74-836	d1 d2 y9 **	(C(6) x Columbia)G d1 d2 x L69-4755,y9*	Chlorophyll	IV	Clark
PI547614	L74-838	G d1 d2 Y11 y11	(C(6) x Columbia)G d1 d2 x L65-1237,Y11 y11	Chlorophyll	IV	Clark
PI547615	L74-851	d1 d2 y3	L67-1000,d1 d2 x L63-2346,y3	Chlorophyll	IV	Clark
PI547616	L74-852	d1 d2 y7 y8	L69-4663,d1 d2 x L63-1792,y7 y8	Chlorophyll	IV	Clark
PI591492	L74-854	d1	L69-4663 d1 d2 x L69-4659 G1 d1	Chlorophyll	IV	Clark
PI547618	L74U-6710	ln Pd1 Rps1	L62-1579,ln x (Clark 63 x L62-1686,Pd1)	combination	IV	Clark
PI547820	L75-0570	ms2	Wells(6) x T259	male sterility	II	Other
PI547821	L75-0587	ms2	Beeson(6) x T259	male sterility	I	Other
PI547834	L75-3735	Rps1-c	Wm(6) x Lee 68	Disease Resistance	III	Williams
PI547619	L75-3901	Rps1-c	C(6) x Arksoy	Disease Resistance	IV	Clark
PI547836	L75-6111	e2	Wm(6) x [SL12,Wayne-l r Rpm Rps1(6) x (Clark(6) x PI 86.024)e2]	maturity	II	Williams
PI547837	L75-6141	Rpm Rps1	Wm(6) x SL12, Wayne-Rpm Rps1; = Wm x Union	Disease Resistance	III	Williams
PI547620	L75-6426	i-k r t *	L68-2063,r t w1* x L70-4209,i-k*	Pigmentation	IV	Clark
PI547621	L75-6433	i-k r w1 *	L68-2063,r t w1* x L70-4209,i-k*	Pigmentation	IV	Clark
PI547622	L75-6439	i-k r t w1 *	L68-2063,r t w1* x L70-4209,i-k*	Pigmentation	IV	Clark
PI547623	L75-6551	Rpm	C x (Clark 63(6) x Kanrich)	Disease Resistance	IV	Clark
PI547624	L75-6631	e2 hb *	L72-1495,e2*(6) x PI 229.342	combination	III	Clark
PI547625	L75-6648	Pd2 *	L6(6) x T264	Pubescence Type	IV	Clark

PI547626	L75-6697	ab *	L6(6) x PI 47.131	leaf	IV	Clark
PI547628	L76-1010	mi G t *	L6 x [L68-2063,r t w*(5) x (Laredo x Harosoy)]	Pigmentation	IV	Clark
PI547629	L76-1101	i-k t *	L68-2063,r t w1* x L70-4209,i-k*	Pigmentation	IV	Clark
PI547630	L76-1113	i-k w1 *	L68-2063,r t w1* x L70-4209,i-k*	Pigmentation	IV	Clark
PI547631	L76-1122	i-k t w1 *	L68-2063,r t w1* x L70-4209,i-k*	Pigmentation	IV	Clark
PI547632	L76-1149	v1 *	L6(6) x T93	Chlorophyll	IV	Clark
PI591493	L76-1162	G1	C x L69-4666 G1 d2	Chlorophyll	IV	Clark
PI547633	L76-1169	Rpm *	L6 x (Clark 63(6) x Kanrich)	Disease Resistance	IV	Clark
PI547634	L76-1291	pa1	C(6) x Higan	Pubescence Type	IV	Clark
PI547838	L76-1988	Rps2 Rj2	Wm(6) x (Harosoy(5) x D54-2437)	combination	III	Williams
PI547839	L76-1994	I Rps2 Rj2	Wm(6) x (Harosoy(5) x D54-2437)	combination	III	Williams
PI547840	L76-2023	t Rps2 Rj2	Wm(6) x (Harosoy(5) x D54-2437)	combination	III	Williams
PI547635	L76-2060	Rps2 (Rj2 rj2)	C(6) x (H(5) x D54-2437,Rps2 Rj2)	combination	IV	Clark
PI547636	L76-2096	e2 l2 Rps1-c rxp	L6(2) x (L63-3117,e2(4) x PI 229.342)	transferred together	II	Clark
PI547637	L76-2100	l2 Rps1-c rxp	L6(6) x PI 229.342	transferred together	IV	Clark
PI547638	L76-2107	Rps1-c rxp	L6(6) x PI 229.342	Disease Resistance	IV	Clark
PI547822	L76-612	e2 I r Rps1	L15 x (SL12(5) x Merit)	combination	III	Other
PI547627	L76-865	dt1 E1 t e3	L63-2404,e3 x L66-546,dt1 E1 t	combination	IV	Clark
PI547823	L77-1585	Rps2 Rj2	Corsoy(6) x (Harosoy(5) x D54-2437)	combination	II	Other
PI547841	L77-1727	Rps1-c	Wm(6) x (Clark 63(3) PI 229.342)	Disease Resistance	III	Williams
PI547890	L77-1794	Rps1-k	Wm(7) x Kingwa	Disease Resistance	III	Williams
PI547842	L77-1863	Rps1-b hm	Wm(7) x Harrel (L26)	combination	III	Williams
PI547639	L77-2015	Rps1-k	C(6) x Kingwa	Disease Resistance	IV	Clark
PI547640	L77-2050	dt1 Rps1-b hm	C(6) x Harrel	transferred together	IV	Clark
PI547641	L77-2061	Rps1-b (not hm)	C(6) x Harrel,Rps1-b hm	Disease Resistance	IV	Clark
PI547824	L77-2152	e2 I r Rps1	L15 x (SL12(5) x Merit)	combination	III	Other
PI547642	L77-2654	lb1 Lb2	L65-701,lb1(6) x PI 196.166	leaf	IV	Clark

PI547843	L77-5632	Im	Wm(6) x L69-5343,Clark-I r Im*	Pigmentation	III	Williams
PI547825	L78-189	Rps1-k	Corsoy(8) x Kingwa	disease resistance	II	Other
PI547845	L78-3079	L2 Im	Wm(6) x L69-5343,Clark-I r Im*	Pigmentation	III	Williams
PI547846	L78-3083	L2	Wm(6) x L69-5343,Clark-I r Im*	Pigmentation	III	Williams
PI547847	L78-3130	cytoplasm	Wisconsin Black x Wm(6)	cytoplasm	III	Williams
PI547644	L78-3263	hb *	L6(6) x PI 229.342	herbicide sensitivity	IV	Clark
PI547844	L78-379	Rsv1	Wm(6) x PI 96.983	Disease Resistance	III	Williams
PI547643	L78-434	Rsv1 *	L6(6) x PI 96.983	Disease Resistance	IV	Clark
PI547849	L79-1250	Dt2 Rps1-k	Will x Wm 82	Disease Resistance	III	Williams
PI547850	L79-1270	Dt2 Im	Will x L75-6867,Im	combination	III	Williams
PI547645	L79-1308	ms2 *	L6(6) x T259H	male sterility	IV	Clark
PI547646	L79-1380	Rps1-c	C(6) x Higan	Disease Resistance	IV	Clark
PI547647	L79-1404	l2 Rps1-c	C(6) x Arksoy	transferred together	IV	Clark
PI547648	L79-1685	lw1 Lw2 t	L65-600,lw1 t(6) x T117,Lw2	combination	IV	Clark
PI547586	L79-1800	Dt2 S *	L6 x (L67-592,S x L62-1251,Dt2)	Stem Growth	IV	Clark
PI547649	L79-1815	Pd1 Pd2 rxp?	L62-1686,Pd1 x (L6(6) x T264)Pd2	Pubescence Type	IV	Clark
PI547786	L79-842	Dt2 E1 T S	L71-1106,E1 T S x L74-59,Dt2 E1 T	combination	IV	Harosoy
PI547848	L79-908	W1 Rps1-c	Wm(6) x Lee 68	Pigmentation	III	Williams
PI547826	L80-5015	Rps1-c Rps2 Rj2	Corsoy 79 x L77-1585,Rps2 Rj2	combination	II	Other
PI547851	L80-5227	Dt2 Rsv1	Will x (Wm(6) x PI 96.983)	combination	III	Williams
PI547852	L80-5372	W1 Rps1-c	Wm(6) x (Clark 63(6) x PI 229.342)	Pigmentation	III	Williams
PI547853	L80-5427	Rpm	Wm x L75-6125,Rpm Rps1; = Wm(2) x Union	Disease Resistance	III	Williams
PI547854	L80-5452	Im Rps1-c	Wm 79,Rps1-c x L75-6867,Im	Pigmentation	III	Williams
PI547650	L80-5879	dt1 E1 t e2 e3	L70-4478,dt1 E1 t e2* x L71-920,e2 e3	combination	III	Clark
PI547651	L80-5882	dt1 e2 e3 rxp?	L70-4478,dt1 E1 t e2* x L71-920,e2 e3	combination	II	Clark
PI547652	L80-5914	E1 t e2 e3	L70-4478,dt1 E1 t e2* x L71-920,e2 e3	Maturity	III	Clark

PI547787	L81-4075	pa1 pa2	L67-271,pa1 x L70-4112,pa2	Pubescence Type	II	Harosoy
PI547827	L81-4274	Dt1	Elf(6) x Williams	stem growth	III	Other
PI547855	L81-4308	Dt2 Rpm Rps1	Will x L75-6125,Rpm1 Rps1	combination	III	Williams
PI547856	L81-4352	Rps1-c Rps2 Rj2	Wm 79,Rps1-c x L76-2013,Rps2 Rj2	combination	III	Williams
PI547857	L81-4420	Rps1-k Rsv1	L78-379,Rsv1 x Wm 82,Rps1-k	Disease Resistance	III	Williams
PI547653	L81-4651	pa1 pa2	L70-4558,pa2 x L76-1291,pa1	Pubescence Type	IV	Clark
PI547654	L81-4659	e2 *	L6(6) x Calland	Maturity	II	Clark
PI547655	L81-4858	rj1 *	L6(2) x L63-1889	Nutrient Response	IV	Clark
PI547656	L81-4871	ti *	L6(6) x PI 157.440	seed composition	IV	Clark
PI547657	L81-4945	w4 *	L6(6) x PI 81.763	Pigmentation	IV	Clark
PI547658	L81-5080	I r w1 Rps1 rps1	L12 x L64-2281 sib,t w1	combination	IV	Clark
PI547587	L81-5082	r w1 *	L12 x L64-2281 sib,t w1	Pigmentation	IV	Clark
PI591497	L81-5122	i t-r w1	L70-4497 i t w16 x T136	pigmentation	IV	Clark
PI547828	L82-1011	dt1	Amsoy 71(6) x PI 151.440	Stem growth	II	Other
PI547829	L82-1187	Rps1-k Rps2 Rj2	L77-1585,Rps2 Rj2 x (Corsoy(8) x Kingwa)Rps1-k	combination	II	Other
PI547788	L82-1449	Rps2 Rmd-c Rj2	H(6) x D54-2437	combination	II	Harosoy
PI547859	L82-1560	Dt2 Rpm Rps1-k	L79-1178,Dt2 Rpm Rps1 x L79-1224,Dt2 Rps1-k	combination	III	Williams
PI591521	L82-1657	Rpm1 Rps1 Rps2 Rmd-c Rj2	L75-6141 Rpm1 Rps1 x L76-1988 Rps2 Rmd-c Rj2	combination	III	Williams
PI547860	L82-1858	Rpm Rps1-c Rps2 Rj2	L81-4352,Rps1-c Rps2 Rj2 x (L75-6141,Rpm Rps1 x L76-1988,Rps2 Rj2)	combination	III	Williams
PI547891	L82-2020	Ti-b	Wm(6) x Jefferson	Seed composision	III	Williams
PI547892	L82-2024	rmd Ti-b	Wm(6) x Jefferson	seed composition	III	Williams
PI547861	L82-2045	dt1 Ti-c	Wm(6) x PI 196.172	seed composition	III	Williams
PI547893	L82-2051	Ti-c	Wm(6) x PI 196.172	Seed composision	III	Williams
PI591486	L82-2249	dt1 E1 t e2 e3 Rps1 rxp	L70-4478 dt1 E1 t e2 Rpsl rxp x L71-920 e2 e3	combination	III	Clark
PI547659	L82-2669	i r t w1 *	L66-14,i Rps1 rxp x (L12 x L64-2281 sib,t w1)	Pigmentation	IV	Clark

PI547858	L82-753	Dt2 Rpm Rsv1	L79-1178,Dt2 Rpm Rps1 x L80-5227,Dt2 Rsv1	combination	III	Williams
PI591526	L82-951	Dt2 Rsv1-m	Will6 x Marshall Rsv1-m	combination	III	Williams
PI547830	L83-0214	Rsv1	PI 65.549(6) x PI 96.983	disease resistance	II	Other
PI547831	L83-0215	Rsv1	PI 65.549(6) x PI 96.983	disease resistance	II	Other
PI547816	L83-4387	ti	Amsoy 71(6) x PI 157.440	seed composition	II	Other
PI547863	L83-4483	Dt2 Rpm Rps1 Rsv1	L79-1178,Dt2 Rpm Rps1 x L80-5227,Dt2 Rsv1	combination	III	Williams
PI547864	L83-4494	Dt2 Rps1 Rsv1	L79-1178,Dt2 Rpm Rps1 x L80-5227,Dt2 Rsv1	combination	III	Williams
PI547865	L83-4527	Dt2 Rps1-k Rsv1	L79-1224,Dt2 Rps1-k x L80-5227,Dt2 Rsv1	combination	III	Williams
PI547866	L83-4744	Rpm Rsv1	L78-379,Rsv1 x L80-5493,Rpm Rps1-k	Disease Resistance	III	Williams
PI547867	L83-4752	Rpm Rps1-k Rsv1	L78-379,Rsv1 x L80-5493,Rpm Rps1-k	Disease Resistance	III	Williams
PI547862	L83-570	Rps3	Wm(6) x PI 86.972-1	Disease Resistance	III	Williams
PI547660	L83-693	i ti *	i mutation in L6(6) x PI 157.440	combination	IV	Clark
PI547661	L83-841	I t w1 **	L12 x L64-2281 sib,t w1	Pigmentation	IV	Clark
PI547662	L83-879	I t *	L12 x L64-2281 sib,t w1	Pigmentation	IV	Clark
PI547663	L83-900	r t **	L12 x L64-2281 sib,t w1	Pigmentation	IV	Clark
PI547664	L83-930	i r t *	L66-14,i* x (L12 x L64-2281 sib,t w1)	Pigmentation	IV	Clark
PI547665	L83-942	i r w1 *	L66-14,i Rps1 rxp x (L12 x L64-2281 sib,t w1)	Pigmentation	IV	Clark
PI547666	L83-964	dt1 L1	L68-1562,L1* x L63-3016,dt1	combination	IV	Clark
PI547668	L84-1135	t w4 *	L6(6) x (Laredo x Harosoy)	Pigmentation	IV	Clark
PI547669	L84-1231	I w1 **	L12 x L64-2281 sib,t w1	Pigmentation	IV	Clark
PI547868	L84-2003	i (not Ti-b)	mutation in Wm(6) x Jefferson found in 1982 at Urbana	Pigmentation	III	Williams
PI591513	L84-2112	Rsv1-m	Wm x (Will6 x Marshall)	Disease Resistance	III	Williams
PI591514	L84-2157	e2 Rsv1-m	Wm x (Will6 x Marshall e2 Rsv1-m)	combination	II	Williams
PI547869	L84-2235	I	Williams(6) x (Clark 63(2) x PI 86150)	pigmentation	III	Williams
PI547870	L84-2237	rmd	Wm(6) x (Clark 63(2) x PI 86.150)	Disease Resistance	III	Williams
PI547789	L84-307	E2 e3	L64-4584,E2 x L73-1543,e3	Maturity	II	Harosoy
PI547791	L85-129	Rps1-c hm?	H(6) x Higan	combination	II	Harosoy

PI547792	L85-144	l2 Rps1-c hm?	H(6) x Higan	Transferred together	II	Harosoy
PI547670	L85-1467	t	C(6) x PI 84.987	Pigmentation	IV	Clark
PI547871	L85-2029	dt1	Wm(6) x (Clark 63(2) x PI 86.150)	Stem Growth	III	Williams
PI547872	L85-2196	sun	Wm(6) x PI 229.324	Seed composision	III	Williams
PI547873	L85-2308	Rpv	Wm(6) x Dorman	Disease Resistance	III	Williams
PI547874	L85-2352	Rps4	Wm(6) x PI 86.050	Disease Resistance	III	Williams
PI547875	L85-2378	Rpp1 Rps1-k	Wm 82(6) x PI 200.492	Disease Resistance	III	Williams
PI547876	L85-3059	Rps5	Wm(6) x PI 91.160	Disease Resistance	III	Williams
PI547671	L86-1078	I t *	L12 x L64-2281 sib,t w1	Pigmentation	IV	Clark
PI547672	L86-1084	I t	L12 x L64-2281 sib,t w1	Pigmentation	IV	Clark
PI547673	L86-1092	r t	L12 x L64-2281 sib,t w1	Pigmentation	IV	Clark
PI547674	L86-1096	I t w1 **	L12 x L64-2281 sib,t w1	Pigmentation	IV	Clark
PI547675	L86-1098	I t w1	L12 x L64-2281 sib,t w1	Pigmentation	IV	Clark
PI547877	L86-1436	lx1	Wm(6) x PI 408.251	Seed composition	III	Williams
PI547878	L86-1752	Rpp2 Rps1-k	Wm 82(6) x PI 230.970	Disease Resistance	III	Williams
PI547794	L86-493	Rps1 Rps2 Rmd Rj2	L2,Rps1 x (H(5) x D54-2437)Rps2 Rmd Rj2	combination	II	Harosoy
PI547793	L86L-4	E2 E5	L64-4830,E5 x L74-27,E2*	Maturity	V	Harosoy
PI591504	L87-0174	Rpm2	Wm6 x PI 88.788	Disease Resistance	III	Williams
PI547879	L87-0482	Rpp4 Rps1-k	Wm 82(6) x PI 459.025	Disease Resistance	III	Williams
PI547880	L88-5492	i	mutant found in Williams in 1980 from a farm on Windsor Road, Champaign, IL	Pigmentation	III	Williams
PI547881	L88-5495	i Rps1-c	mutant found in Williams(6) x Lee 68 in 1975 at Urbana (L75-3774)	combination	III	Williams
PI547882	L88-8012	dt1 i Ti-c	i mutant selected from Wm(6) x PI 196.172	combination	III	Williams
PI547883	L88-8025	dt1	Wm(6) x PI 408.251	Stem Growth	III	Williams
PI591522	L88-8153	e2	Wm6 x Altona	combination	II	Williams
PI547884	L88-8226	rmd	Wm(6) x PI 86.972-1	Disease Resistance	III	Williams
PI547885	L88-8431	Rsv2	Wm(6) x Raiden,PI 360.844	Disease Resistance	III	Williams

PI547886	L88-8440	r Rsv2	Wm(6) x Raiden (PI 360.844)	combination	III	Williams
PI591505	L88-8470	Rps1	Wm2 x Union, BC4 Wm with Rps1 from Mukden	Disease Resistance	III	Williams
PI547887	L88-8488	Rpm Rps1-k	Wm 82,Rps1-k x (Wm x L75-6125,Rpm Rps1)	Disease Resistance	III	Williams
PI547888	L88-8502	Rpm Rps1-b hm	L75-6125,Rpm Rps1 x L77-1818,Rps1-b hm	combination	III	Williams
PI591527	L88-8629	Dt2 e2 Rsv1-m	Will6 x Marshall e2 Rsv1-m	combination	II	Williams
PI547889	L88-8739	Dt2 Rpm Rps1-k Rsv1	L79-1224,Dt2 Rps1-k x (L79-1178,Dt2 Rpm Rps1 x L80-5230,Dt2 Rsv1)	combination	III	Williams
PI591507	L89-1541	Rps3-b	Wm6 x PI 82.312N	Disease Resistance	III	Williams
PI591508	L89-1550	e2 Rps3-b	Wm6 x PI 82.312N	combination	II	Williams
PI591523	L89-1553	e2	Wm6 x PI 82.312N	combination	II	Williams
PI591511	L89-1581	Rps6	Wm6 x Altona	Disease Resistance	III	Williams
PI591531	L89-2435	I	Wm6 x (Harosoy5 x D54-2437)	Pigmentation	III	Williams
PI591537	L89-2621	Sp1-an Rps1-k	Wm 826 x Chestnut	combination	III	Williams
PI591538	L89-2634	i Sp1-an Rps1-k	Wm 826 x Chestnut	combination	III	Williams
PI591546	L90-4683	Rps2 Rmd-c (rj2)	H6 x D54-2437	combination	II	Harosoy
PI591547	L90-4711	(rps2) Rmd-c Rj2	H6 x D54-2437	combination	II	Harosoy
PI591544	L90-7656	G1	H6 x PI 81.763	Pigmentation	II	Harosoy
PI591503	L90-7978	rmd	Wm6 x Jefferson	Disease Resistance	III	Williams
PI591536	L90-8003	sp1 Rps1-k	Wm 826 x T293, Altona	combination	III	Williams
PI591534	L90-8047	le Rps1-k	Wm 826 x Wilson Five	combination	III	Williams
PI591487	L91-8052	dt1-t Rps1 rxp	L6 Rpsl rxp6 x Soysota	combination	IV	Clark
PI591488	L91-8060	dt1-t Rps1 rxp	L6 Rpsl rxp6 x Peking	combination	IV	Clark
PI591509	L91-8347	Rps3-b	Wm6 x PI 172.901	Disease Resistance	III	Williams
PI591528	L91-8520	Eu1-a Rps1-k	Wm 826 x Columbia	combination	III	Williams
PI591539	L91-8558	sun ti Rps1-k	Kunitz(Wm 826 x PI 157.440, Kum Du) x L85-2196(Wm6 x PI 229.324, Itachi)	combination	III	Williams
PI591519	L91-8765	(rps2) rmd Rj2	L76-1988 Rps2 Rmd-c Rj2 x L82-2024 rmd Ti-b	combination	III	Williams

PI591520	L91-8839	(rps2) Rmd-c Rj2	L76-1988 Rps2 Rmd-c Rj2 x L82-2024 rmd Ti-b	combination	III	Williams
PI591518	L91-8915	Rps2 rmd (rj2)	L76-1988 Rps2 Rmd-c Rj2 x L82-2024 rmd Ti-b	combination	III	Williams
PI591489	L92-1166	e4	C6 x PI 297.550, Urosajnaja	combination		Clark
PI591490	L92-1195	E5	C x ancestor of L94-1110	combination	IV	Clark
PI591484	L92-7229	rmd	C6 x PI 317.334B	Disease Resistamce	IV	Clark
PI591485	L92-7259	e2 rmd	L63-3117 e26 x PI 317.334B	combination	II	Clark
PI591540	L92-7600	W1	Wm6 x Clark	Pigmentation	III	Williams
PI591524	L92-7647	e2	Wm6 x L63-3117 (Clark6 x PI 86.024 e2)	combination	II	Williams
PI591525	L92-7677	e2 Rps1-k	Wm 826 x L63-3117(Clark6 x PI 86.024 e2)	combination	II	Williams
PI591510	L92-7857	Rps3-c	Wm6 x PI 340.046	Disease Resistance	III	Williams
PI591517	L92-7963	rmd Rps3	Wm6 x PI 86.972-1	Disease Resistance	III	Williams
PI591516	L92-8580	Rsv2	Wm6 x PI 483.084, Suweon 97	Disease Resistance	III	Williams
PI591500	L92-9511	k1 k2	L67-3483 k2 x L67-3479 k1	pigmentation	IV	Clark
PI591501	L92-9515	i k2	L67-3483 k2 x L67-3469 i	pigmentation	IV	Clark
PI591548	L93-2589	s-t	H6 x L67-3243 e2 s-t from (C6 x PI 86.024 e2) x (C6 x Chief s-t)	Stem growth	II	Harosoy
PI591496	L93-2677	B1 e2	L63-3117 e26 x PI 65.388	combination	II	Clark
PI591495	L93-2740	d1 d2 y3	L69-4663 d1 d2 x L63-2346 y3	Chlorophyll	IV	Clark
PI591494	L93-2748	G1 d1 d2 cyt-G1	L62-1027 cyt-G1 x L64-2545 G1 d1 d2	Chlorophyll	IV	Clark
PI591530	L93-3103	G2	Wm6 x Ogden	Pigmentation	III	Williams
PI591512	L93-3258	Rps7	Wm6 x Harosoy	Disease Resistance	III	Williams
PI591506	L93-3312	Rps1-d	Wm6 x PI 103.091	Disease Resistance	III	Williams
PI591515	L93-3327	rsv1-t	Wm6 x Ogden	Disease Resistance	III	Williams
PI591529	L93-3423	G1 Rps1-k	Wm 826 x Columbia	combination	III	Williams
PI591533	L93-3539	I r Rsv2 Rps2 Rmd-c Rj2	L76-1994 I Rps2 Rmd-c Rj2 x L88-8440 r Rsv2	combination	III	Williams
PI591535	L93-7290	lx3 Rps1-k	Wm 826 x PI 417.458, Wase Natsu	combination	III	Williams
PI591532	L93-7333	I r Rsv2	L76-1994 I Rps2 Rmd-c Rj2 x L88-8440 r Rsv2	combination	III	Williams

PI591491	L94-1110	e2 E5	L63-3117 e26 x L64-4830(Harosoy6 x PI 80.837)	combination	IV	Clark
PI591502	L94-1365	i k2 r t	L67-3483 k2 x L83-930 i r t	pigmentation	IV	Clark
PI546039	OT89-01	e3 Dt1	PI 196529/7*Maple Arrow	combination	0	Other
PI546040	OT89-02	e3 dt1	PI 196529/7*Maple Arrow	combination	0	Other
PI546041	OT89-03	e4 I	McCall/7*Maple Amber	combination	0	Other
PI546042	OT89-04	e4 ii	McCall/7*Maple Amber	combination	0	Other
PI546043	OT89-05	t e1 e3 e4 Dt1	PI438477/2*Evans/7*L62-667	combination	0	Harosoy
PI546044	OT89-06	t e1 e3 e4 dt1	OT89-05//L67-153	combination	0	Harosoy
PI546045	OT89-07	e3 e4	PI 438477/2*Evans/5*Evans-e3	maturity	0	Other
PI546046	OT89-08	Dt1	L67-153/7*Maple Presto	stem growth	0	Other
PI546047	OT89-09	dt1	L67-153/7*Maple Presto	stem growth	0	Other
PI546048	OT89-10	Ln	OX611/8*Maple Presto	leaf	0	Other
PI546049	OT89-11	ln	OX611/8*Maple Presto	leaf	0	Other
PI546050	OT89-12	Rj1	L64-2671/7*Maple Presto	nutrient response	0	Other
PI546051	OT89-13	rj1	L64-2671/7*Maple Presto	nutrient response	0	Other
PI546052	OT89-14	Ab	'Kingwa'/7*Maple presto	leaf	0	Other
PI546053	OT89-15	ab	'Kingwa'/7*Maple presto	leaf	0	Other
PI591429	OT93-26	T E1 e2 e3 e4 e5 DT1	OT89-5/L71-802	combination	0	Harosoy
PI591430	OT93-28	t E1 e2 e3 e4 e5 Dt1	OT89-5/L71-802	combination	0	Harosoy
PI591433	OT94-37	t e1 e2 e3 E4 e5 dt1	PI 438477/Evans (K613-5-2)//7*L62-667/3/L67-153	combination	0	Harosoy
PI591434	OT94-39	t e1 e2 E3 e4 e5 dt1	PI 438477/Evans (K613-5-2)//7*L62-667/3/L67-153	combination	0	Harosoy
PI591435	OT94-41	t e1 e2 E3 e4 e5 Dt1	PI 438477/Evans (K613-5-2)//7*L62-667/3/L67-153	combination	I	Harosoy
PI591431	OT94-49	T E1 e2 e3 e4 e5 dt1	OT89-5/L71-802//OT89-6	combination	0	Harosoy
PI591432	OT94-51	t E1 e2 e3 e4 e5 dt1	OT89-5/L71-802//OT89-6	combination	0	Harosoy
PI548218	T235	wm	mutation in Harosoy found in 1957 at Urbana	Pigmentation	II	Mut
PI548220	T238	k3	mutation in x-rayed Clark found in 1956 at Columbia, Missouri	Pigmentation	IV	Mut
PI548221	T239	k2	mutation in Harosoy found in 1961 at Urbana	Pigmentation	II	Mut

PI548228	T251H	mn	mutation in Harosoy(5) x T139 found in 1961 at Urbana	Stem Growth	II	Mut
PI548230	T253	y20 k2	mutation in T239(k2) found in 1963 at Urbana	Chlorophyll	III	Mut
PI548244	T267H	ms1 (Tonica)	mutation in Harosoy found in 1955 at Tonica, Illinois	male sterility	II	Mut
PI602447	BARC-14 nodulated	Rj1	D76-8070(4) X Clark rj1	nodulated	V	Other
PI602448	BARC-14 non-nodulated	rj1	D76-8070(4) X Clark rj1	non-nodulated	V	Other
PI602449	BARC-15 nodulated	Rj1	CX797-21(4) X Clark rj1	nodulated	IV	Other
PI602450	BARC-15 non-nodulated	rj1	CX797-21(4) X Clark rj1	non-nodulated	IV	Other
PI602451	BARC-16 nodulated	Rj1	Essex(4) X Clark rj1	nodulated	V	Other
PI602452	BARC-16 non-nodulated	rj1	Essex(4) X Clark rj1	non-nodulated	V	Other
PI603180	A94-671-2	k2 T w1	Harsoy-k2 (T239)	pigmentation	I	Harosoy
PI603181	A94-672-1	k2 T W1	Harsoy-k2 (T239)	pigmentation	I	Harosoy
PI603182	A94-683-1	k2 t W1	Harsoy-k2 (T239)	pigmentation	I	Harosoy
PI603183	A94-719-1	k2 t w1	Harsoy-k2 (T239)	pigmentation	I	Harosoy
PI666149	TH001	w2	Nezumisaya x Harosoy(6)	pigmentation	II	Harosoy
PI547503	L68-2056	I r t w1 *	L12 x L64-2281 sib,t w1	Pigmentation	IV	Clark
PI547504	L68-2061	r w1 *	L12 x L64-2281 sib,t w1	Pigmentation	IV	Clark
PI547505	L68-2063	r t w1 *	L12 x L64-2281 sib,t w1	Pigmentation	IV	Clark
PI547506	L68-2073	i t	L67-3469,i x L64-2281 sib,t wl	Pigmentation	IV	Clark
PI547507	L68-2077	i w1	L67-3469,i x L64-2281 sib,t wl	Pigmentation	IV	Clark
PI547508	L68-2082	k1 t1	L67-3479,k1 x L64-2281 sib,t w1	Pigmentation	IV	Clark
PI547509	L68-2085	k1 w1	L67-3479,k1 x L64-2281 sib,t w1	Pigmentation	IV	Clark
PI547510	L68-2093	k1 t w1	L67-3479,k1 x L64-2281 sib,t w1	Pigmentation	IV	Clark
PI547511	L68-2105	I k1 r	L67-3479,k1 x L12,I r*	Pigmentation	IV	Clark
PI547512	L68-2106	k1 r	L67-3479,k1 x L12,I r*	Pigmentation	IV	Clark
PI547513	L68-2130	I k1	L67-3479,k1 x L12,I r*	Pigmentation	IV	Clark

PI547594	L68-236	i(wild)	PI 101.404A x C(6)	Pigmentation	IV	Clark
PI547595	L68-237	i Rps1	PI 101.404A x C(6)	transferred together	IV	Clark
PI547804	L68-4064	Rpm	W(10) x Kanrich	Disease resistance	III	Other
PI547805	L68-4172	Rpm *	L10 x [Chippewa 64(5) x (Clark(2) x Kanrich)]	disease resistance	I	Other
PI547806	L68-4216	I r Rpm *	L16 x SL7	combination	I	Other
PI547807	L68-4242	I t w1 Rpm *	L10 x (Chippewa 64(4) x S62X30:1)	combination	I	Other
PI547808	L68-4291	E2 *	L10(6) x Clark	maturity	I	Other
PI547705	L68-560	y7 y8	H(6) x T138	Chlorophyll	II	Harosoy
PI547706	L68-582	L1 *	L2(6) x Seneca	Pigmentation	II	Harosoy
PI547707	L68-694	E1	H(6) x PI 196.166	Maturity	IV	Harosoy
PI547708	L68-758	Rps1 rxp	H(4) x L2,Rps1 rxp	Disease Resistance	II	Harosoy
PI547809	L69-4124	Rpm Rps1	L15,Rps1 x SL9,Rpm	Disease resistance	III	Other

Supplementary Table 2

Supplementary Table 2 Table showing each trait mapped in this study, along with its alternate alleles, and the isolines of these traits in the USDA Soybean Isolines. Not all NILs listed here were used in the study due to lack of SNP information on one or both parents.

Trait	Additional alleles	Description of Gene Transferred	NILs
ab	Ab	Delayed leaf abscission	PI547575 PI546052 PI546053
d1		Nuclear "stay green" chlorophyll presence after senescence	PI547691 PI547426 PI547709 PI547711 PI547443 PI547445 PI547746 PI547551 PI547552 PI547565 PI547776 PI547777 PI547600 PI547602 PI547603 PI547577 PI547582 PI547607 PI547613 PI547616 PI547618 PI547649 PI591495
d2		Nuclear "stay green" chlorophyll presence after senescence	PI547691 PI547426 PI547701 PI547710 PI547711 PI547444 PI547445 PI547515 PI547565

			PI547613 PI547616 PI547649 PI591495
dt1	Dt1 dt1-t	Determinate stem	PI547729 PI547488 PI547599 PI547546 PI547552 PI547554 PI547601 PI547602 PI547603 PI547572 PI547627 PI547640 PI547650 PI547651 PI547827 PI547861 PI591486 PI547666 PI547883
Dt2		Semi-determinate stem	PI547409 PI547681 PI547458 PI547725 PI547734 PI547489 PI547437 PI547569 PI547835 PI547851
E1	e1	Late maturity	PI547767 PI547431 PI547432 PI547436 PI547702 PI547747 PI547775 PI547551 PI547552

			PI547553 PI547554 PI547572 PI547627 PI547650 PI547652 PI591486 PI547707
e2	E2	Early maturity	PI547768 PI547432 PI547437 PI547533 PI547541 PI547542 PI547551 PI547552 PI547605 PI547606 PI547567 PI547568 PI547572 PI547783 PI547784 PI547785 PI547636 PI547822 PI547824 PI547651 PI547652 PI547654 PI547793
e3	e3	Early maturity and low photoperiod sensitivity to incandescent light	PI547716 PI547747 PI547533 PI547627 PI547650 PI547651 PI547652 PI591486
G		Green seed coat	PI547691 PI547426 PI547701

			PI547709 PI547443 PI547515
hm	hm? (not hm)	Metribuzin sensitive	PI547842 PI547640 PI547641 PI547791 PI547792 PI547888
i	I i(wild) i-i i-k I-I	Black seed coat with R T brown with r T imperfect black with R t W1 or buff with R t w1 or r t	PI547408 PI547463 PI547464 PI547771 PI547725 PI547770 PI547727 PI547800 PI547735 PI547736 PI547494 PI547801 PI547699 PI547772 PI547502 PI547448 PI547449 PI547527 PI547530 PI547560 PI547574 PI547605 PI547606 PI547567 PI547568 PI547822 PI547824 PI591533 PI591532 PI547594 PI547595
Im		Non-mottling (Non-mottling under SMV infection)	PI547447

			PI547448 PI547519 PI547814 PI547815 PI547567 PI547843 PI547845
L1		Black pod	PI547441 PI547597 PI547546 PI547666 PI547706
l2	L2	Tan pod	PI547714 PI547715 PI547731 PI547700 PI547440 PI547496 PI547518 PI547636 PI547637 PI547845 PI547846 PI547647 PI547792
lo		Oval leaflet few-seeded pod	PI547414 PI547692 PI547745 PI547522 PI547530
lw1		Wavy leaf (Requires lw2 no effect with T or individually)	PI547724 PI547470 PI547735 PI547485
n		Abnormal hilum abscission	PI547752 PI547556 PI547557
Np		Phosphorous tolerant	PI547417

			PI547462 PI547466 PI547696 PI547726 PI547727
P1		Glabrous (Pubescence density)	PI547410 PI547412 PI547715 PI547682 PI547723 PI547801 PI547502
p2		Puberulent (Pubescence Density) dwarf seed coat cracks partly male sterile	PI547713 PI547449 PI547566
pa1		Semi-appressed pubescence (upper leaf surface)	PI547457 PI547733 PI547480 PI547481 PI547482 PI547742 PI547581 PI547582 PI547583 PI547634 PI547787 PI547653
pa2		Appressed pubescence with pa1	PI547480 PI547481 PI547482 PI547742 PI547744 PI547528 PI547529 PI547581 PI547582 PI547583 PI547787 PI547653
Ps	Ps-s	Sparse pubescence	PI547456 PI547457 PI547723

			PI547730 PI547480 PI547499 PI547529 PI547532 PI547583
R	r r-m	Black seed pigment with T imperfect black with t W1 or buff with t w1	PI547410 PI547411 PI547765 PI547463 PI547464 PI547592 PI547473 PI547693 PI547735 PI547736 PI547494 PI547801 PI547502 PI547447 PI547448 PI547519 PI547449 PI547527 PI547530 PI547556 PI547560 PI547814 PI547815 PI547605 PI547606 PI547567 PI547568 PI547886 PI591533 PI591532
Rj2	rj2	Ineffective nodulation with Rhizobium strains b7 b14 and b122.	PI509547 PI547826 PI591519 PI591518 PI591533
rmd	Rmd Rmd-c	Susceptible to powdery mildew	PI547892

			PI591519 PI591518 PI591533
Rps1	rps1 Rps1-a Rps1-b Rps1-c Rps1-d Rps1-k	Resistant to to Phytophthora rot races 1 2 10 13 16.	PI548531 PI518669 PI542044 PI547677 PI547403 PI547405 PI547679 PI547406 PI547795 PI547797 PI547798 PI547476 PI547619 PI547636 PI547637 PI547638 PI547822 PI547841 PI547842 PI547639 PI547640 PI547641 PI547824 PI547646 PI547647 PI547848 PI547826 PI547852 PI547857 PI547860 PI591486 PI547791 PI547792 PI547595 PI547708
Rps2	rps2	Resistant to Phytophthora rot races 1-2.	PI509547 PI547826 PI591519 PI591518

			PI591533
Rsv2		Resistant to Soybean Mosaic potyvirus Infection	PI547885 PI547886 PI591533 PI591532
rxp	rxp?	Resistant to bacterial pustule.	PI547403 PI547404 PI547679 PI547406 PI547797 PI547636 PI547637 PI547638 PI591486 PI547708
S	s-t	Short internode length	PI547462 PI547731 PI547732 PI547488 PI547489 PI547482 PI547483 PI547553 PI547554 PI547608
t	T t-r	Grey pubescence	PI547451 PI547465 PI547431 PI547470 PI547590 PI547432 PI547697 PI547726 PI547702 PI547435 PI547496 PI547527 PI547747 PI547775 PI547542 PI547551 PI547552

			PI547553 PI547554 PI547572 PI547783 PI547627 PI547650 PI547652 PI591486 PI547668
td		Light tawny to near-grey pubescence with T	PI547478 PI547516 PI547523
ti	Ti-b Ti-c (not Ti-b)	Kunitz trypsin inhibitor absent	PI542044 PI547656 PI547891 PI547892 PI547861 PI547893
w1	W1	White flower	PI547420 PI547766 PI547465 PI547516 PI547517 PI547518 PI547848 PI547852
w4		Near-white flower	PI547498 PI547524 PI547750 PI547751 PI547668
wm		Magenta flower	PI547541 PI547563 PI547564
y3		Leaves turn rusty yellow with g	PI547688 PI547452 PI547427 PI591495
y7		New leaves very light green in cool weather with y8	PI547418 PI547616 PI547705

y8		New leaves very light green in cool weather with y7	PI547418 PI547616 PI547705
y9		Yellow-green plant	PI547712 PI547446 PI547611 PI547613

Supplementary Table 3

Supplementary Table 3 This table summarizes the parental contribution for each line in the full USDA soybean isoline collection.

NIL	recurrent contribution	donor contribution	parent similarity	Pedigree	Recurrent group
PI597653	0.75186	0.169103	0.701212	Hawkeye x Harosoy	Harosoy
PI597654	0.762623	0.153381	0.701212	Hawkeye x Harosoy	Harosoy
PI597655	0.770164	0.157979	0.701212	Hawkeye x Harosoy	Harosoy
PI597656	0.760769	0.15789	0.701212	Hawkeye x Harosoy	Harosoy
PI597660	0.75836	0.162003	0.701212	Hawkeye x Harosoy	Harosoy
PI597661	0.765742	0.155068	0.701212	Hawkeye x Harosoy	Harosoy
PI597662	0.751737	0.165958	0.701212	Hawkeye x Harosoy	Harosoy
PI597657	0.739124	0.170525	0.701212	Hawkeye x Harosoy	Harosoy
PI597658	0.754561	0.16393	0.701212	Hawkeye x Harosoy	Harosoy
PI597659	0.760215	0.153359	0.701212	Hawkeye x Harosoy	Harosoy
PI547895	0.865206	0.036894	0.686074	Clark 63(9) x Hill	Clark
PI509547	0.770785	0.05328	0.607652	Clark 63(9) x Hardee	Clark
PI548531	0.938046	0.054979	0.710195	Ch(8) x Blackhawk	Other
PI518669	0.956057	0.043633	0.686858	Corsoy(6) x Lee 68	Other
PI542044	0.915508	0.071535	0.590138	Wm 82(6) x PI157440	Williams
PI547677	0.841045	0.063928	0.716279	H(8) x Blackhawk	Harosoy
PI547403	0.986621	0.006274	0.545342	(C(7) x CNS)rxp x (C(6) x Blackhawk)Rps 1	Clark
PI547404	0.986929	0.007104	0.545342	C(8) x CNS	Clark
PI547405	0.986023	0.009535	0.69577	C(8) x Blackhawk	Clark
PI547679	0.893249	0.104229	0.969701	Harosoy 63 x L3rxp	Harosoy
PI547406	0.989309	0.008753	0.545342	L8rxp x L7Rps1	Clark
PI547406	0.989524	0.006552	0.69577	L8rxp x L7Rps1	Clark

PI547408	0.975956	0.022803	0.896008	C(6) x T201	Clark
PI547409	0.971825	0.026862	0.702067	C(6) x T117	Clark
PI547410	0.963247	0.03501	0.649311	C(6) x T145	Clark
PI547411	0.962245	0.030551	0.649311	C(6) x T145	Clark
PI547412	0.98891	0.008698	0.649311	C(6) x T145	Clark
PI547451	0.936654	0.061807	0.652329	C(6) x T204	Clark
PI547413	0.99295	0.003886	0.652329	C(6) x T204	Clark
PI547414	0.988262	0.009725	0.652329	C(6) x T204	Clark
PI547681	0.965256	0.028122	0.708175	H(6) x T117	Harosoy
PI547714	0.944834	0.022941	0.6851	H(6) x T145	Harosoy
PI547715	0.982429	0.0142	0.6851	H(6) x T145	Harosoy
PI547682	0.984001	0.010414	0.6851	H(6) x T145	Harosoy
PI547716	0.825212	0.041777	0.6798	H(6) x T204	Harosoy
PI547688	0.985056	0.007806	0.684529	H(6) x T139	Harosoy
PI547765	0.988293	0.005091	0.684529	H(6) x T139	Harosoy
PI547690	0.952886	0.011591	0.6798	H(6) x T204	Harosoy
PI547795	0.901398	0.048425	0.710195	Ch(10) x Blackhawk	Other
PI547417	0.979949	0.016793	0.758127	C(6) x Chief	Clark
PI547418	0.977114	0.021517	0.769867	C(6) x T138	Clark
PI547419	0.98347	0.015691	0.896008	C(6) x T201	Clark
PI547452	0.952297	0.029789	0.720627	C(6) x T139	Clark
PI547420	0.970266	0.026323	0.720627	C(6) x T139	Clark
PI547458	0.97185	0.024255	0.702067	(C(6) x T117)Dt2 x (C(6) x T204)ln	Clark
PI547462	0.984898	0.013588	0.758127	C(6) x Chief	Clark
PI547766	0.975132	0.008534	0.68624	H(6) x Peking	Harosoy
PI547463	0.973916	0.017335	0.896008	(C(6) x T201)l x (C(6) x T145)r	Clark
PI547465	0.997117	0.001287	0.652329	(C(6) x T139)w1 x (C(6) x T204)t	Clark
PI547691	0.943971	0.052208	0.641683	H(6) x Columbia	Harosoy
PI547426	0.979858	0.016333	0.622125	C(6) x Columbia	Clark
PI547427	0.979586	0.019226	0.720627	L62-1027cyt-G x (C(6) x T139)y3	Clark
PI547466	0.976608	0.019445	0.758127	L6 x (C(5) x Chief)	Clark
PI547797	0.947063	0.030347	0.558009	(Ch(8) x CNS) x (Ch(10) x Blackhawk)	Other
PI547456	0.959105	0.036706	0.627923	C(6) x Higan	Clark
PI547457	0.924652	0.046386	0.627923	C(6) x Higan	Clark

PI547767	0.948837	0.044142	0.641683	H(6) x Columbia	Harosoy
PI547768	0.983223	0.011643	0.708175	H(6) x T117	Harosoy
PI547771	0.983405	0.014105	0.708175	H(6) x T117	Harosoy
PI547725	0.971285	0.026252	0.708175	H(6) x T117	Harosoy
PI547592	0.99462	0.003307	0.627923	C(6) x Higan	Clark
PI547695	0.943806	0.050885	0.719035	H(6) x T201	Harosoy
PI547473	0.976922	0.017827	0.896008	L6 x L11I r	Clark
PI547723	0.979325	0.016885	0.686811	H(6) x Higan	Harosoy
PI547431	0.972857	0.024857	0.632106	C(6) x T175	Clark
PI547692	0.985835	0.009101	0.689496	H(6) x T205	Harosoy
PI547798	0.387757	0.525354	0.855442	W(6) x Clark 63	Williams
PI547724	0.969479	0.019846	0.682937	H(6) x T176	Harosoy
PI547693	0.987791	0.008552	0.682937	H(6) x T176	Harosoy
PI547770	0.982322	0.01635	0.682937	H(6) x T176	Harosoy
PI547470	0.949958	0.048522	0.688973	C(6) x T176	Clark
PI547590	0.955617	0.043102	0.688973	C(6) x T176	Clark
PI547471	0.978	0.015298	0.648931	C(6) x PI196166	Clark
PI547476	0.982971	0.014583	0.506107	PI101404A x C(6)	Clark
PI547478	0.957916	0.036264	0.539259	L6(6) x Sooty	Clark
PI547728	0.981722	0.009887	0.719035	L2 x (H(6) x T201)	Harosoy
PI547432	0.937238	0.058766	0.647433	L62-1932e2 x L65-3366E1 t	Clark
PI547432	0.947181	0.044461	0.632106	L62-1932e2 x L65-3366E1 t	Clark
PI547696	0.978061	0.012164	0.711502	H(6) x (C(6) x Chief)	Harosoy
PI547697	0.986967	0.003952	0.706179	H(6) x Clark	Harosoy
PI547726	0.975418	0.011912	0.705014	H(6) x L9(Clark-Np)	Harosoy
PI547727	0.984326	0.005513	0.705014	H(6) x L9(Clark-Np)	Harosoy
PI547800	0.688556	0.22427	0.60076	W(5) x L68-2045Clark-I P1 r	Williams
PI547734	0.952134	0.038698	0.708175	L2 x (H(6) x T117)	Harosoy
PI547436	0.985219	0.011316	0.632106	C(6) x T175	Clark
PI547729	0.951761	0.039856	0.686811	H(6) x Higan	Harosoy
PI547730	0.943781	0.048569	0.686811	H(6) x Higan	Harosoy
PI547735	0.976195	0.015544	0.682937	H(6) x T176	Harosoy
PI547736	0.977892	0.016192	0.682937	H(6) x T176	Harosoy
PI547485	0.991717	0.006158	0.688973	C(6) x T176	Clark
PI547731	0.979373	0.014428	0.686811	H(6) x Higan	Harosoy

PI547700	0.974983	0.021269	0.686811	H(6) x Higan	Harosoy
PI547702	0.972895	0.022516	0.714092	H(6) x PI196166	Harosoy
PI547732	0.954343	0.032498	0.686811	H(6) x Higan	Harosoy
PI547733	0.966722	0.028108	0.686811	H(6) x Higan	Harosoy
PI547488	0.948456	0.042285	0.758127	(C(6) x Chief)s-t x L63-3297dt1	Clark
PI547489	0.918197	0.011732	0.758127	(C(6) x Chief)s-t x L62-1251Dt2	Clark
PI547437	0.957653	0.027925	0.702067	L62-1932e2 x L62-1251Dt2	Clark
PI547437	0.943653	0.051904	0.647433	L62-1932e2 x L62-1251Dt2	Clark
PI547494	0.470059	0.519166	0.989354	L66-14i* x L12I r*	Clark
PI547801	0.693813	0.222325	0.60076	W(5) x L68-2045Clark-I P1 r	Williams
PI547699	0.989958	0.004192	0.706179	H(6) x Clark	Harosoy
PI547435	0.989199	0.009254	0.627923	C(6) x Higan	Clark
PI547480	0.952351	0.045153	0.627923	C(6) x Higan	Clark
PI547481	0.967017	0.027246	0.627923	C(6) x Higan	Clark
PI547482	0.960478	0.037887	0.627923	C(6) x Higan	Clark
PI547483	0.949324	0.047363	0.627923	C(6) x Higan	Clark
PI547772	0.982325	0.014027	0.641683	H(6) x Columbia	Harosoy
PI547701	0.96889	0.01704	0.641683	H(6) x Columbia	Harosoy
PI547440	0.975006	0.018118	0.627923	C(6) x Higan	Clark
PI547496	0.975288	0.020508	0.627923	C(6) x Higan	Clark
PI547441	0.942784	0.046678	0.648432	L6(6) x Seneca	Clark
PI547499	0.982047	0.009063	0.627923	(C(6) x Higan)Ps-s x L63-2435pc	Clark
PI547502	0.972813	0.021265	0.649311	L62-1058I x (C(6) x T145)P1 r	Clark
PI547709	0.972029	0.018852	0.641683	H(6) x Columbia	Harosoy
PI547710	0.9623	0.018939	0.641683	H(6) x Columbia	Harosoy
PI547711	0.974251	0.016166	0.641683	H(6) x Columbia	Harosoy
PI547712	0.935301	0.03822	0.69798	L2(6) x T135	Harosoy
PI547443	0.961072	0.033772	0.622125	C(6) x Columbia	Clark
PI547444	0.962655	0.034664	0.622125	C(6) x Columbia	Clark
PI547445	0.941815	0.015143	0.622125	C(6) x Columbia	Clark
PI547515	0.989545	0.009166	0.622125	C(6) x Columbia	Clark
PI547446	0.989725	0.007539	0.754539	L6(6) x T135	Clark
PI547516	0.971606	0.020004	0.648432	L6(6) x Seneca	Clark
PI547517	0.978723	0.016981	0.648432	L6(6) x Seneca	Clark

PI547518	0.982018	0.016126	0.652329	C(6) x T204	Clark
PI547447	0.957329	0.035071	0.732224	L12(6) x Hawkeye	Clark
PI547448	0.962042	0.028602	0.732224	L12(6) x Hawkeye	Clark
PI547519	0.941506	0.052883	0.732224	L12(6) x Hawkeye	Clark
PI547742	0.888453	0.057434	0.686811	H(6) x Higan	Harosoy
PI547713	0.96174	0.026224	0.717704	L2(6) x T31	Harosoy
PI547449	0.985527	0.007876	0.700143	L12(6) x T31	Clark
PI547744	0.956424	0.039814	0.686811	H(6) x Higan	Harosoy
PI547745	0.977793	0.016237	0.6798	(H(6) x T204)ln x (H(6) x T204)lo	Harosoy
PI547522	0.977007	0.020275	0.652329	(C(6) x T204)ln x L62-1615lo	Clark
PI547523	0.940956	0.051936	0.778588	L6(6) x Grant	Clark
PI547527	0.968123	0.023412	0.732224	L12(6) x Hawkeye	Clark
PI547528	0.953022	0.044993	0.627923	C(6) x Higan	Clark
PI547529	0.955734	0.041127	0.627923	C(6) x Higan	Clark
PI547530	0.981705	0.0126	0.652329	L12 x L62-1615lo	Clark
PI547531	0.987897	0.009701	0.652329	L12 x L62-1579ln	Clark
PI547532	0.98413	0.013142	0.637952	L12 x L63-2999Ps	Clark
PI547746	0.979045	0.013927	0.704325	L2 x L62-801Pd1	Harosoy
PI547747	0.968941	0.009018	0.6798	L62-667e3 x L67-2324E1 T	Harosoy
PI547747	0.964022	0.015473	0.714092	L62-667e3 x L67-2324E1 T	Harosoy
PI547533	0.976395	0.016988	0.641136	L63-3117e2 x L63-2404e3	Clark
PI547533	0.976045	0.017363	0.647433	L63-3117e2 x L63-2404e3	Clark
PI547775	0.970615	0.026233	0.704325	L67-2324E1 T x L64-4830E5	Harosoy
PI547775	0.97892	0.014245	0.714092	L67-2324E1 T x L64-4830E5	Harosoy
PI547599	0.979303	0.014268	0.641136	L63-3297dt1 x L62-1579ln	Clark
PI547599	0.981299	0.010964	0.652329	L63-3297dt1 x L62-1579ln	Clark
PI547752	0.980171	0.015177	0.634767	L2(6) x Soysota	Harosoy
PI547541	0.9547	0.036715	0.702424	L6(6) x T235	Clark

PI547542	0.948072	0.046219	0.702424	L6(6) x T235	Clark
PI547546	0.961118	0.022765	0.648432	(L6(6) x Seneca)L1* x L63-3297dt1	Clark
PI547551	0.959816	0.034249	0.641778	L66-531dt1 E1 t e2 x L62-1686Pd1	Clark
PI547552	0.954376	0.038097	0.641778	L66-531dt1 E1 t e2 x L62-1686Pd1	Clark
PI547553	0.973105	0.025571	0.758127	L65-3366E1 t x L64-1731s-t Np	Clark
PI547554	0.450229	0.535943	0.990019	L66-531 dt1 E1 t e2 x L67-3207dt1 s-t	Clark
PI547554	0.96274	0.023852	0.758127	L66-531 dt1 E1 t e2 x L67-3207dt1 s-t	Clark
PI547555	0.992644	0.006018	0.740589	C(6) x T219H	Clark
PI547556	0.953696	0.040322	0.609078	L6(6) x Soysota	Clark
PI547557	0.986279	0.006218	0.609078	L6(6) x Soysota	Clark
PI547560	0.977215	0.017953	0.652329	L12 x L62-1579ln	Clark
PI547577	0.962115	0.036155	0.896008	L12 x L63-1889rj1	Clark
PI547562	0.983973	0.011541	0.647433	L12 x L64-1344Lf1	Clark
PI547563	0.970954	0.025179	0.702424	L6(6) x T235	Clark
PI547564	0.955565	0.038698	0.702424	L6(6) x T235	Clark
PI547565	0.969703	0.011838	0.622125	(L12(5) x T31)p2* x (C(6) x Columbia)d1 d2	Clark
PI547566	0.930732	0.059358	0.700143	(L12(5) x T31)p2* x (C(6) x Columbia)d1 d2	Clark
PI547776	0.969097	0.025117	0.704325	L63-1212ln x L62-801Pd1	Harosoy
PI547776	0.976426	0.015241	0.6798	L63-1212ln x L62-801Pd1	Harosoy
PI547777	0.921289	0.073318	0.960765	(L63-1212ln x Harosoy 63) x L62-801Pd1	Harosoy
PI547778	0.922936	0.071331	0.960765	L63-1212ln x Harosoy 63	Harosoy
PI547600	0.987792	0.006433	0.641778	L62-1579ln x L62-1686Pd1	Clark

PI547600	0.988822	0.004749	0.652329	L62-1579ln x L62-1686Pd1	Clark
PI547601	0.975525	0.0189	0.641136	L62-1579ln x (L63-3297dt1 x Clark 63)	Clark
PI547601	0.977086	0.016183	0.652329	L62-1579ln x (L63-3297dt1 x Clark 63)	Clark
PI547602	0.989576	0.008615	0.641778	L63-3297dt1 x L62-1686Pd1	Clark
PI547602	0.987833	0.011341	0.641136	L63-3297dt1 x L62-1686Pd1	Clark
PI547603	0.98076	0.014665	0.641136	Clark 63 x (L63-3297dt1 x L62-1686Pd1)	Clark
PI547603	0.981015	0.014251	0.641778	Clark 63 x (L63-3297dt1 x L62-1686Pd1)	Clark
PI547575	0.973604	0.021555	0.570817	L6(6) x Kingwa	Clark
PI547576	0.991574	0.003479	0.570817	L6(6) x Kingwa	Clark
PI547577	0.987528	0.01088	0.641778	L12 x L63-1889rj1	Clark
PI547578	0.970399	0.025929	0.896008	L12 x L63-1889rj1	Clark
PI547580	0.985599	0.011046	0.742253	L6(6) x T255	Clark
PI547581	0.983227	0.015079	0.641136	L67-497pa1 pa2 x L63-2435pc	Clark
PI547581	0.983613	0.014781	0.627923	L67-497pa1 pa2 x L63-2435pc	Clark
PI547582	0.947426	0.036188	0.641778	L67-497pa1 pa2 x L62-1686Pd1	Clark
PI547582	0.938637	0.050983	0.627923	L67-497pa1 pa2 x L62-1686Pd1	Clark
PI547583	0.970392	0.02698	0.627923	L67-497pa1 pa2 x L63-2999Ps	Clark
PI547583	0.972122	0.023845	0.637952	L67-497pa1 pa2 x L63-2999Ps	Clark
PI547814	0.788426	0.113253	0.656369	SL12(6) x Merit	Other
PI547815	0.77692	0.122563	0.656369	SL12(6) x Merit	Other
PI547605	0.942828	0.054846	0.706179	L12(6) x Harosoy	Clark
PI547606	0.951437	0.03986	0.892229	L12(6) x Chippewa	Clark
PI547567	0.789373	0.074783	0.732224	L12(6) x Hawkeyee2 Im*	Clark
PI547568	0.887224	0.074569	0.732224	L12(6) x Hawkeye	Clark
PI547760	0.988568	0.002573	0.582581	L2(6) x Kingwa	Harosoy

PI547569	0.965107	0.031151	0.702067	L6 x L62-1251Dt2	Clark
PI547572	0.858153	0.052509	0.732224	(L12(6) x Hawkeye)Im* x L66-531dt1 E1 t e2	Clark
PI547607	0.983664	0.012124	0.641778	(L63-3297dt1 x L62-1579ln) x(L63-3297dt1 x L62-1686Pd1)	Clark
PI547607	0.983624	0.01199	0.652329	(L63-3297dt1 x L62-1579ln) x(L63-3297dt1 x L62-1686Pd1)	Clark
PI547832	0.922269	0.071715	0.682605	Wm(6) x T259H	Williams
PI547584	0.958491	0.036586	0.646103	L6(6) x T260H	Clark
PI547783	0.957597	0.037264	0.706179	L2(6) x Clark	Harosoy
PI547835	0.92723	0.063425	0.635147	Wm(6) x (Clark(6) x T117)	Williams
PI547784	0.978317	0.014956	0.706179	L2(6) x Clark	Harosoy
PI547608	0.942747	0.051413	0.758127	L12 x (C(6) x Chief)	Clark
PI547785	0.980123	0.015383	0.708175	L64-4584E2 x L64-4830E5	Harosoy
PI547611	0.985902	0.007881	0.655086	L62-1027cyt-G x L69-4755y9*	Clark
PI547611	0.974922	0.021394	0.754539	L62-1027cyt-G x L69-4755y9*	Clark
PI547613	0.974212	0.0188	0.622125	(C(6) x Columbia)G d1 d2 x L69-4755y9	Clark
PI547616	0.97491	0.022928	0.769867	L69-4663d1 d2 x L63-1792y7 y8	Clark
PI547616	0.983789	0.014101	0.622125	L69-4663d1 d2 x L63-1792y7 y8	Clark
PI547618	0.970585	0.021136	0.641778	L62-1579ln x (Clark 63 x L62-1686Pd1)	Clark
PI547618	0.978291	0.008981	0.652329	L62-1579ln x (Clark 63 x L62-1686Pd1)	Clark
PI547619	0.971807	0.026721	0.66288	C(6) x Arksoy	Clark
PI547624	0.915386	0.055122	0.642182	L72-1495e2*(6) x PI229342	Clark

PI547625	0.842904	0.119917	0.692538	L6(6) x T264	Clark
PI547632	0.985452	0.010676	0.70606	L6(6) x T93	Clark
PI547634	0.726678	0.132248	0.627923	C(6) x Higan	Clark
PI547636	0.898857	0.081563	0.642182	L6(2) x (L63-3117e2(4) x PI229342)	Clark
PI547637	0.927764	0.064378	0.642182	L6(6) x PI229342	Clark
PI547638	0.939067	0.05144	0.642182	L6(6) x PI229342	Clark
PI547627	0.950587	0.033297	0.641136	L63-2404e3 x L66-546dt1 E1 t	Clark
PI547627	0.385408	0.593308	0.988569	L63-2404e3 x L66-546dt1 E1 t	Clark
PI547841	0.873962	0.076516	0.601806	Wm(6) x (Clark 63(3) PI229342)	Williams
PI547842	0.929915	0.063118	0.610005	Wm(7) x Harrel (L26)	Williams
PI547639	0.935795	0.030922	0.570817	C(6) x Kingwa	Clark
PI547640	0.972312	0.0268	0.659815	C(6) x Harrel	Clark
PI547641	0.941957	0.056382	0.659815	C(6) x HarrelRps1-b hm	Clark
PI547843	0.712824	0.205307	0.843512	Wm(6) x L69-5343Clark-I r Im*	Williams
PI547845	0.826612	0.16769	0.843512	Wm(6) x L69-5343Clark-I r Im*	Williams
PI547846	0.837785	0.156388	0.843512	Wm(6) x L69-5343Clark-I r Im*	Williams
PI547644	0.965668	0.030222	0.642182	L6(6) x PI229342	Clark
PI547645	0.983829	0.013746	0.744225	L6(6) x T259H	Clark
PI547646	0.91526	0.049194	0.627923	C(6) x Higan	Clark
PI547647	0.979778	0.017421	0.66288	C(6) x Arksoy	Clark
PI547649	0.974657	0.021496	0.692538	L62-1686Pd1 x (L6(6) x T264)Pd2	Clark
PI547848	0.893183	0.099719	0.653897	Wm(6) x Lee 68	Williams
PI547852	0.932118	0.05858	0.601806	Wm(6) x (Clark 63(6) x PI229342)	Williams
PI547650	0.55576	0.429654	0.989259	L70-4478dt1 E1 t e2* x L71-920e2 e3	Clark

PI547651	0.833489	0.15871	0.989259	L70-4478dt1 E1 t e2* x L71-920e2 e3	Clark
PI547652	0.61266	0.373722	0.989259	L70-4478dt1 E1 t e2* x L71-920e2 e3	Clark
PI547787	0.951592	0.043632	0.686811	L67-271pa1 x L70-4112pa2	Harosoy
PI547827	0.776388	0.17076	0.813379	Elf(6) x Williams	Other
PI547857	0.902212	0.074456	0.614377	L78-379Rsv1 x Wm 82Rps1-k	Williams
PI547653	0.937717	0.042079	0.627923	L70-4558pa2 x L76-1291pa1	Clark
PI547654	0.954897	0.039236	0.749786	L6(6) x Calland	Clark
PI547655	0.974613	0.020774	0.896008	L6(2) x L63-1889	Clark
PI547656	0.976464	0.020572	0.619629	L6(6) x PI157440	Clark
PI547860	0.915246	0.065263	0.598432	L81-4352Rps1-c Rps2 Rj2 x (L75-6141Rpm Rps1 x L76-1988Rps2 Rj2)	Williams
PI547860	0.802957	0.18302	0.826925	L81-4352Rps1-c Rps2 Rj2 x (L75-6141Rpm Rps1 x L76-1988Rps2 Rj2)	Williams
PI547891	0.927977	0.062992	0.615589	Wm(6) x Jefferson	Williams
PI547892	0.920065	0.075419	0.615589	Wm(6) x Jefferson	Williams
PI547861	0.902093	0.091128	0.615946	Wm(6) x PI196172	Williams
PI547893	0.929799	0.063392	0.615946	Wm(6) x PI196172	Williams
PI591486	0.37215	0.498315	0.966849	L70-4478 dt1 E1 t e2 Rpsl rxp x L71-920 e2 e3	Clark
PI591486	0.676828	0.17904	0.989259	L70-4478 dt1 E1 t e2 Rpsl rxp x L71-920 e2 e3	Clark
PI547666	0.903403	0.030459	0.647433	L68-1562L1* x L63-3016dt1	Clark
PI547666	0.907098	0.024713	0.648432	L68-1562L1* x L63-3016dt1	Clark
PI547791	0.96302	0.024709	0.686811	H(6) x Higan	Harosoy
PI547792	0.976794	0.015796	0.686811	H(6) x Higan	Harosoy

PI547872	0.916008	0.072369	0.598764	Wm(6) x PI229324	Williams
PI547873	0.915887	0.074993	0.646911	Wm(6) x Dorman	Williams
PI547877	0.935755	0.056318	0.582913	Wm(6) x PI408251	Williams
PI547793	0.831493	0.038052	0.704325	L64-4830E5 x L74-27E2*	Harosoy
PI547883	0.892026	0.070306	0.582913	Wm(6) x PI408251	Williams
PI547885	0.910463	0.084501	0.604563	Wm(6) x RaidenPI360844	Williams
PI547886	0.920057	0.069576	0.604563	Wm(6) x Raiden (PI360844)	Williams
PI591519	0.931235	0.06013	0.615589	L76-1988 Rps2 Rmd-c Rj2 x L82-2024 rmd Ti-b	Williams
PI591518	0.928682	0.066788	0.615589	L76-1988 Rps2 Rmd-c Rj2 x L82-2024 rmd Ti-b	Williams
PI591495	0.92519	0.066029	0.951236	L69-4663 d1 d2 x L63-2346 y3	Clark
PI591533	0.806521	0.178094	0.853541	L76-1994 I Rps2 Rmd-c Rj2 x L88-8440 r Rsv2	Williams
PI591533	0.906567	0.085954	0.604563	L76-1994 I Rps2 Rmd-c Rj2 x L88-8440 r Rsv2	Williams
PI591532	0.912562	0.081973	0.604563	L76-1994 I Rps2 Rmd-c Rj2 x L88-8440 r Rsv2	Williams
PI546052	0.965932	0.019416	0.589449	'Kingwa'/7*Maple presto	Other
PI546053	0.936855	0.052739	0.589449	Kingwa'/7*Maple presto	Other
PI602447	0.932709	0.060781	0.66452	D76-8070(4) X Clark rj1	Other
PI602448	0.933407	0.061054	0.66452	D76-8070(4) X Clark rj1	Other
PI602451	0.895249	0.07596	0.603779	Essex(4) X Clark rj1	Other
PI602452	0.81022	0.117603	0.603779	Essex(4) X Clark rj1	Other
PI547594	0.982976	0.013915	0.506107	PI101404A x C(6)	Clark

PI547595	0.972925	0.025276	0.506107	PI101404A x C(6)	Clark
PI547705	0.968766	0.016727	0.71509	H(6) x T138	Harosoy
PI547706	0.946621	0.049683	0.665423	L2(6) x Seneca	Harosoy
PI547707	0.943238	0.023447	0.714092	H(6) x PI196166	Harosoy
PI547708	0.786279	0.204689	0.99432	H(4) x L2Rps1 rxp	Harosoy

Supplementary Table 4

Supplementary Table 4 Table summarizing the mapping results of this study. Each mapped trait is listed in the first column. Traits annotated with a ‘*’ are ones in which the interval size has been shortened with these results. Traits annotated with ‘**’ were unmapped previously to this study. Additional alleles of the trait that are also isolated in this collection, and a description of the gene according to the USDA Soybean Isoline Collection are also outlined (Bernard et al., 1991). Previous mapping information is listed first to include cloned genes, map it is placed on, chromosome, position/flanking markers, upstream marker locus, and downstream marker locus. Mapping results from this study are provided as the chromosome, interval start, interval end, its size in bp and Mbp, and the total number of introgressions predicted for that trait. Finally, population characteristics are provided to show the number of NILs available for that trait and which of the three commercial recurrent parents were used for this trait.

Trait Isolated	**ab****	**d1**	**d2***
Additional alleles	Ab		
Description of Trait	Delayed leaf abcission	Nuclear "stay green" chlorophyll presence after senescence	Nuclear "stay green" chlorophyll presence after senescence
Type	Leaf Form	Chlorophyll	Chlorophyll

Gene Models		Glyma01g42390	Glyma.11g027200
Map		Glyma 2.0	Glyma 2.0
Previous Chromosome		1	11
Position/Flanking Markers			
Upstream Marker Locus		54554210	2.00E+06
Downstream Marker Locus		54556460	1970366
Interval Chromosome	13	1	11
Interval Start	30086805	53786562	1629870
Inerval End	34775605	55086518	2633828
Interval Size (Mb)	7.683876	7.683876	7.683876
Number of NILS	3	18	8
Number of Intervals Predicted	1	1	1
Recurrent Parents	Clark Harosoy	Clark Harosoy	Clark Harosoy
Reference to Cloned Genes		Fang, C., et al. (2014), Concerted evolution of D1 and D2 to regulate chlorophyll degradation in soybean. Plant J, 77: 700–712. doi:10.1111/tpj.12419	Fang, C., et al.(2014), Concerted evolution of D1 and D2 to regulate chlorophyll degradation in soybean. Plant J, 77: 700–712. doi:10.1111/tpj.12419

dt1*	Dt2	E1	e2
Dt1 dt1-t		e1	E2
Determinate stem	Semi-determinate stem	Late maturity	Early maturity
Stem Growth	Stem Growth	Maturity Time	Maturity Time
Glyma.19g194300	Glyma.18g273600	Glyma.06g207800	Glyma.10g221500
Composite2003	Glyma2.0	Glyma 2.0	Glyma 2.0
19	18	6	10
			136.33cM
5.00E+07	55638209	2.00E+07	44716720
5.00E+07	55646654	20207959	44738268
19	18	6	10
43882137	54576800	19354163	43780076
45273019	56430921	20353073	45629506
7.683876	7.683876	7.683876	7.683876
4	5	5	8
1	1	1	1
Clark Harosoy Williams	Clark Harosoy Williams	Clark Harosoy	Clark Harosoy Williams
Liu, B., et al. (2010). The Soybean Stem Growth Habit Gene Dt1 Is an Ortholog of Arabidopsis TERMINAL FLOWER1. Plant Physiology, 153(1).	Ping, J., et al.(2014). Dt2 is a gain-of-function MADS-domain factor gene that specifies semideterminacy in soybean. The Plant Cell, 26(7), 2831–42.	Xia, Z.,et al. (2012). Positional cloning and characterization reveal the molecular basis for soybean maturity locus E1 that regulates photoperiodic flowering. Proceedings of the National Academy of Sciences, 109(32), E2155–E2164. http://doi.org/10.1073/pnas.1117982109	Watanabe S, et al. (2011). A map-based cloning strategy employing a residual heterozygous line reveals that the GIGANTEA gene is involved in soybean maturity and flowering. Genetics.188(2):395–407.

e3	G**	hm**	i*
e3		hm? (not hm)	I i(wild) i-i i-k I-I
Early maturity and low photoperiod sensitivity to incandescent light	Green seed coat	Metribuzin sensitive	Black seed coat with R T brown with r T imperfect black with R t W1 or buff with R t w1 or r t
Chlorophyll	Chlorophyll	Other	Pigmentation
Glyma.19g41210			
Classical	Classical	Classical	Composite2003
19	1	3	8
	108cM	7cM	48.4cM
5.00E+07			5772438
47642015			7885882
19	1	3	8
45920936	51775991	2495572	6183359
48259684	55375763	5216005	8816346
7.683876	7.683876	7.683876	7.683876
5	6	3	22
3	1	1	1
Clark Harosoy	Clark Harosoy	Clark Harosoy Williams	Harosoy
Watanabe S, Hideshima R, Zhengjun X, et al. (2009) Map-based cloning of the gene associated with the soybean maturity locus E3 . Genetics.;182 (4):1251–1262.			Senda et al. (2002). Analysis of the duplicated CHS1 gene related to the suppression of the seed coat pigmentation in yellow soybeans. Theor. Appl. Genet. 104(6-7):1086-1091

Im**	L1	l2*	lo*
		L2	
Non-mottling (Non-mottling under SMV infection)	Black pod	Tan pod	Oval leaflet few-seeded pod
Pigmentation	Pigmentation	Pigmentation	Leaf_Form
	Glyma19g27460		
	Glyma 1.0	Composite2003	Glyma 2.0
	19	3	19
		1cM	
	34750891	0	46515796
	34752190	467655	50189764
9	19	3	19
12809350	32245731	385844	49107132
21080454	39929607	793778	50555433
7.683876	7.683876	7.683876	7.683876
8	5	10	5
1	2	1	1
Clark Harosoy Williams	Clark Harosoy	Clark Harosoy Williams	Clark Harosoy
			He, Q., et al. (2015). Fine mapping of the genetic locus L1 conferring black pods using a chromosome segment substitution line population of soybean. Plant Breeding, 134(4), 437–445.

lw1**	n*	Np**	P1
Wavy leaf (Requires lw2 no effect with T or individually)	Abnormal hilum abcission	Phosphorous tolerant	Glabrous (Pubescence density)
Leaf_Form	Other	Nutrient_Response	Pubescence_Type
Glyma 2.0	Composite2003	Glyma 2.0	Composite2003
7	4	10	9
	122.62cM		
	43172504		48662337
	50220916		48977064
7	4	10	9
19017836	48009592	339795	48200877
25800983	50798340	2076591	49558866
7.683876	7.683876	7.683876	7.683876
5	3	6	7
1	1	1	3
Clark Harosoy	Clark Harosoy	Clark Harosoy	Clark Harosoy

p2**	pa1*	pa2	Ps*	R*
			Ps-s	r r-m
Puberulent (Pubescence Density) dwarf seed coat cracks partly male sterile	Semi-appressed pubescence (upper leaf surface)	Appressed pubescence with pa1	Sparse pubescence	Black seed pigment with T imperfect black with t W1 or buff with t w1
Pubescence Type	Pubescence Type	Pubescence_Type	Pubescence_Type	Pigmentation
Classical	Composite2003	Composite2003	Composite2003	Composite2003
20	11	13	12	9
62cM	40cM	85.33cM	78.44cM	97.3cM
	6971135	32866056	34078234	42848903
	8151771	33555523	40091314	44329945
20	12	13	12	9
1582950	37092076	31833050	34718187	43968962
2292167	37662189	34231643	34756687	45078638
7.683876	7.683876	7.683876	7.683876	7.683876
5	7	7	6	19
1	4	1	1	2
Clark Harosoy	Clark Harosoy	Clark Harosoy	Clark Harosoy	Clark Harosoy

Rj2*	rmd*	Rps1 *	Rps2*	Rsv2**
rj2	Rmd Rmd-c	rps1 Rps1-a Rps1-b Rps1-c Rps1-d Rps1-k	rps2	
Ineffective nodulation with Rhizobium strains b7 b14 and b122.	Susceptible to powdery mildew	Resistant to to Phytophthora rot races 1 2 10 13 16.	Resistant to Phytophthora rot races 1-2.	Resistant to Soybean Mosaic potyvirus Infection
Nutrient Response	Disease Resistance	Disease Resistance	Disease Resistance	Disease Resistance
Glyma.16g212300				
Glyma 1.0	Composite2003	Composite2003	Composite2003	
16	16	3	16	
	97cM	31.5cM	90.8cM	
4.00E+07	37139330	3465436	37139330	
37068431	37887014	9058213	37887014	
16	16	3	16	13
36657330	37133445	2388393	37323949	29761581
37510824	37445692	5044674	37510824	32459471
7.683876	7.683876	7.683876	7.683876	7.683876
16	6	3	15	5
1	3	1	1	3
Clark Harosoy Williams	Clark Harosoy Williams	Clark Harosoy Williams	Clark Harosoy Williams	Williams
Yang, S., Tang, F., Gao, M., Krishnan, H. B., & Zhu, H. (2010). R gene-controlled host specificity in the legume-rhizobia symbiosis. Proceedings of the National Academy of Sciences of the United States of America, 107(43), 18735–40. http://doi.org/10.1073/pnas.1011957107				

rxp*	S**	t	td**	ti
rxp?	s-t	T t-r		Ti-b Ti-c (not Ti-b)
Resistant to bacterial pustule.	Short internode length	Grey pubescence	Light tawny to near-grey pubescence with T	Kunitz trypsin inhibitor absent
Disease Resistance	Stem Growth	Pigmentation	Pigmentation	Seed composition
		Glyma.06g202300		
Composite2003		Glyma 2.0		Composite2003
17		6		8
35.5cM				150cM
5791692		18731105		45149998
7811432		18738025		45939584
17	13	6	3	8
7128509	38027686	18481405	43513124	43763761
7514242	39207273	19120623	45643162	46569580
7.683876	7.683876	7.683876	7.683876	7.683876
16	4	10	3	3
1	1	1	1	1
Clark Harosoy	Clark Harosoy	Clark Harosoy Williams	Clark Harosoy	Clark Williams

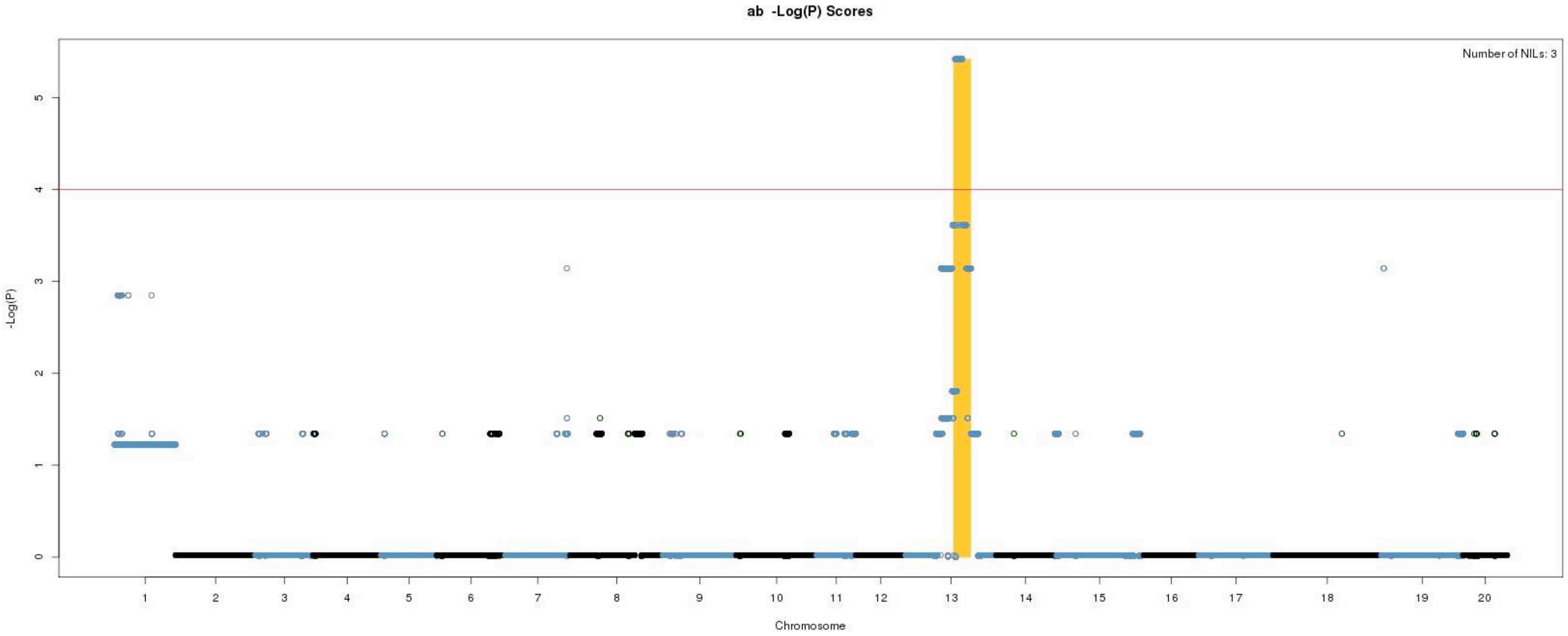
w1	w4	wm	y3**
W1			
White flower	Near-white flower	Magenta flower	Leaves turn rusty yellow with g
Pigmentation	Pigmentation	Pigmentation	Chlorophyll
Glyma.13g072100	Glyma.17g252200	Glyma.13g082300	
Glyma 2.0	Glyma 2.0	Glyma 2.0	
13	17	13	
17312472	40652090	19154278	
17317198	40657097	19159357	
13	17	13	11
17048632	40267171	15543548	2175770
18248678	40705987	21073871	6565408
7.683876	7.683876	7.683876	7.683876

5	5	3	5
1	1	1	3
Clark Harosoy Williams	Clark Harosoy	Clark Harosoy	Clark Harosoy

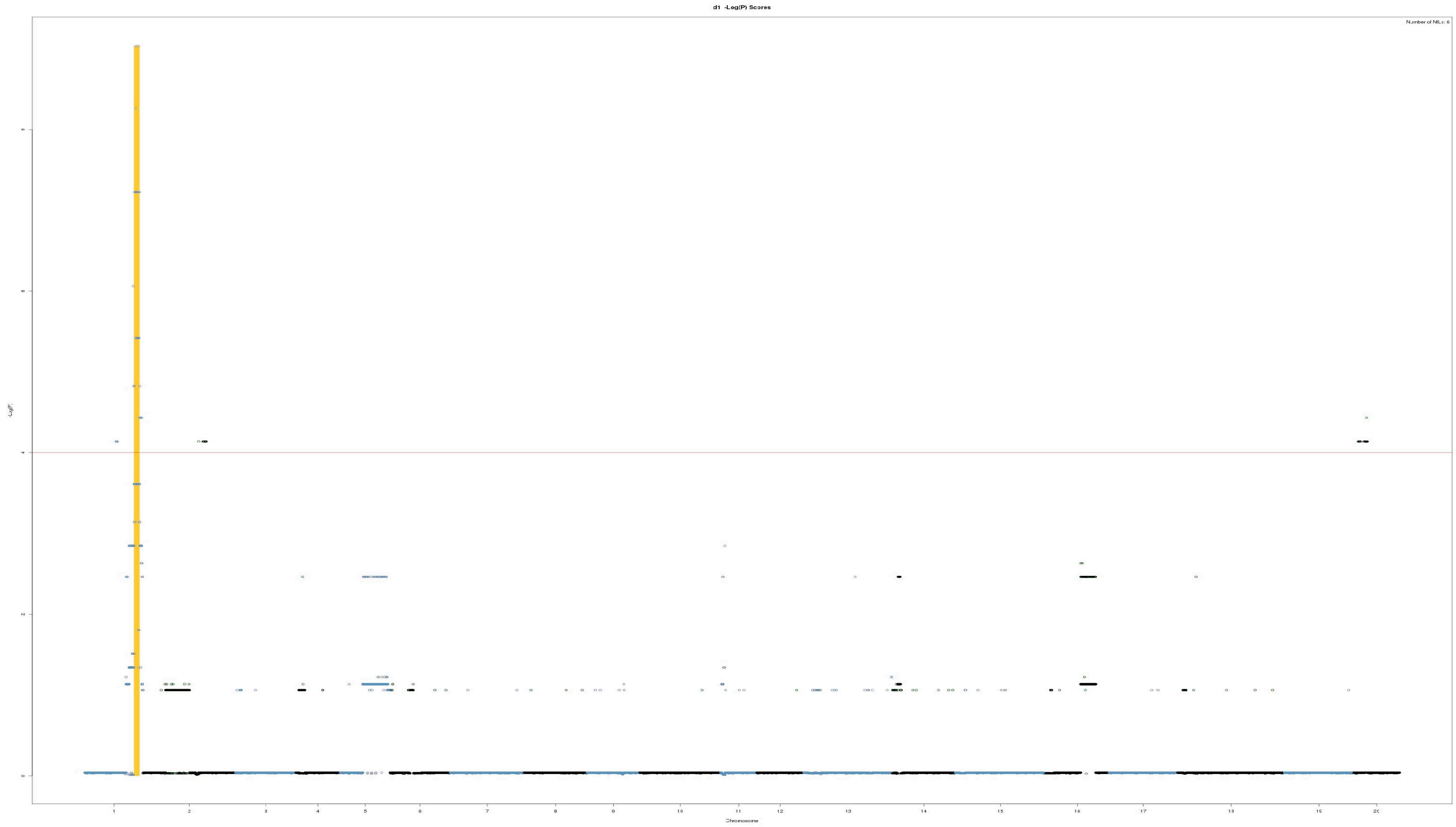
y7/y8**	**y7/y8****	**y9**
New leaves very light green in cool weather with y8	New leaves very light green in cool weather with y7	Yellow-green plant
Chlorophyll	Chlorophyll	Chlorophyll
		Composite2003
		15
		22.5cM
		4135853
		6916577
3	19	15
561263	36161480	1940853
2315408	40236466	7473258
7.683876	7.683876	7.683876
3	3	4
3	3	1
Clark Harosoy	Clark Harosoy	Clark Harosoy

Supplementary Figures 1

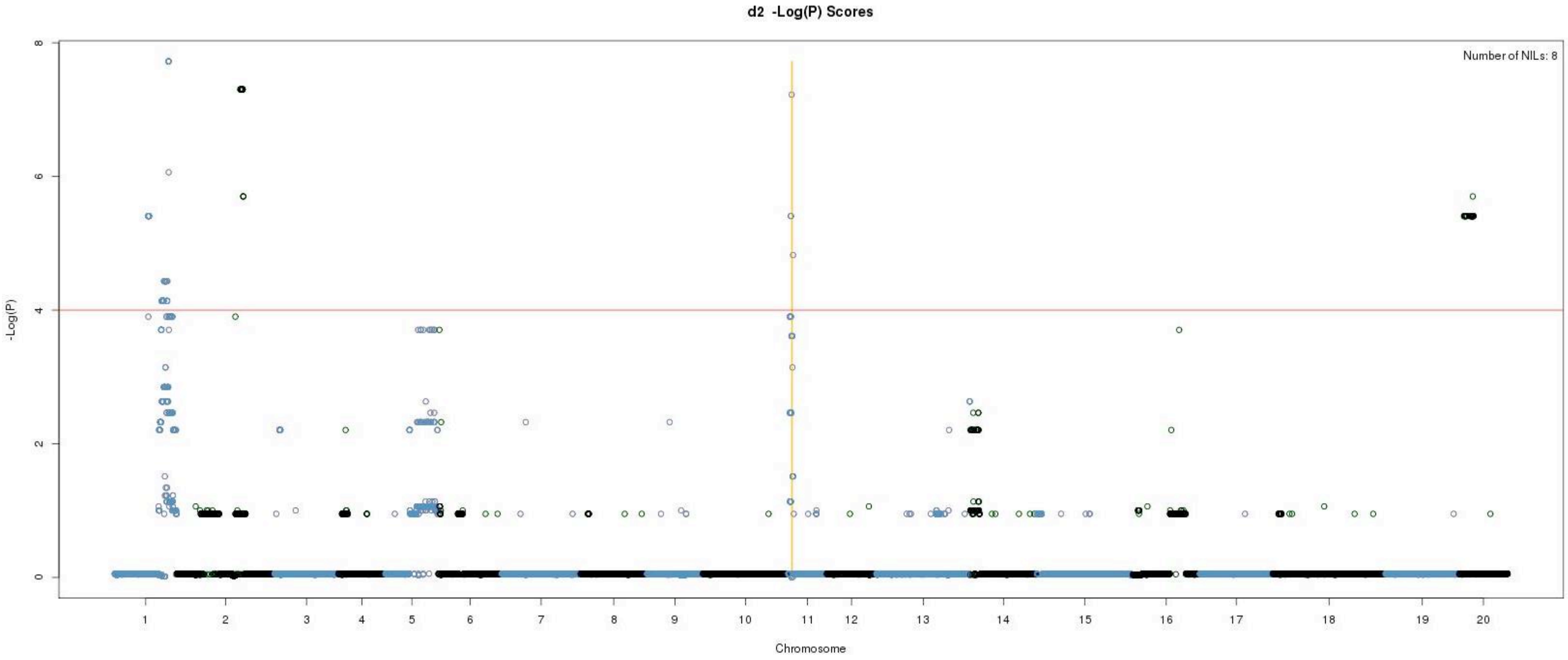
These figures depict –Log(P) values for polymorphic loci in NILs for each trait analyzed in this collection. The red line indicates –Log(P)=4. The gold bars indicate significant introgressions predicted with computational comparative mapping.



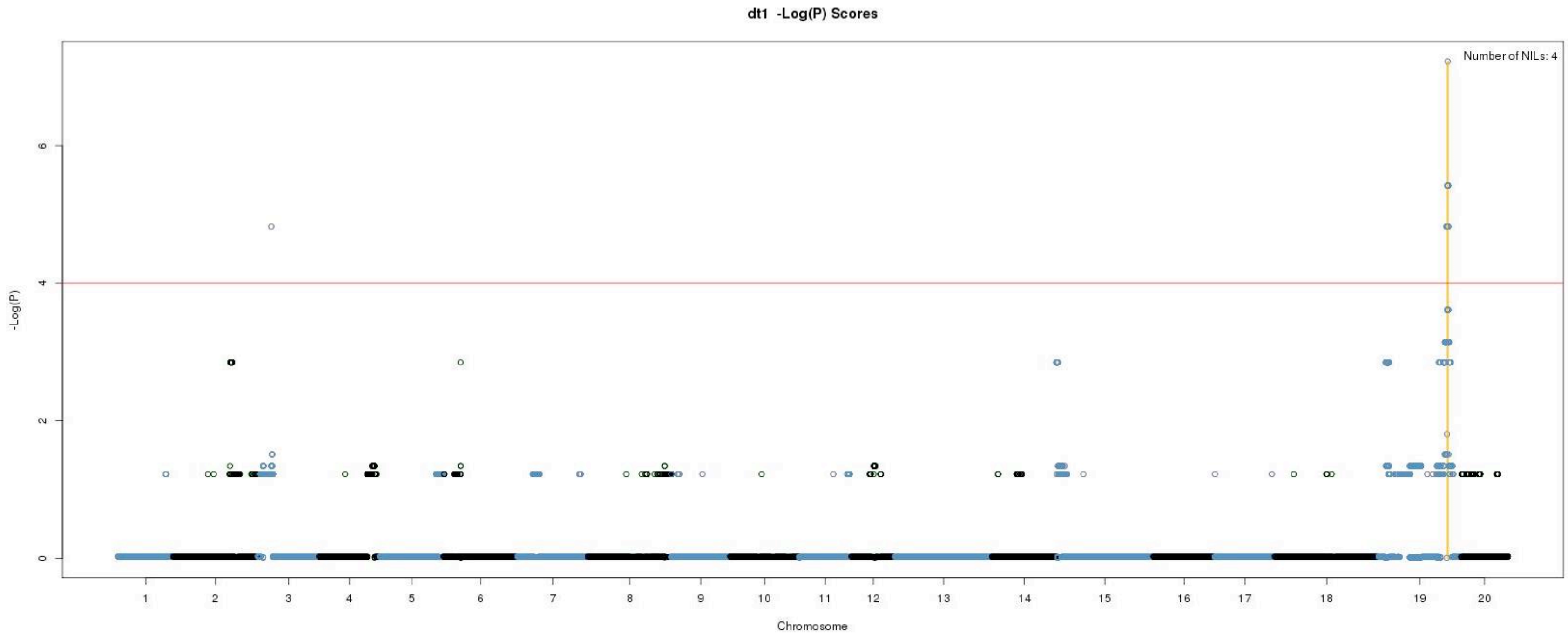
Supplementary Figure 1. 1 -log(P) scores for polymorphic markers in NILs with the trait ab (Delayed leaf abscission). The final interval selected is on chromosome 13.



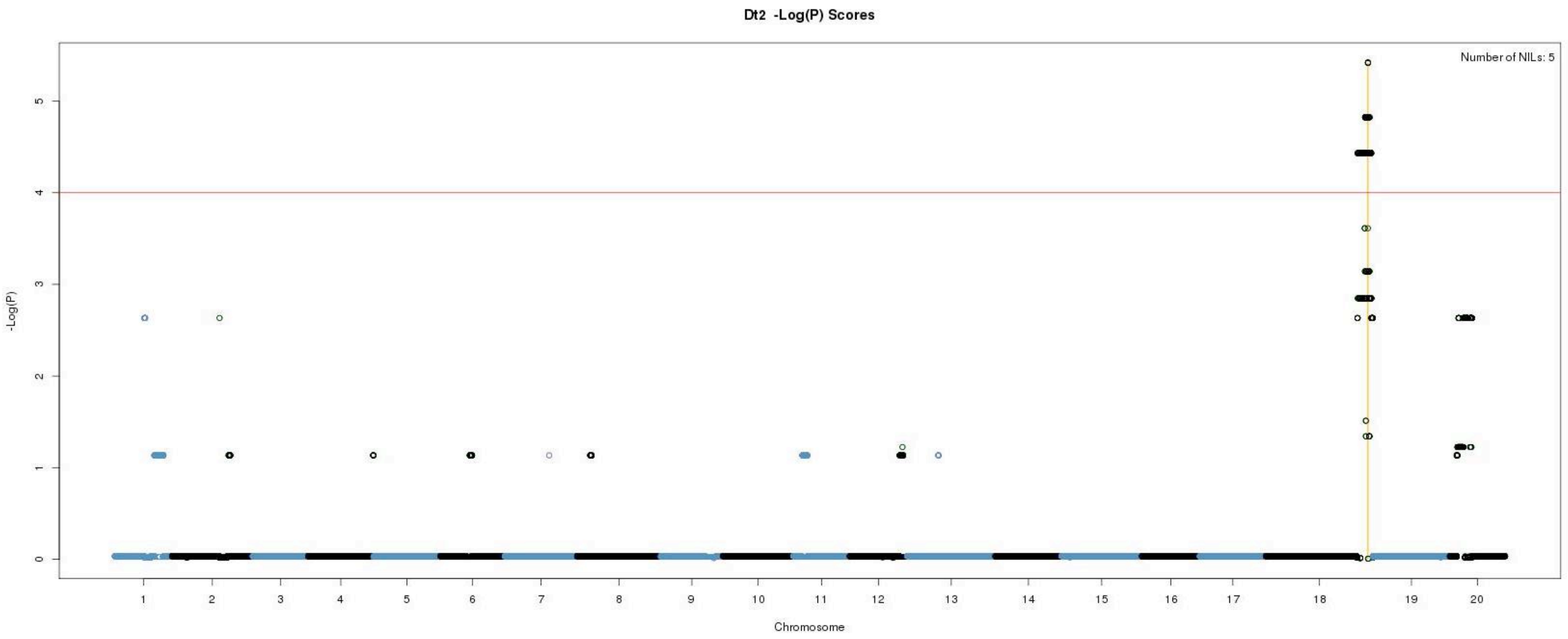
Supplementary Figure 1.2 -log(P) scores for polymorphic markers in NILs with the trait d1 (Nuclear "stay green" chlorophyll presence after senescence). The final interval selected is on chromosome 1.



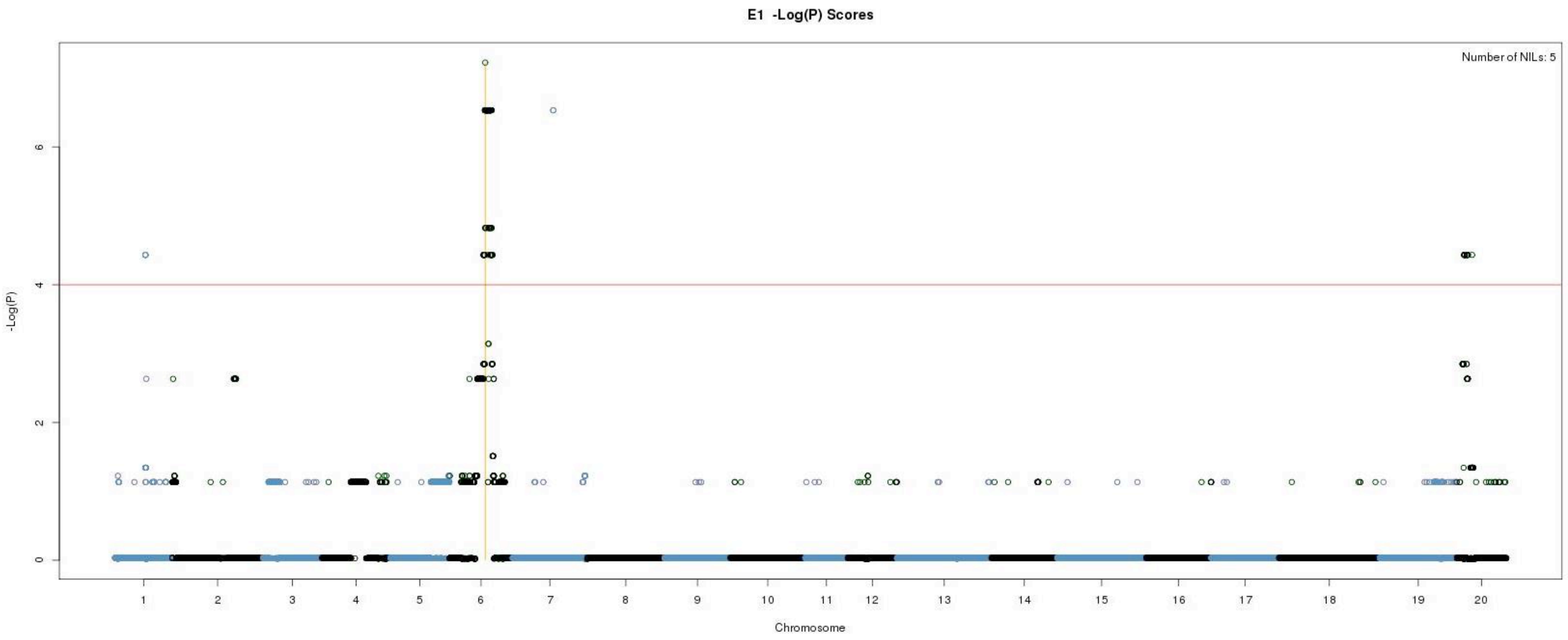
Supplementary Figure 1. 2 -log(P) scores for polymorphic markers in NILs with the trait d2 (Nuclear "stay green" chlorophyll presence after senescence). The final interval selected is on chromosome 11.



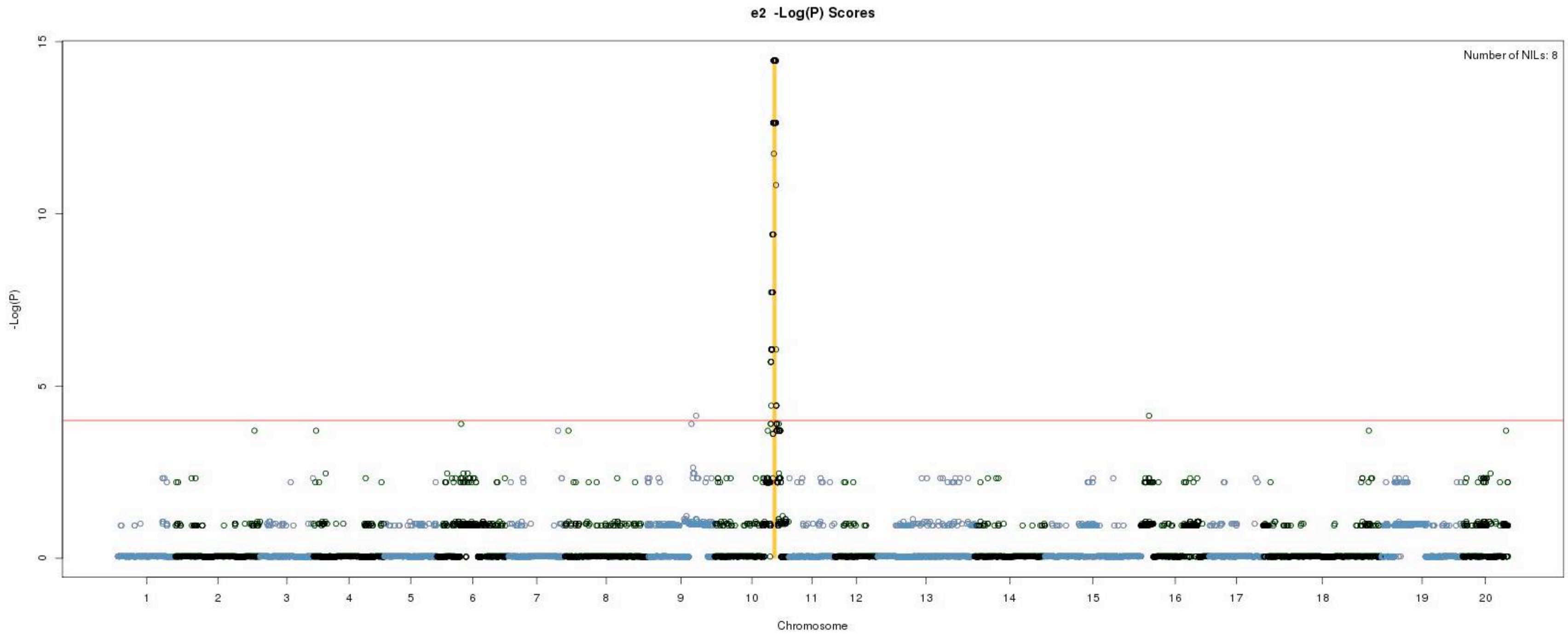
Supplementary Figure 1. 3 -log(P) scores for polymorphic markers in NILs with the trait dt1 (Determinate stem). The final interval selected is on chromosome 19.



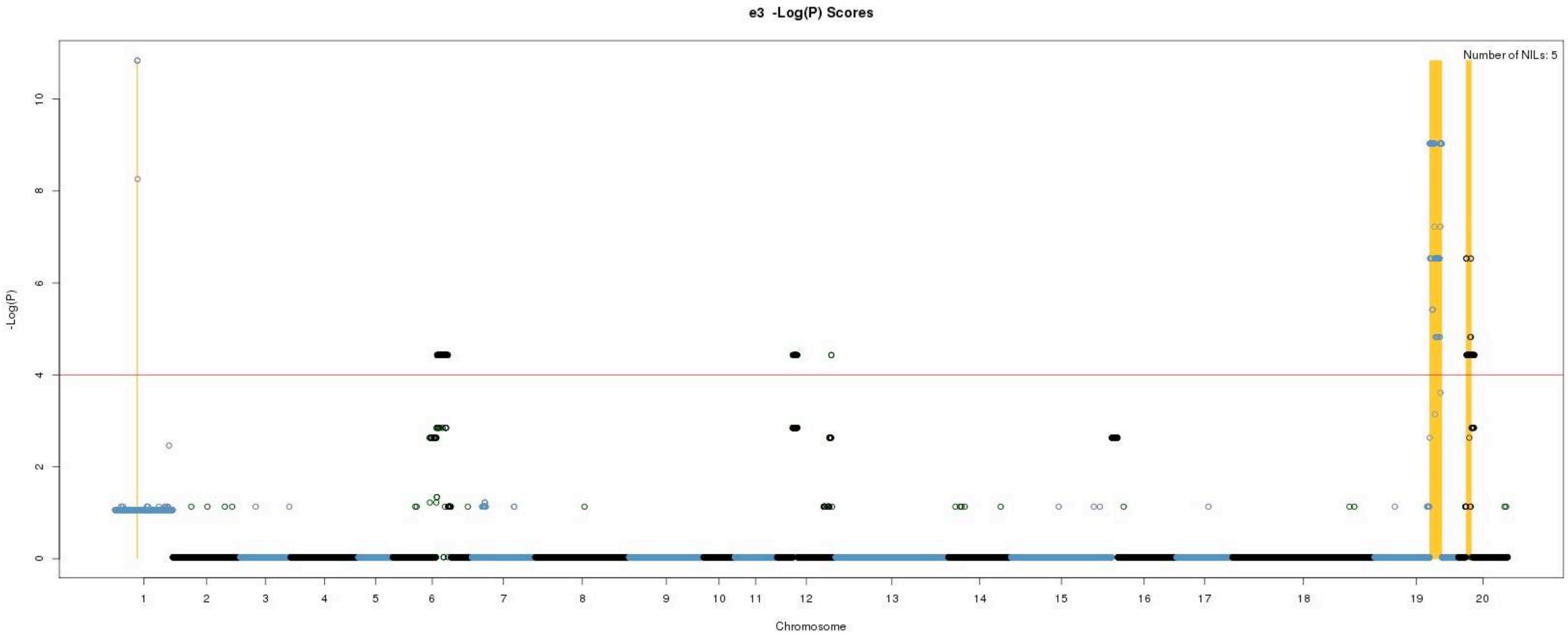
Supplementary Figure 1. 4 - log(P) scores for polymorphic markers in NILs with the trait Dt2 (Semi-determinate stem). The final interval selected is on chromosome 18.



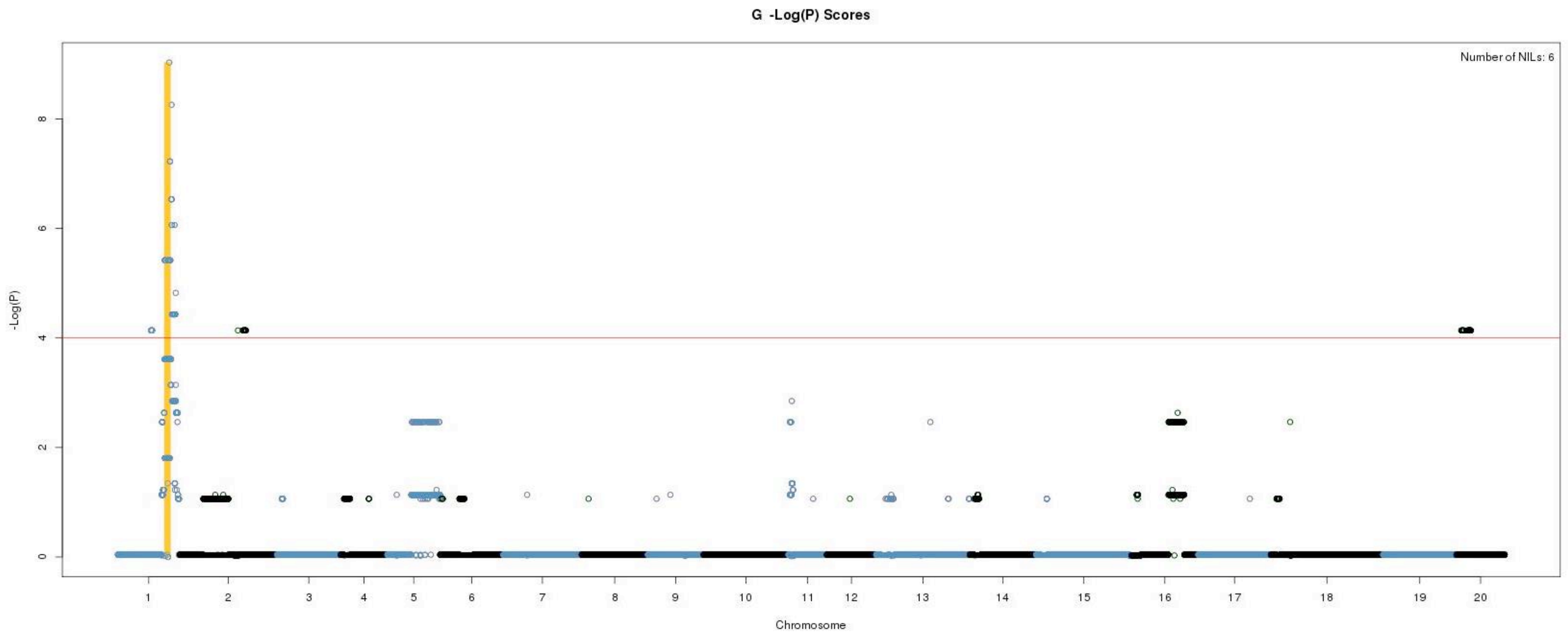
Supplementary Figure 1. 5 -log(P) scores for polymorphic markers in NILs with the trait E1 (Late maturity). The final interval selected is on chromosome 6.



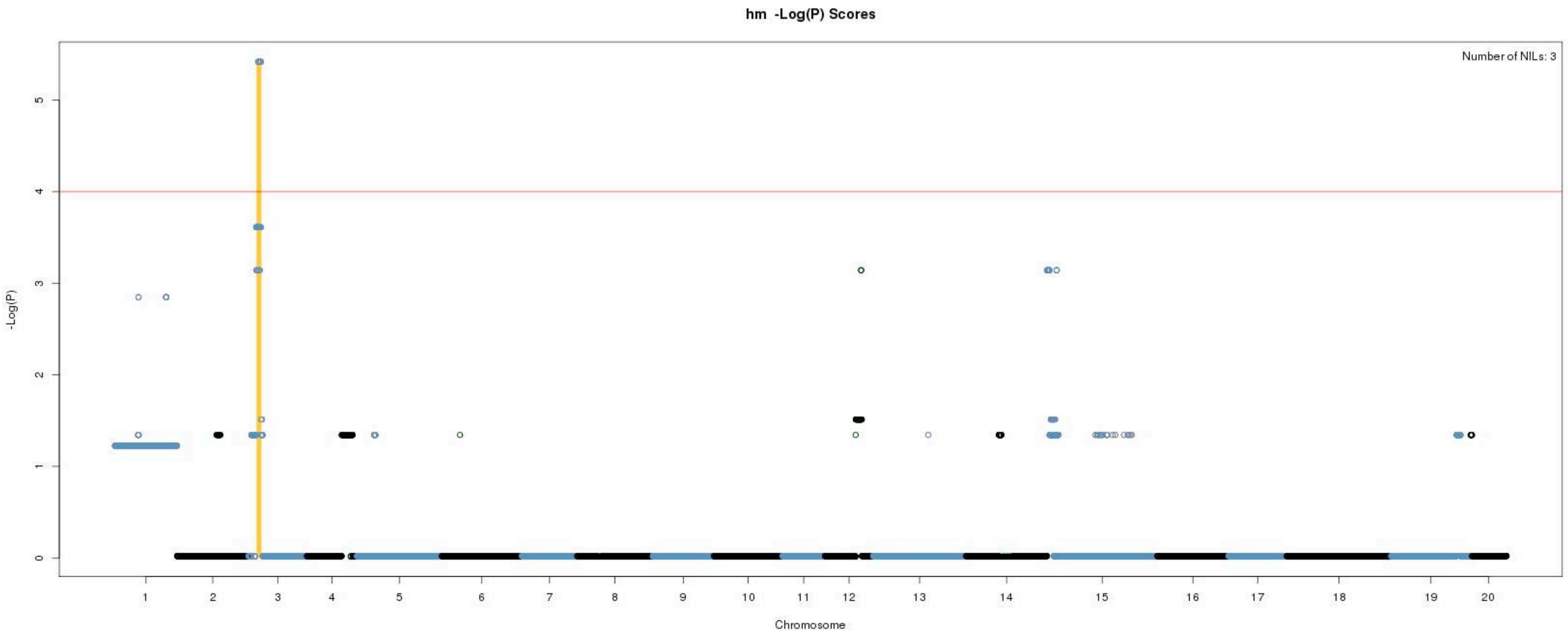
Supplementary Figure 1. 6 - log(P) scores for polymorphic markers in NILs with the trait e2 (Early maturity). The final interval selected is on chromosome 10.



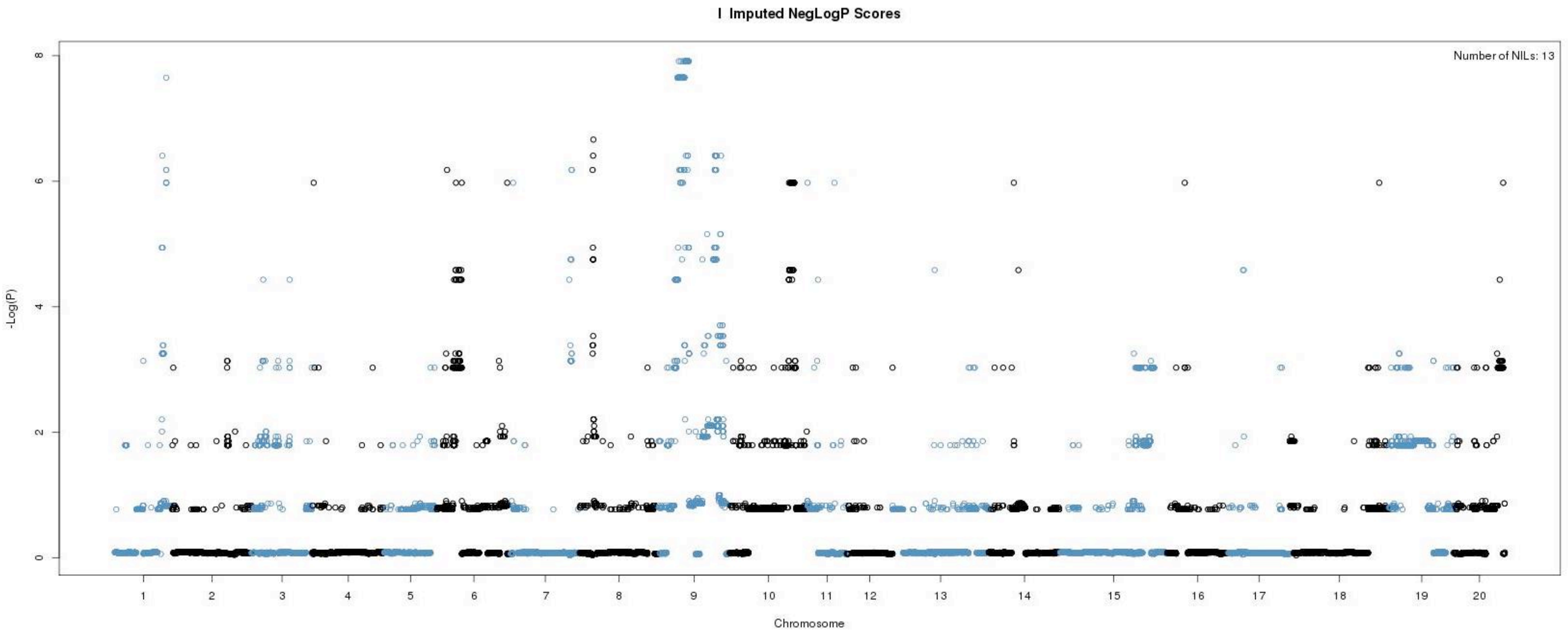
Supplementary Figure 1. 7 - log(P) scores for polymorphic markers in NILs with the trait e3 (Early maturity and low photoperiod sensitivity to incandescent light). The final interval selected is on chromosome 19.



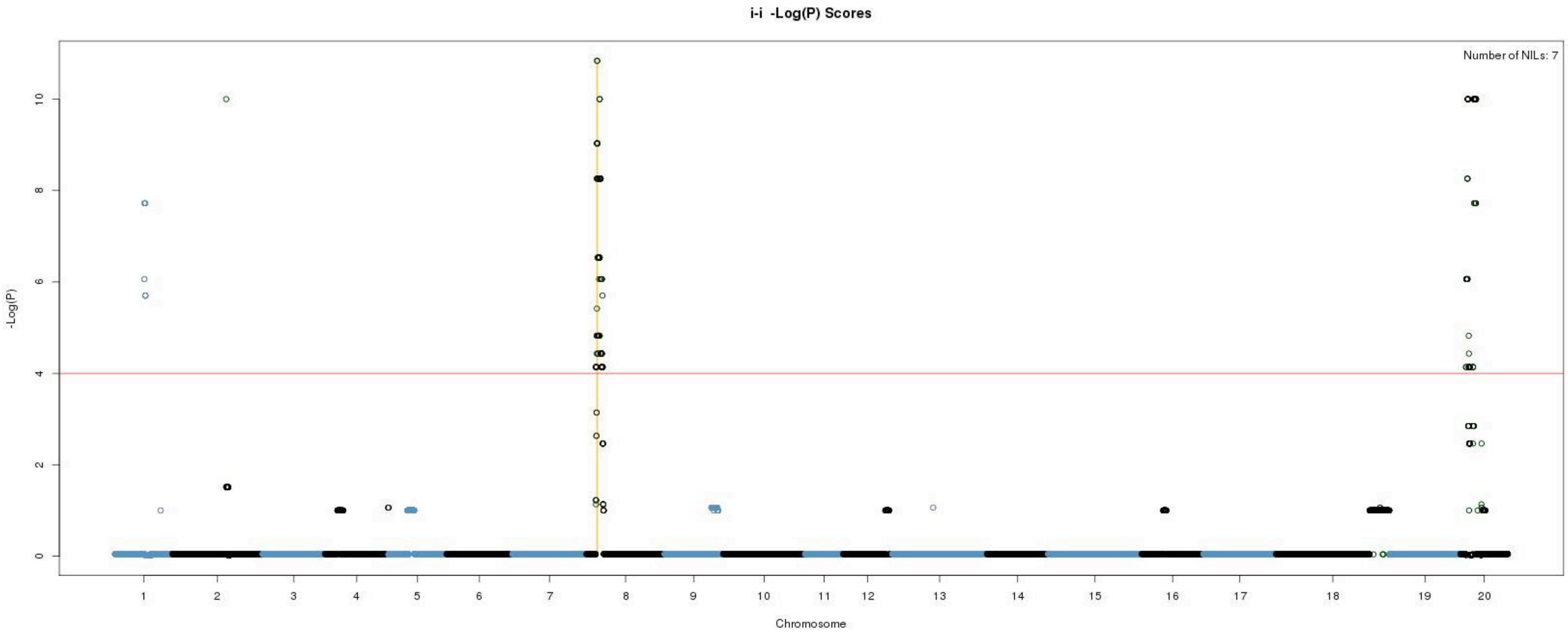
Supplementary Figure 1. 8 - log(P) scores for polymorphic markers in NILs with the trait G (Green seed coat). The final interval selected is on chromosome 1.



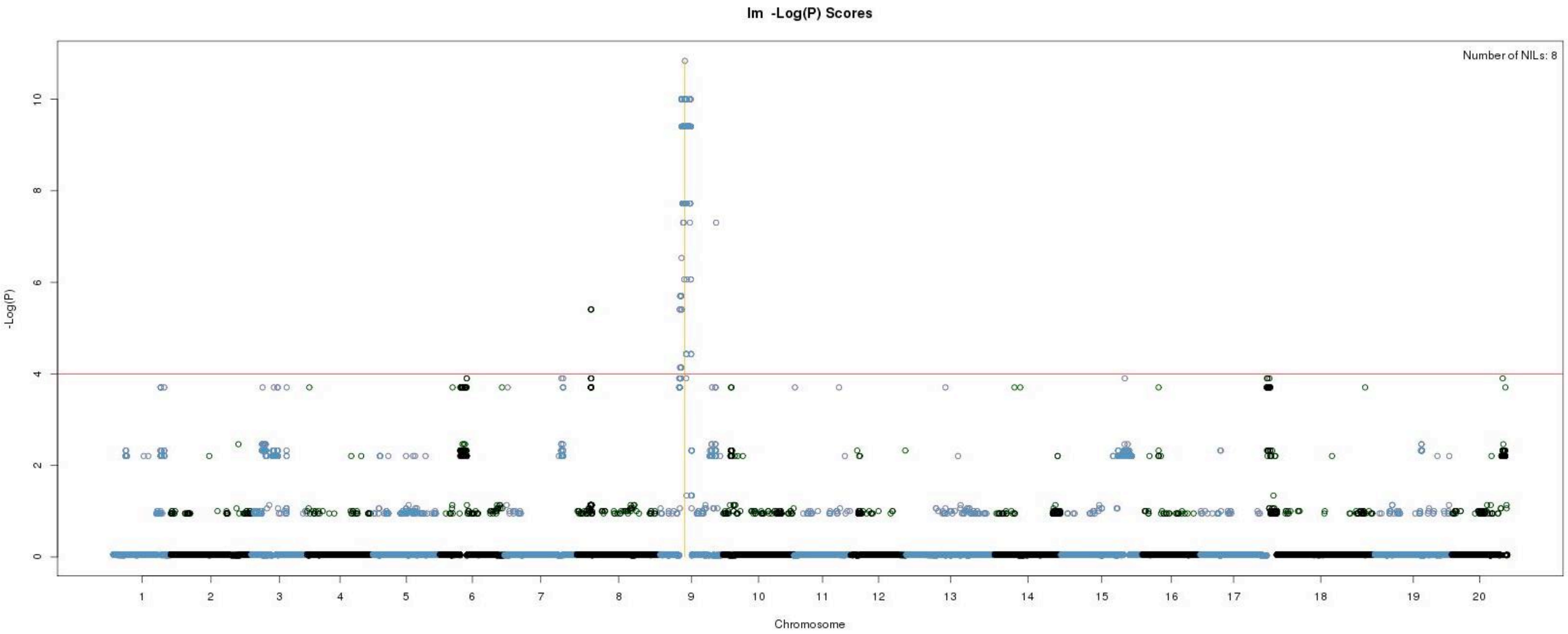
Supplementary Figure 1. 9 - log(P) scores for polymorphic markers in NILs with the trait hm (Metribuzin sensitive). The final interval selected is on chromosome 3.



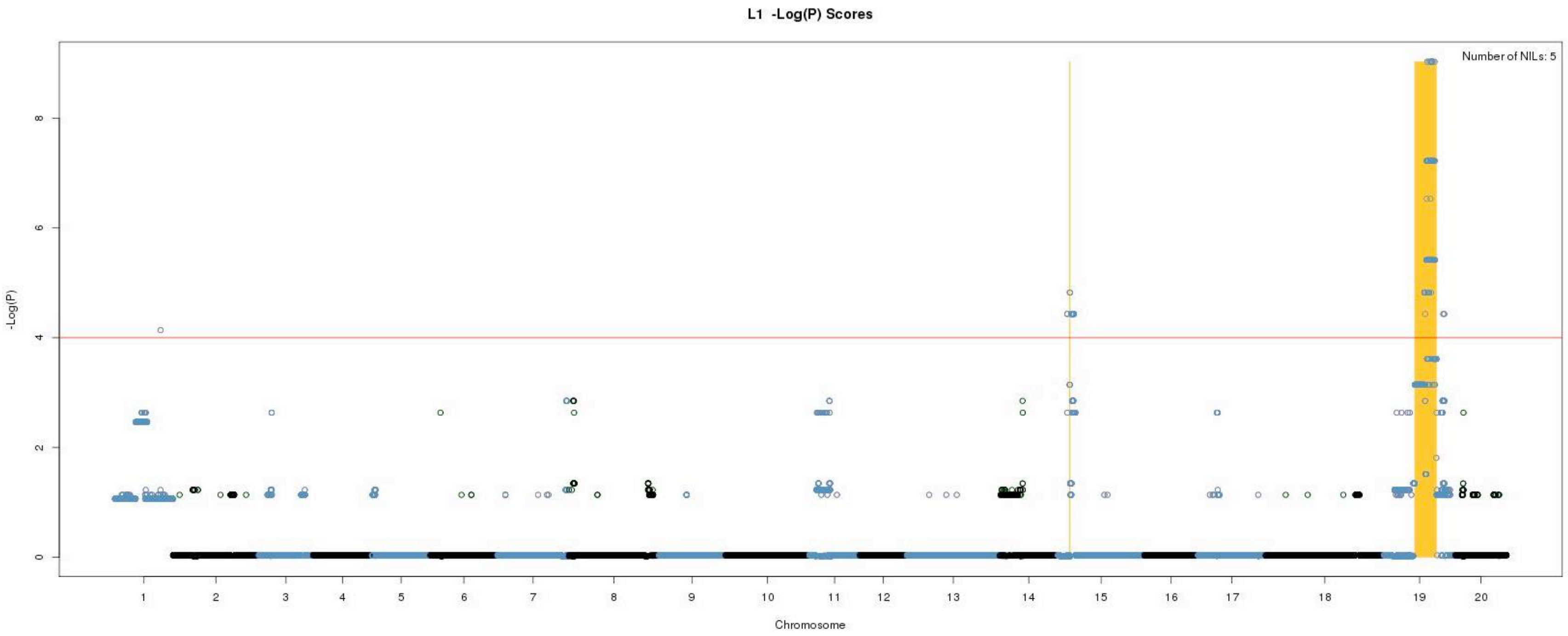
Supplementary Figure 1. 10 - log(P) scores for polymorphic markers in NILs with the trait i (Black seed coat with R T brown with r T imperfect black with R t W1 or buff with R t w1 or r t). The final interval selected is on chromosome 8.



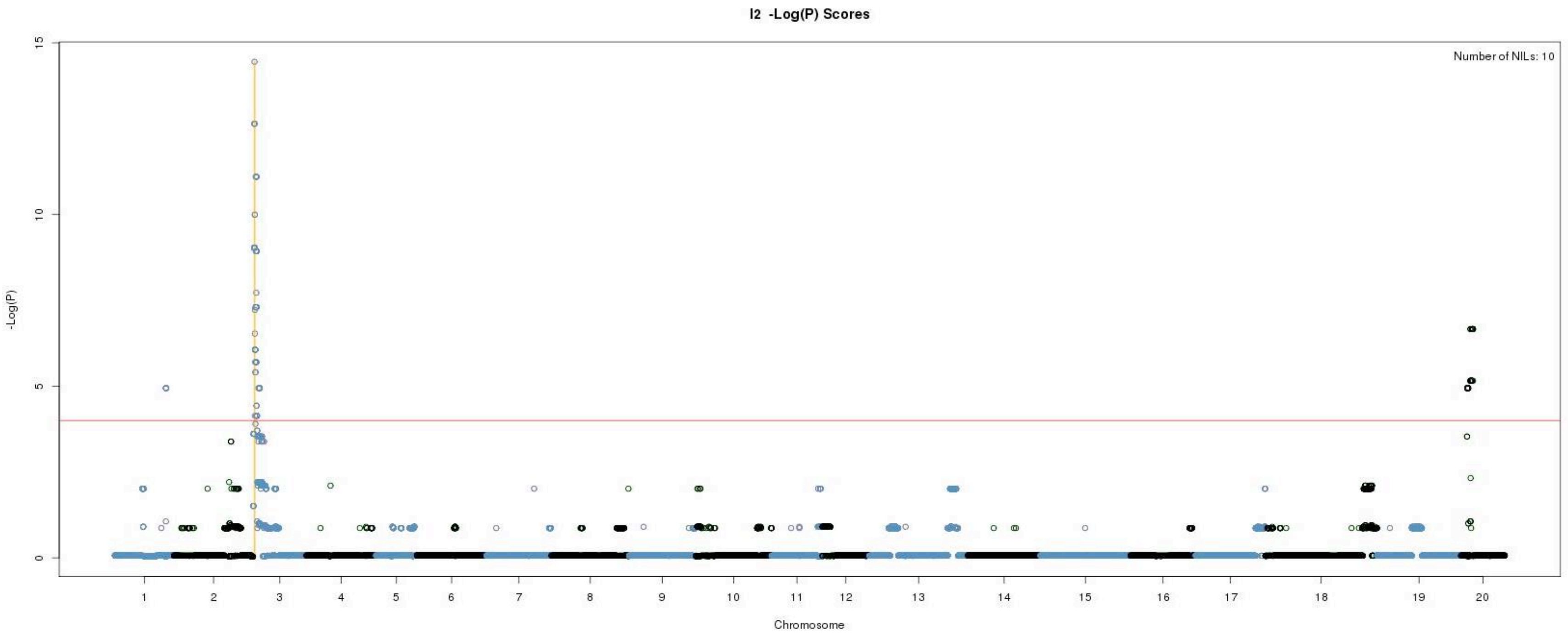
Supplementary Figure 1. 11 - log(P) scores for polymorphic markers in NILs with the trait allele i-i. These were used in combined analysis of I alleles.



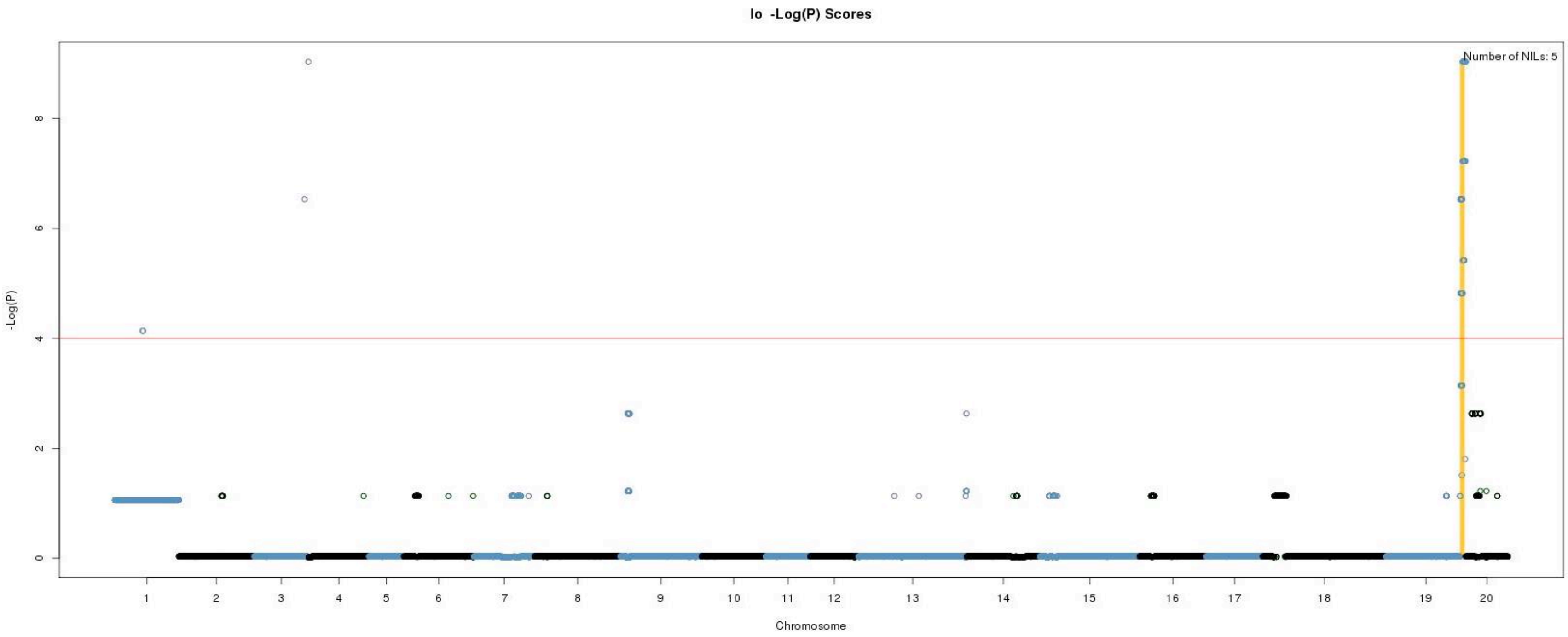
Supplementary Figure 1. 12 - log(P) scores for polymorphic markers in NILs with the trait I_m (non-mottling under SMV). The final interval selected is on chromosome 9.



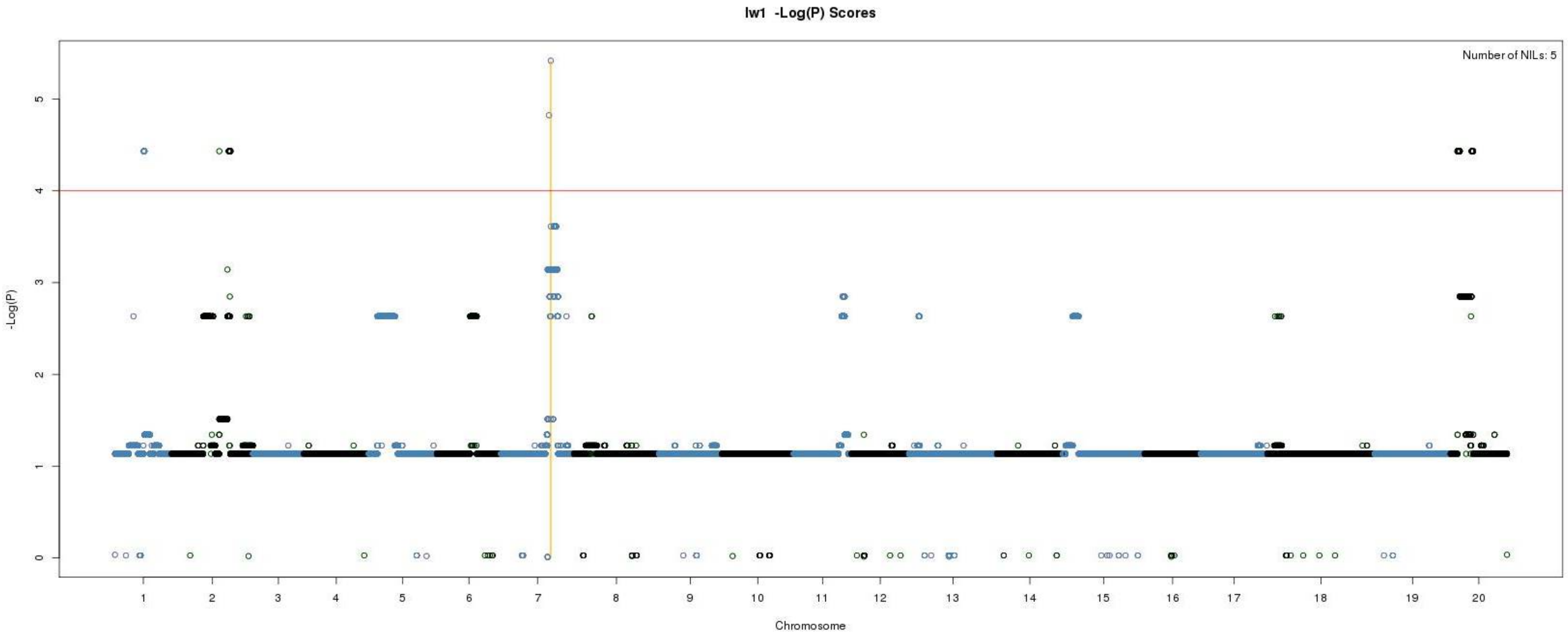
Supplementary Figure 1. 13 - log(P) scores for polymorphic markers in NILs with the trait L1 (Black pod). The final interval selected is on chromosome 19.



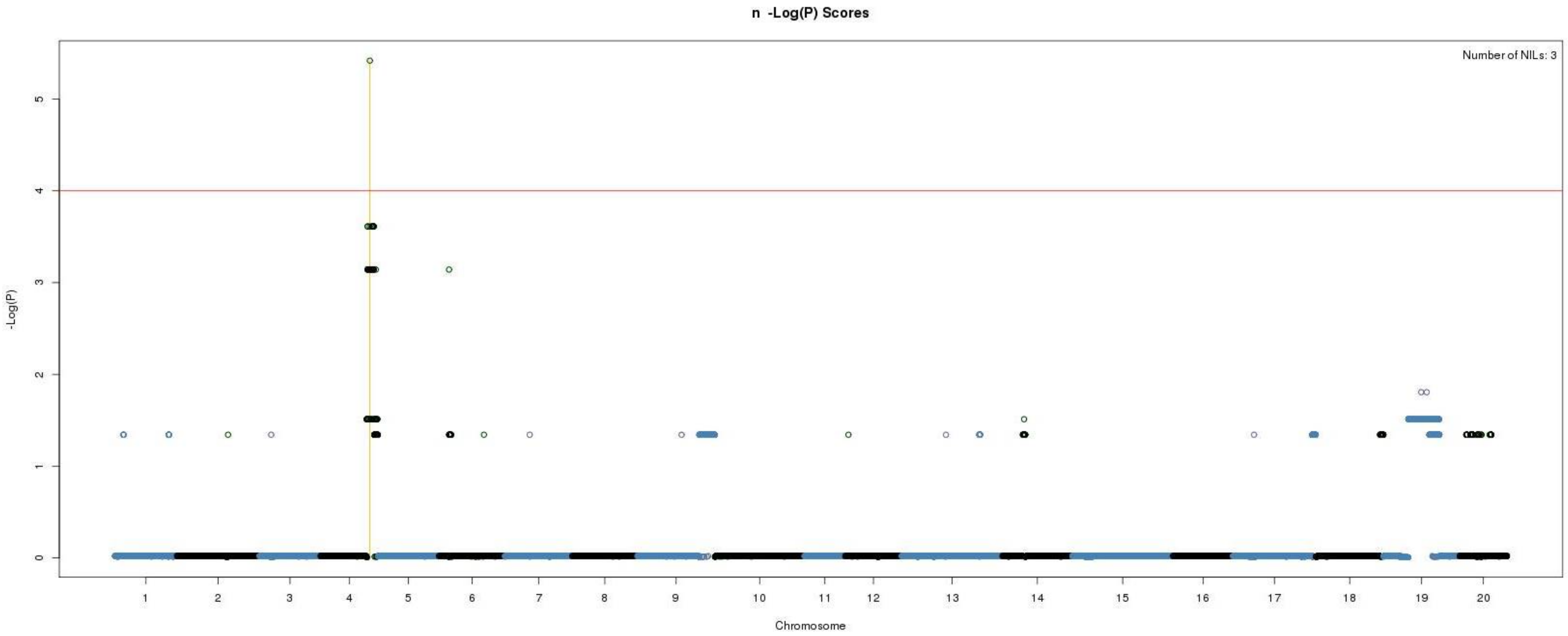
Supplementary Figure 1. 14 - log(P) scores for polymorphic markers in NILs with the trait I2 (Tan pod). The final interval selected is on chromosome 3.



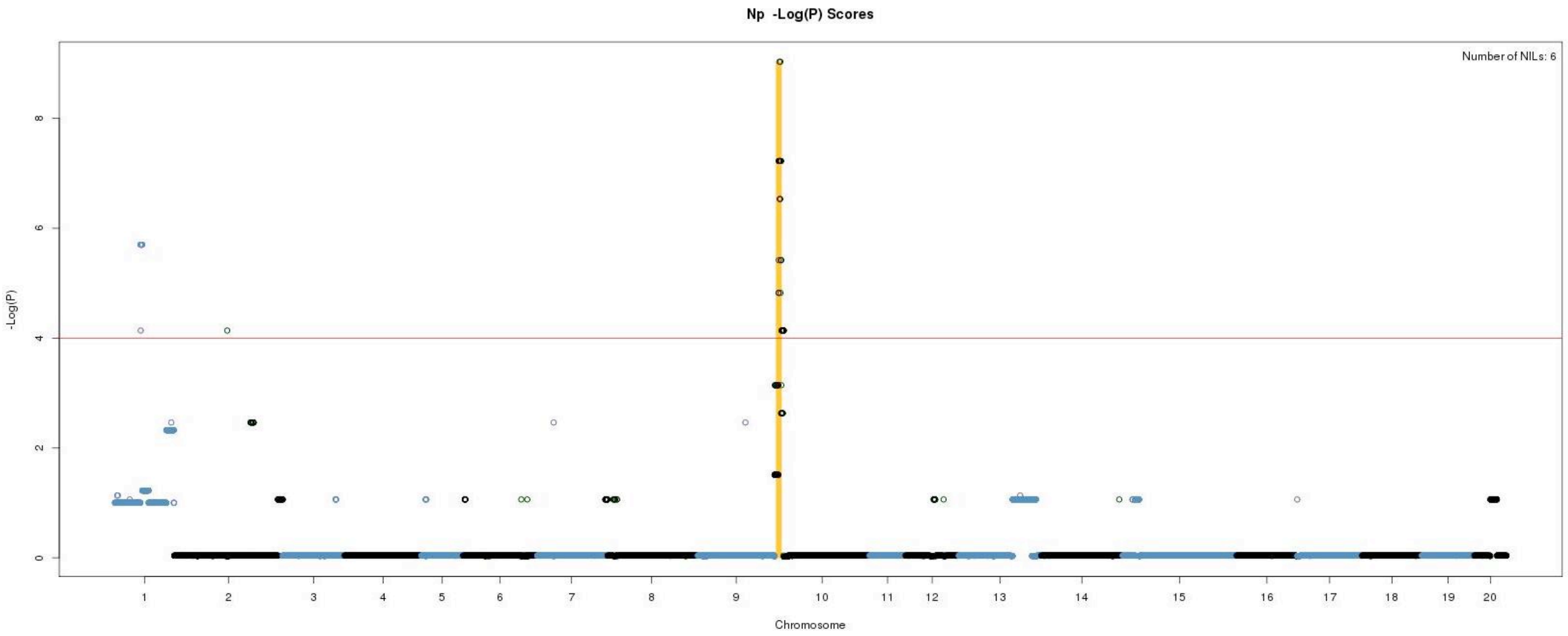
Supplementary Figure 1. 15 - log(P) scores for polymorphic markers in NILs with the trait lo (Oval leaflet few-seeded pod). The final interval selected is on chromosome 19.



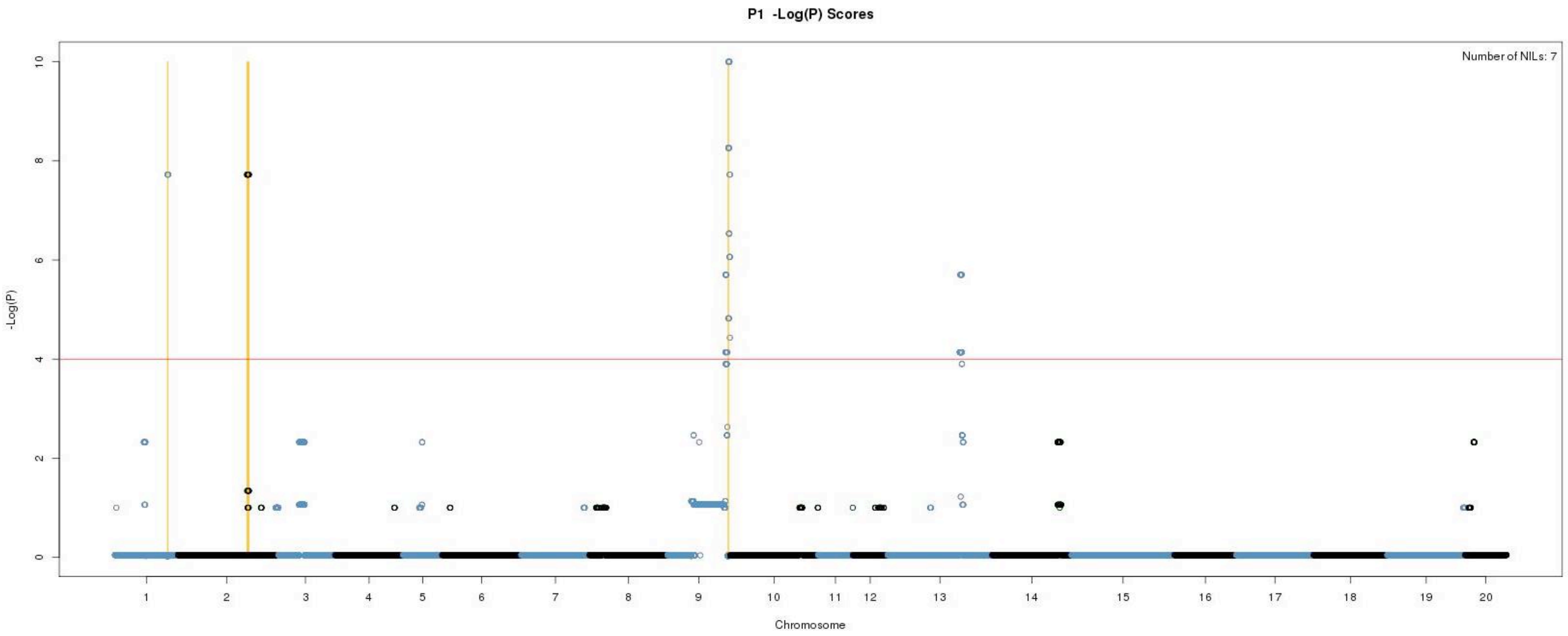
Supplementary Figure 1. 16 - log(P) scores for polymorphic markers in NILs with the trait lw1 (Wavy leaf (Requires lw2 no effect with T or individually)). The final interval selected is on chromosome 7.



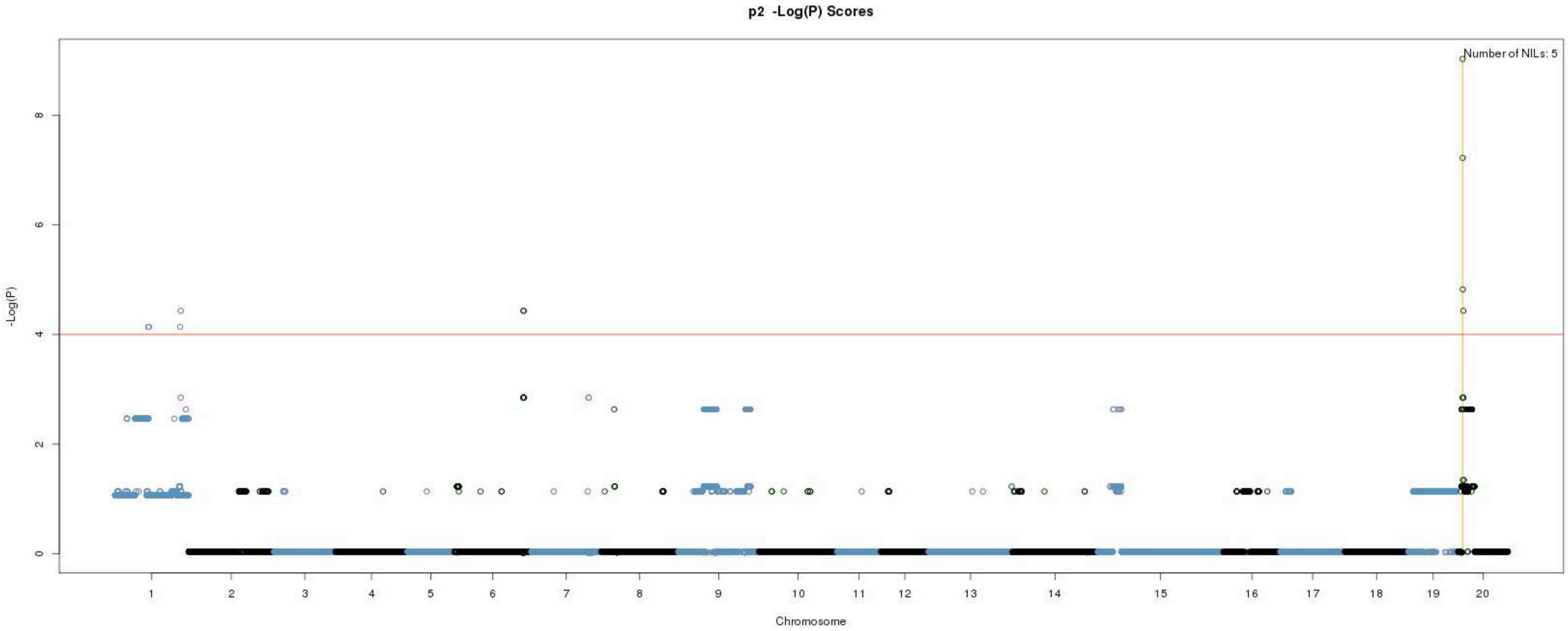
Supplementary Figure 1. 17 - log(P) scores for polymorphic markers in NILs with the trait n (Abnormal hilum abscission). The final interval selected is on chromosome 4.



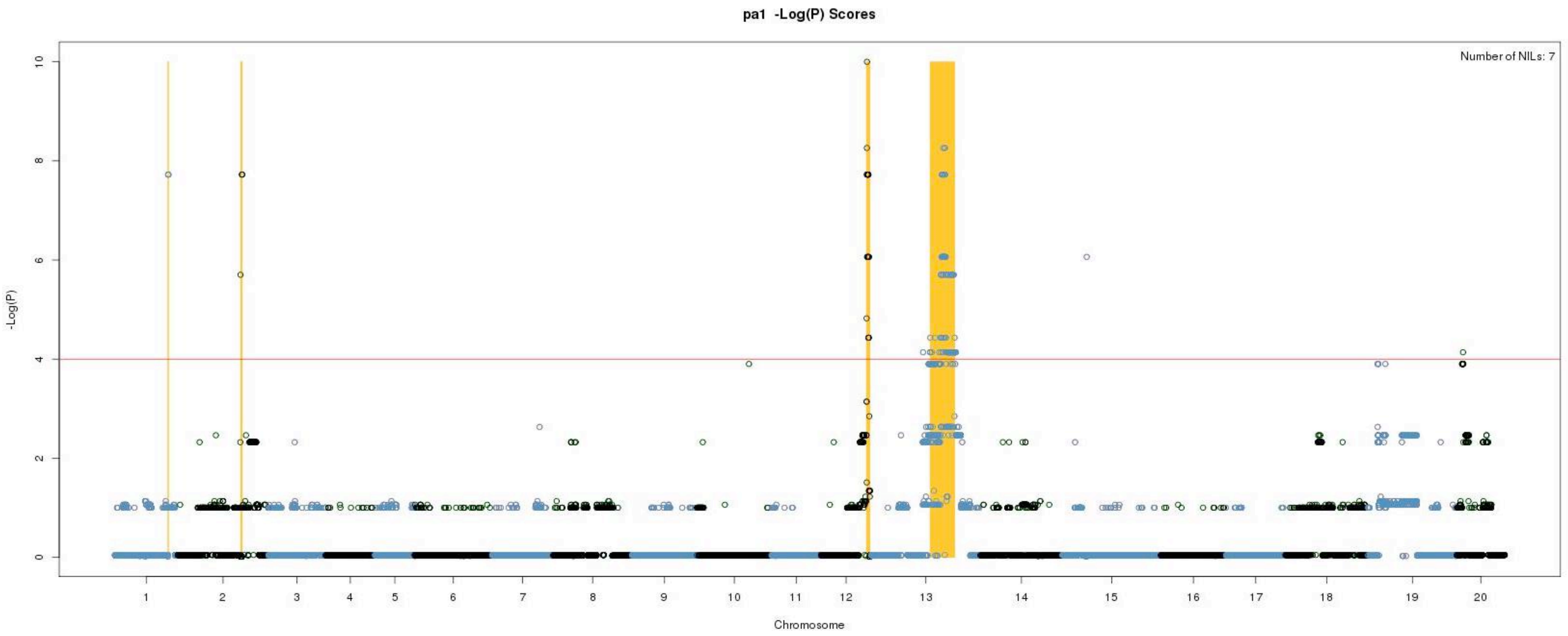
Supplementary Figure 1. 18 - log(P) scores for polymorphic markers in NILs with the trait Np (Phosphorous tolerant). The final interval selected is on chromosome 10.



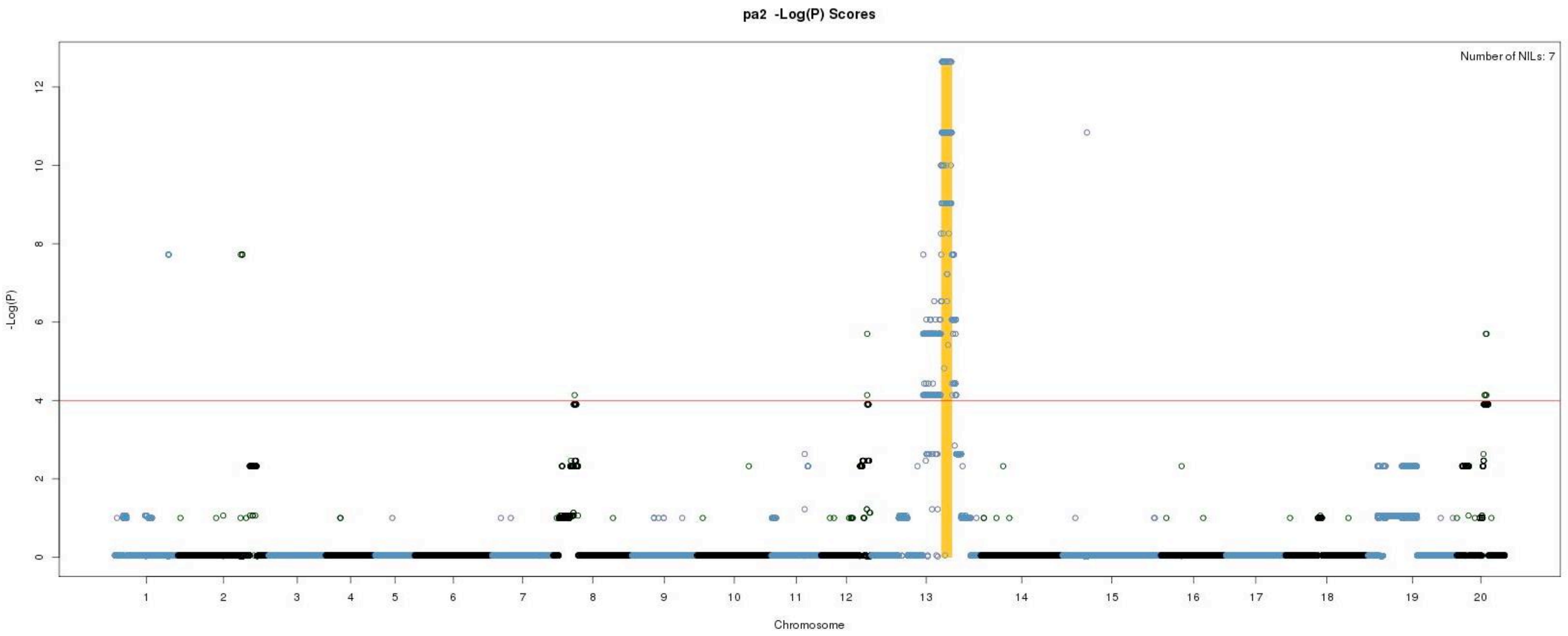
Supplementary Figure 1. 19 - log(P) scores for polymorphic markers in NILs with the trait P1 (Glabrous (Pubescence density)). The final interval selected is on chromosome 9.



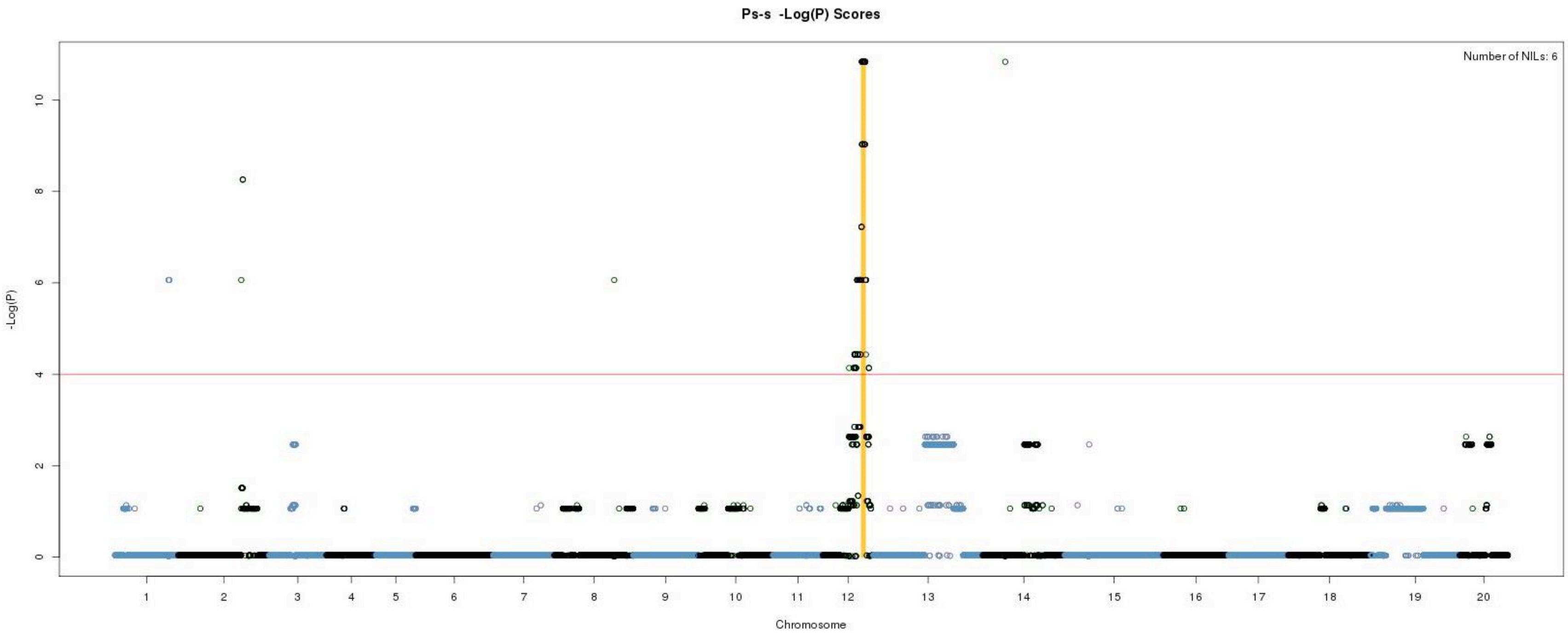
Supplementary Figure 1. 20 - log(P) scores for polymorphic markers in NILs with the trait p2 (Puberulent (Pubescence Density) dwarf seed coat cracks partly male sterile). The final interval selected is on chromosome 20.



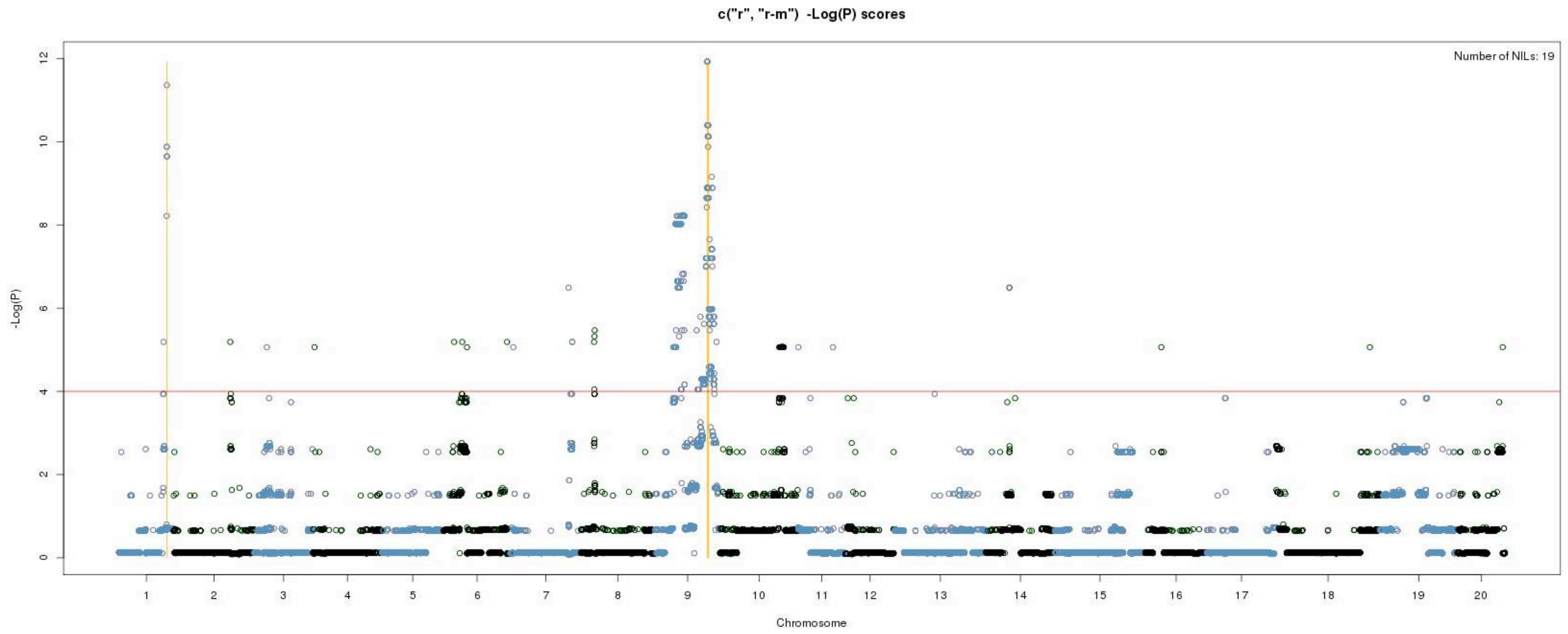
Supplementary Figure 1. 21 - log(P) scores for polymorphic markers in NILs with the trait pa1 (Semi-appressed pubescence (upper leaf surface)). The final interval selected is on chromosome 12.



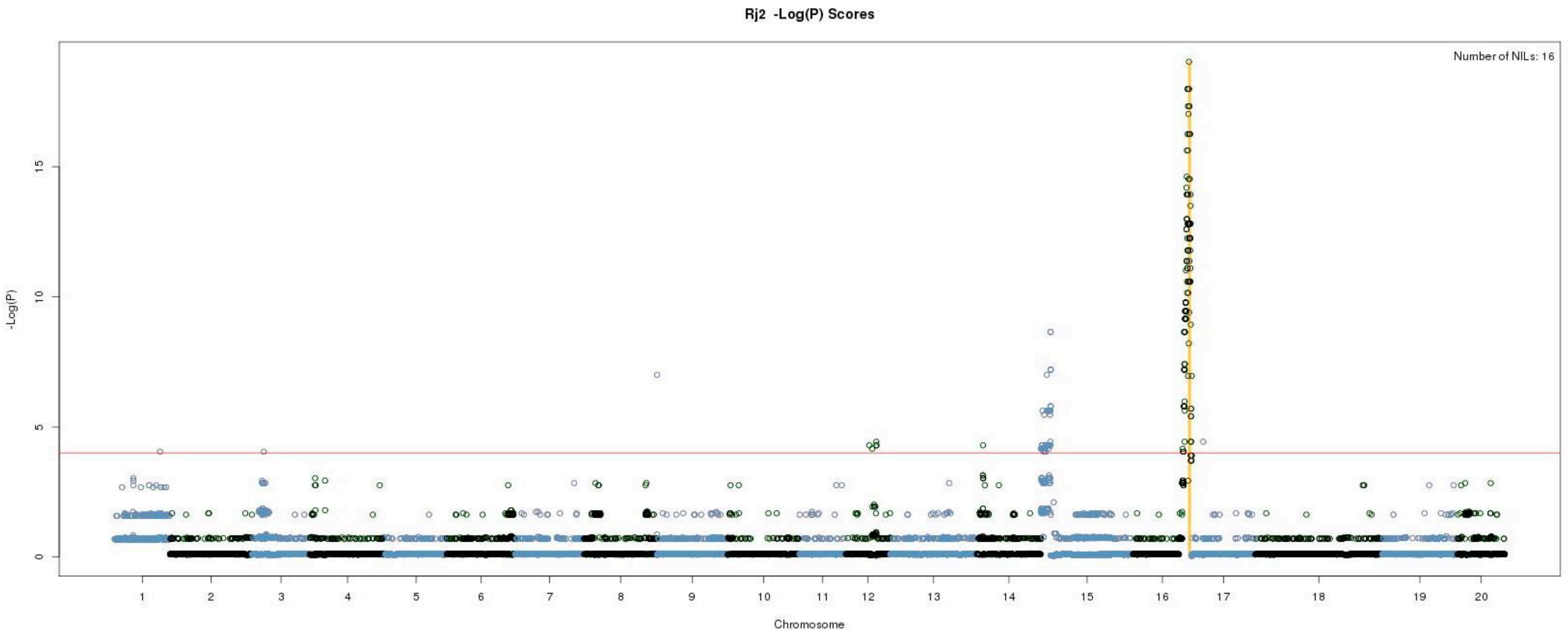
Supplementary Figure 1. 22 - log(P) scores for polymorphic markers in NILs with the trait pa2 (Appressed pubescence with pa1). The final interval selected is on chromosome 13.



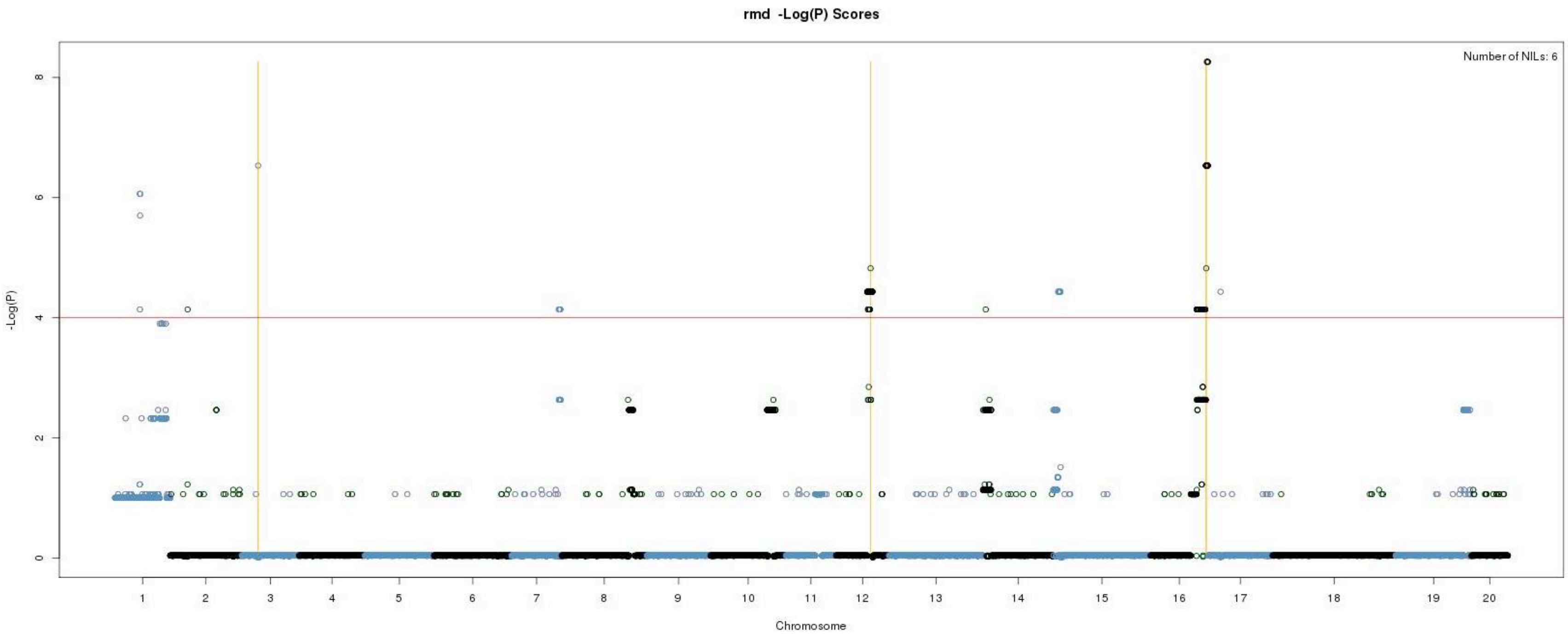
Supplementary Figure 1. 23 - log(P) scores for polymorphic markers in NILs with the trait Ps/Ps-s (Sparse pubescence). The final interval selected is on chromosome 12.



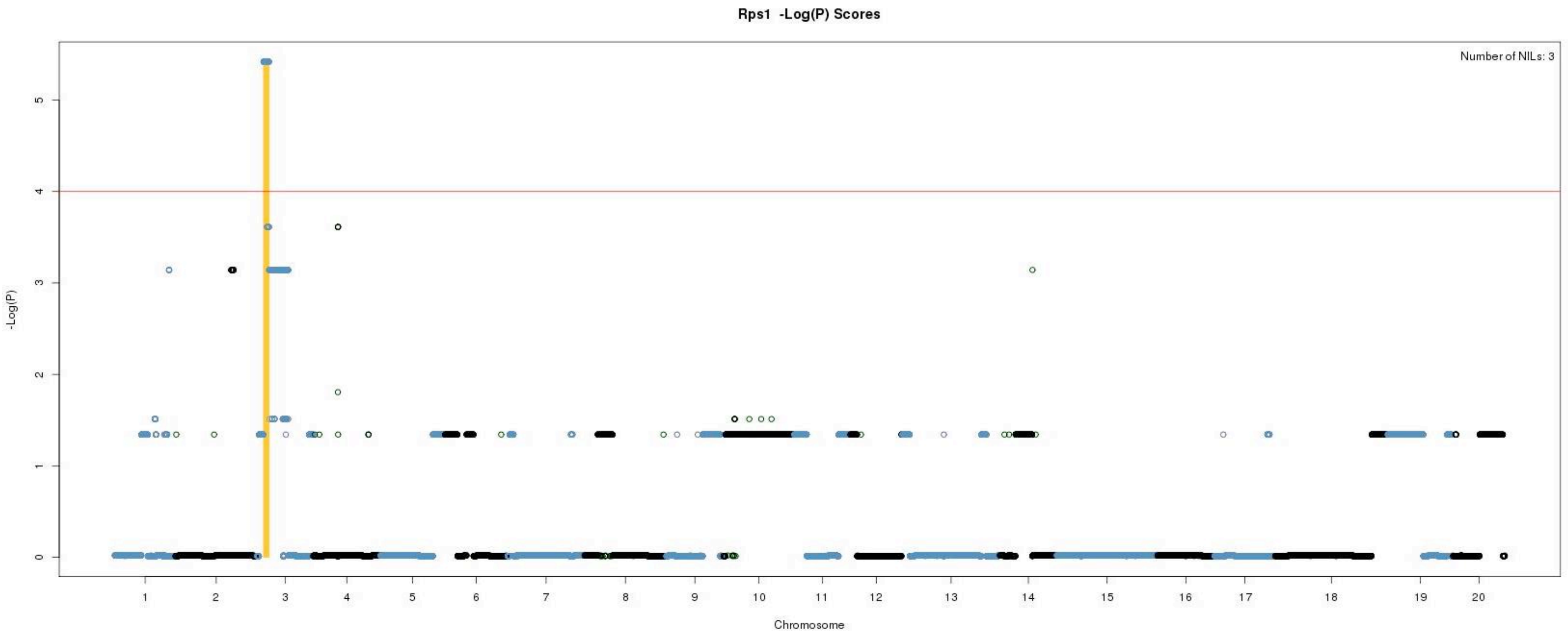
Supplementary Figure 1. 24 -log(P) scores for polymorphic markers in NILs with the trait R (Black seed pigment with T imperfect black with t W1 or buff with t w1). The final interval selected is on chromosome 9.



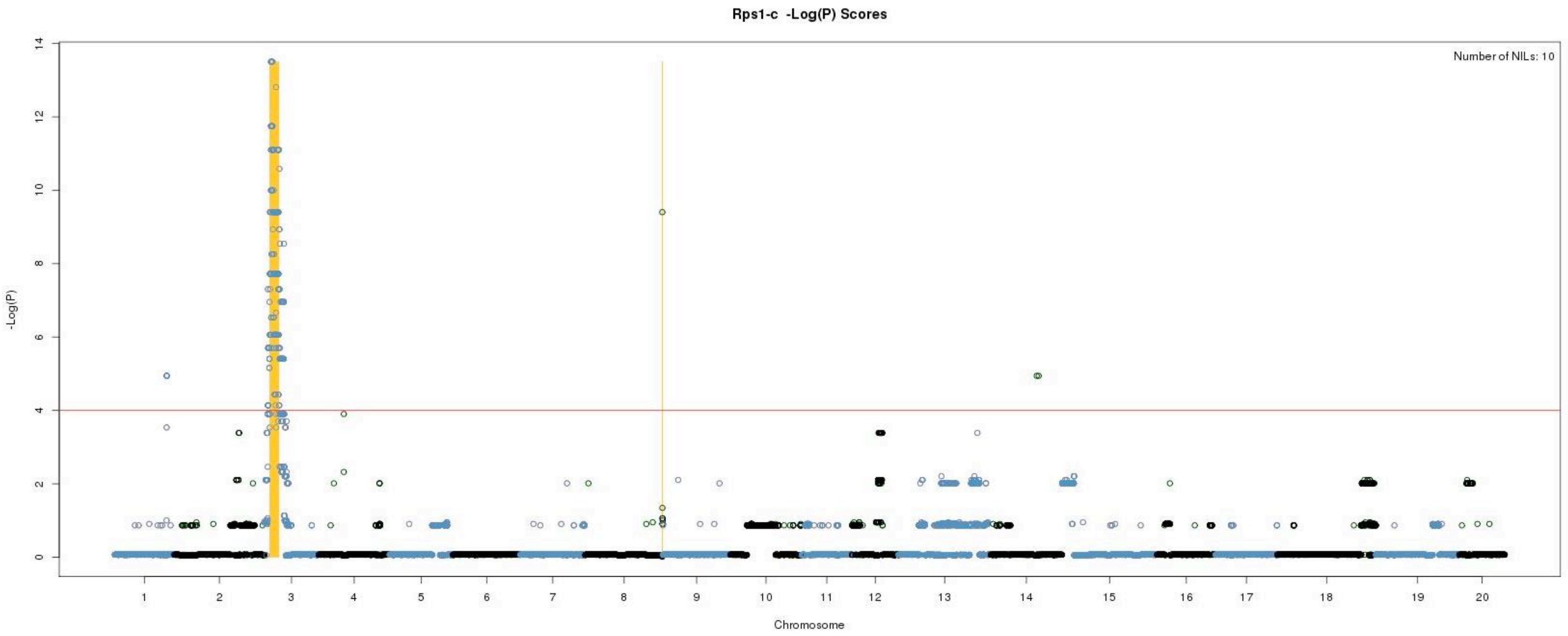
Supplementary Figure 1. 25 - log(P) scores for polymorphic markers in NILs with the trait Rj2 (Ineffective nodulation with Rhizobium strains b7 b14 and b122.). The final interval selected is on chromosome 16.



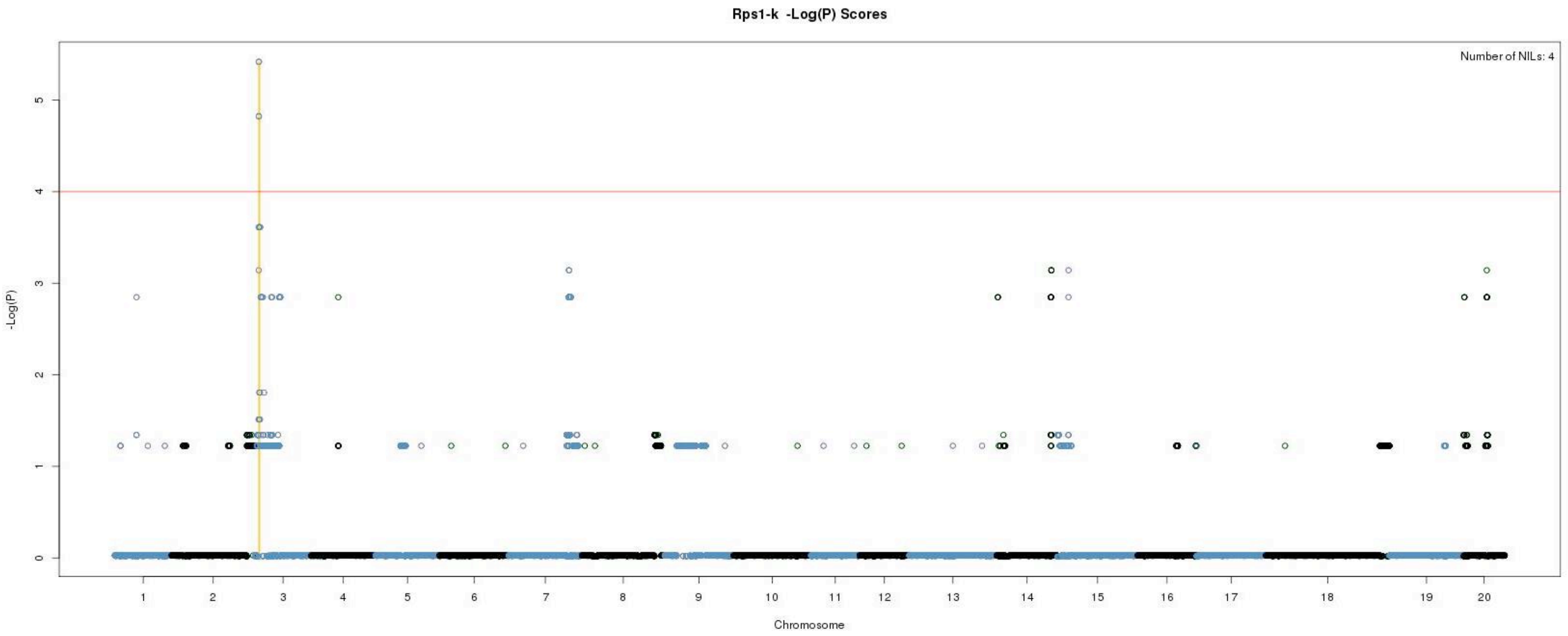
Supplementary Figure 1. 26 - log(P) scores for polymorphic markers in NILs with the trait rmd (Susceptible to powdery mildew). The final interval selected is on chromosome 16.



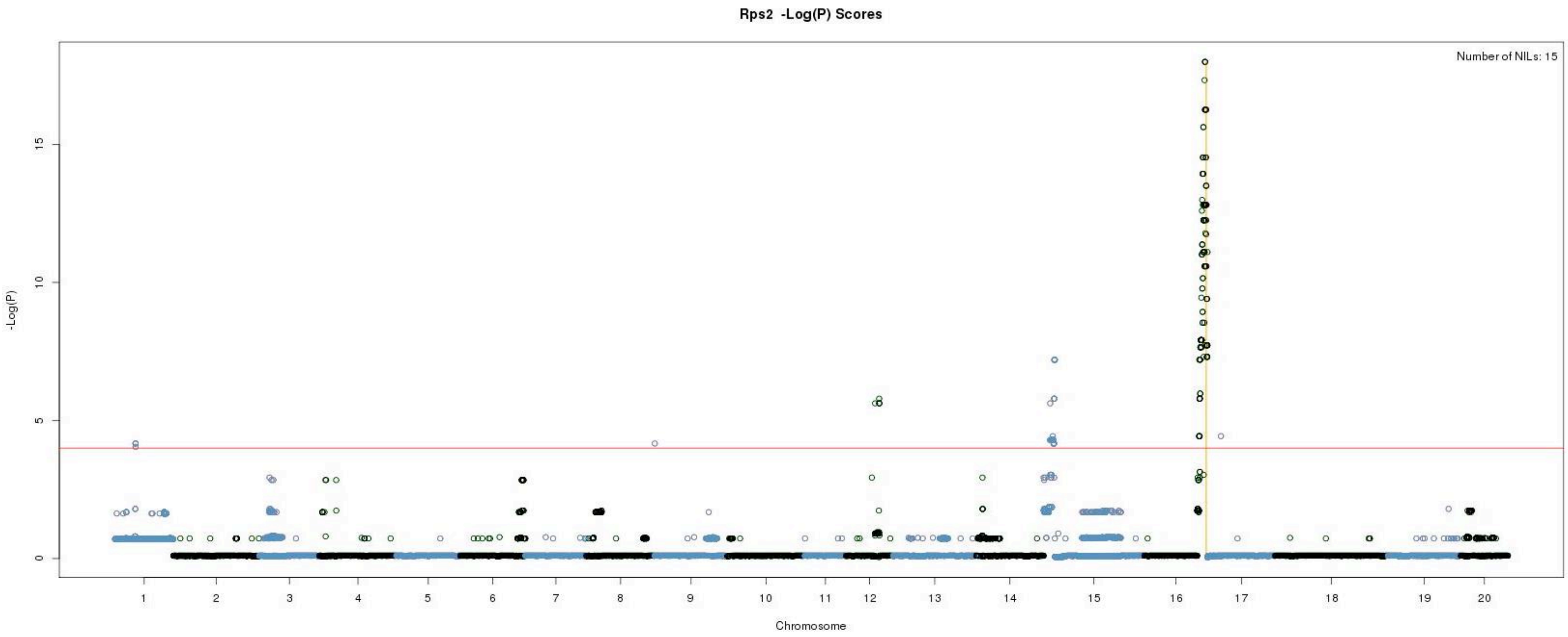
Supplementary Figure 1. 27 - log(P) scores for polymorphic markers in NILs with the trait Rps1 (Resistant to Phytophthora rot races 1 2 10 13 16.). The final interval selected is on chromosome 3.



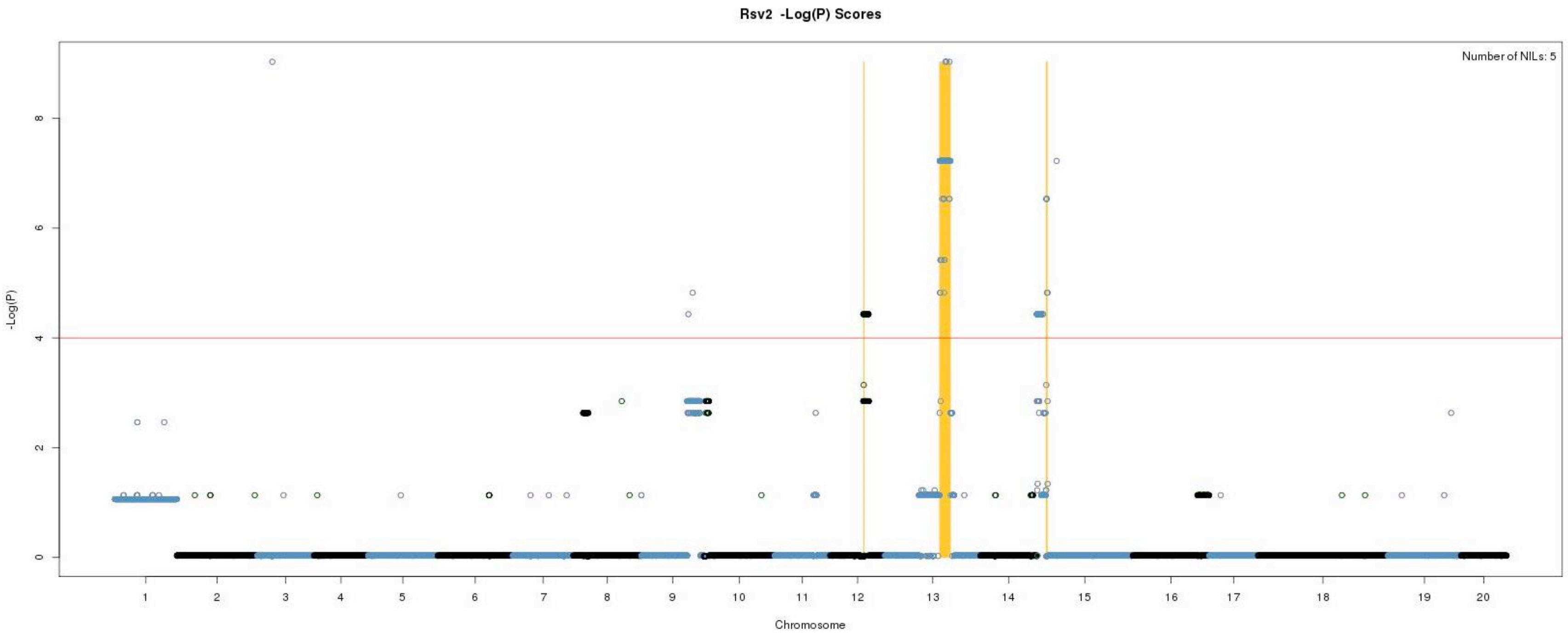
Supplementary Figure 1. 28 - log(P) scores for polymorphic markers in NILs with the trait Rps1-c (Resistant to Phytophthora rot). The final interval selected is on chromosome 3. This allele aided in choosing the final interval.



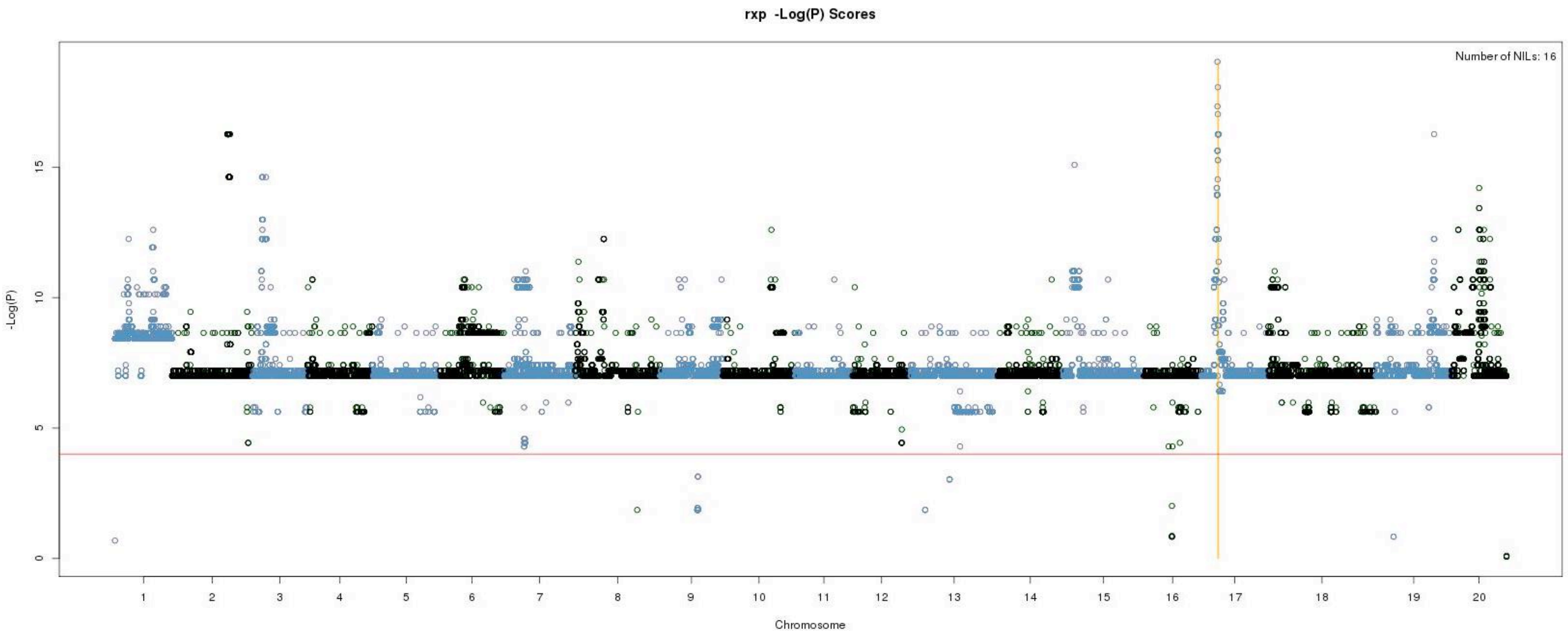
Supplementary Figure 1. 29 - log(P) scores for polymorphic markers in NILs with the trait Rps1-k (Resistant to Phytophthora rot). The final interval selected is on chromosome 3. This allele aided in choosing the final interval.



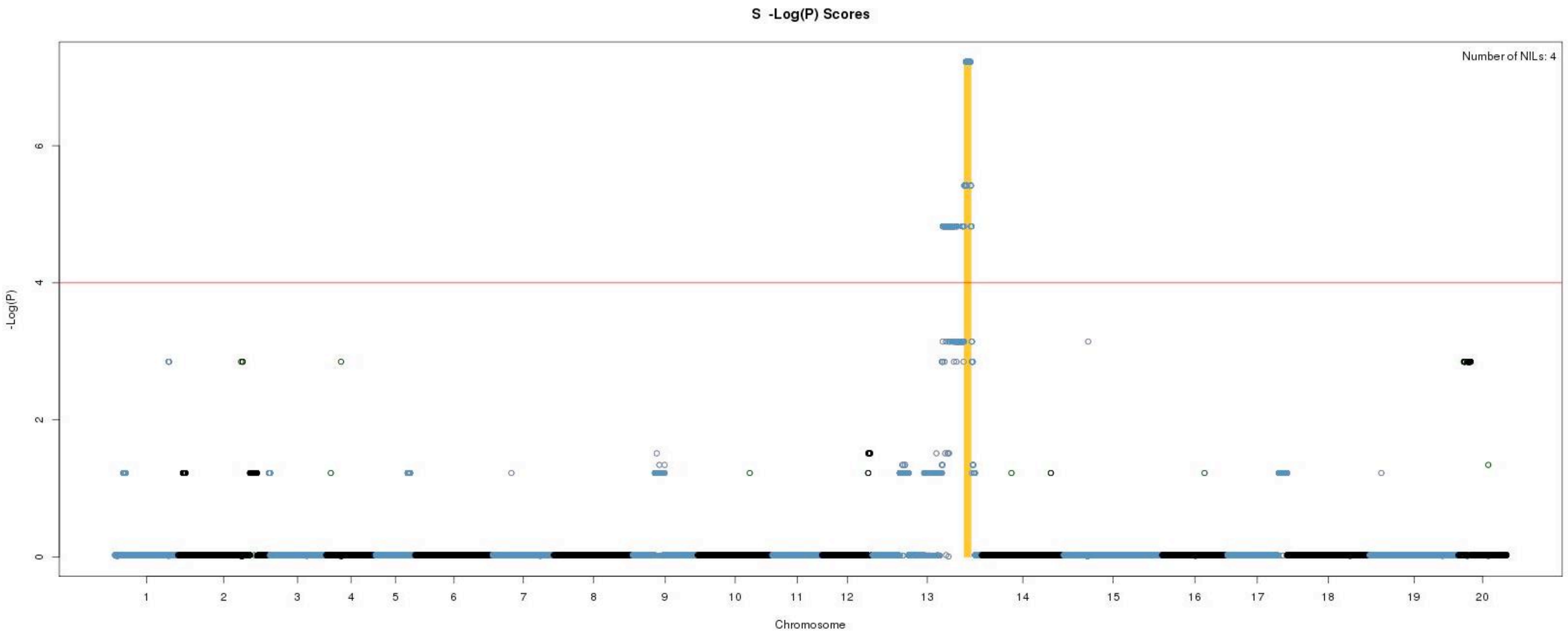
Supplementary Figure 1. 30 - log(P) scores for polymorphic markers in NILs with the trait Rps2 (Resistant to Phytophthora rot races 1-2.). The final interval selected is on chromosome 16.



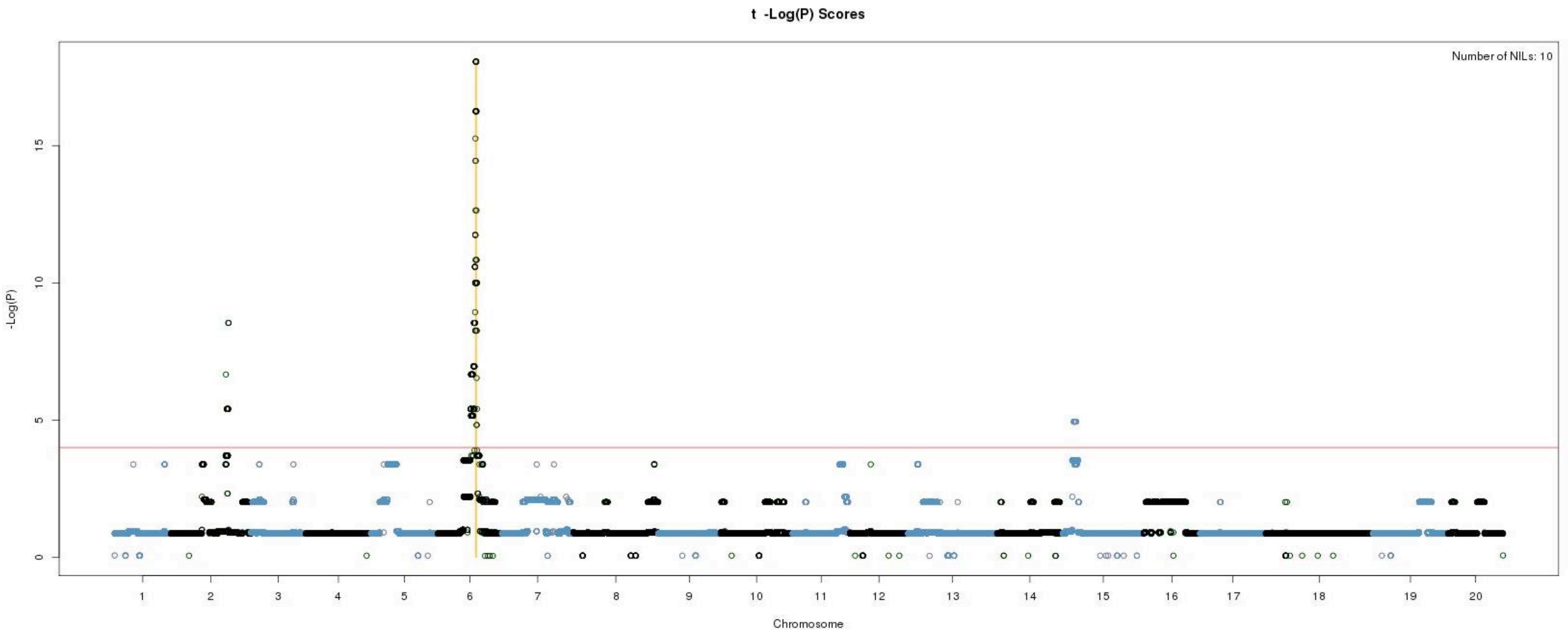
Supplementary Figure 1. 31 - log(P) scores for polymorphic markers in NILs with the trait Rsv2 (Resistant to Soybean Mosaic potyvirus Infection). The final interval selected is on chromosome 13.



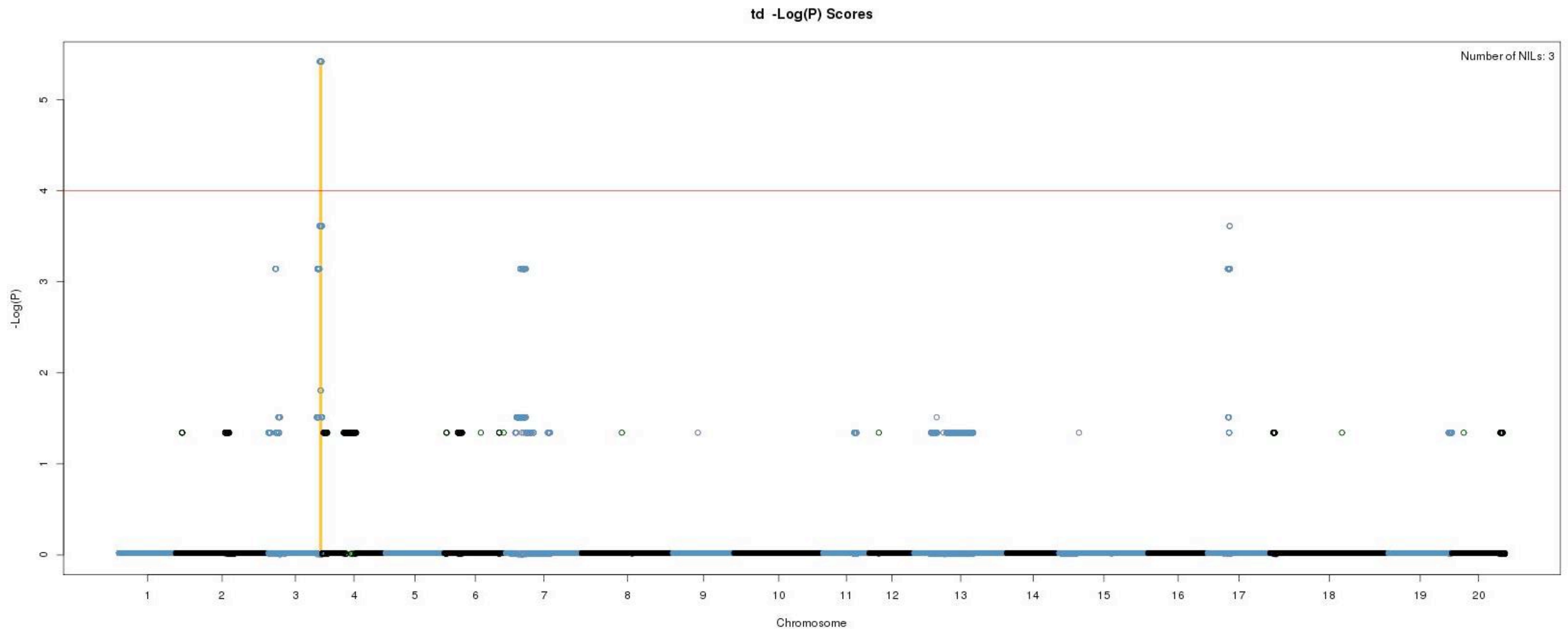
Supplementary Figure 1. 32 - log(P) scores for polymorphic markers in NILs with the trait rxp (Resistant to bacterial pustule.). The final interval selected is on chromosome 17. This is an interesting example where all polymorphic markers were significant according to the threshold, however, the only cluster to pass filtering was the donor parent



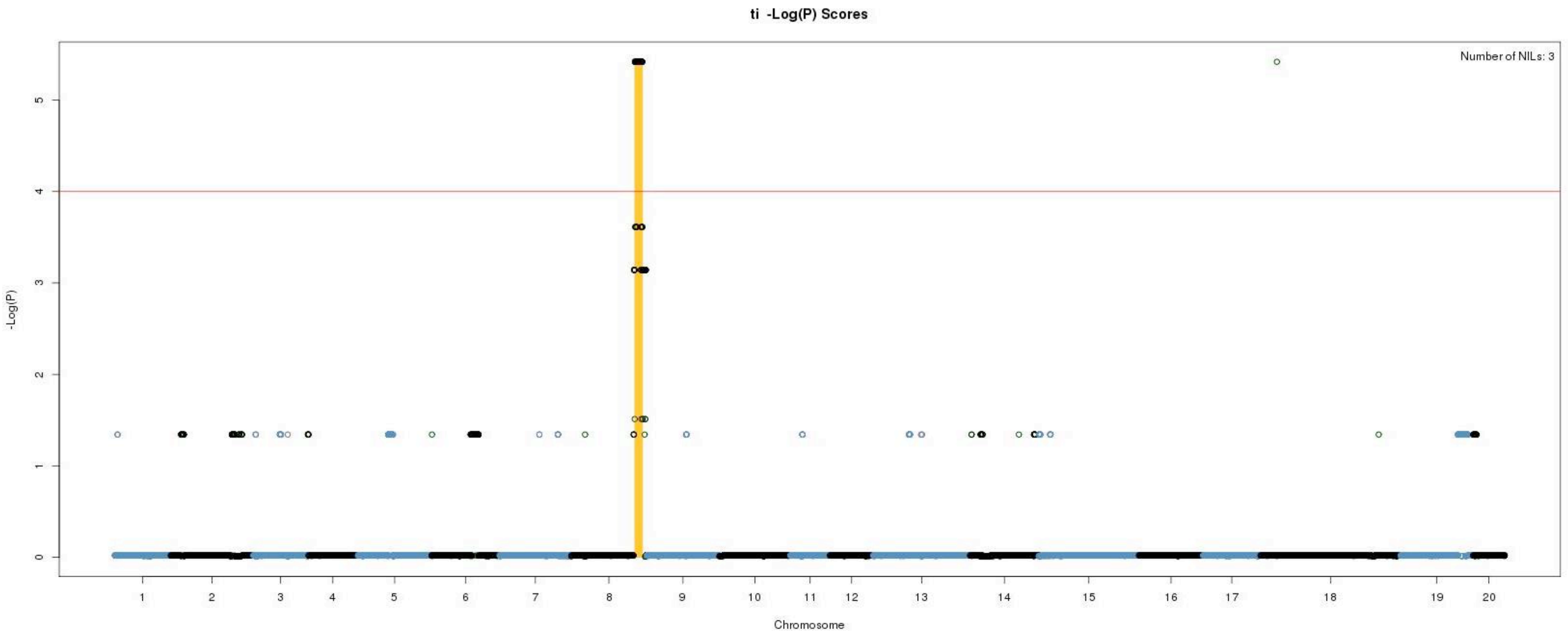
Supplementary Figure 1. 33 - log(P) scores for polymorphic markers in NILs with the trait S (Short internode length). The final interval selected is on chromosome 13.



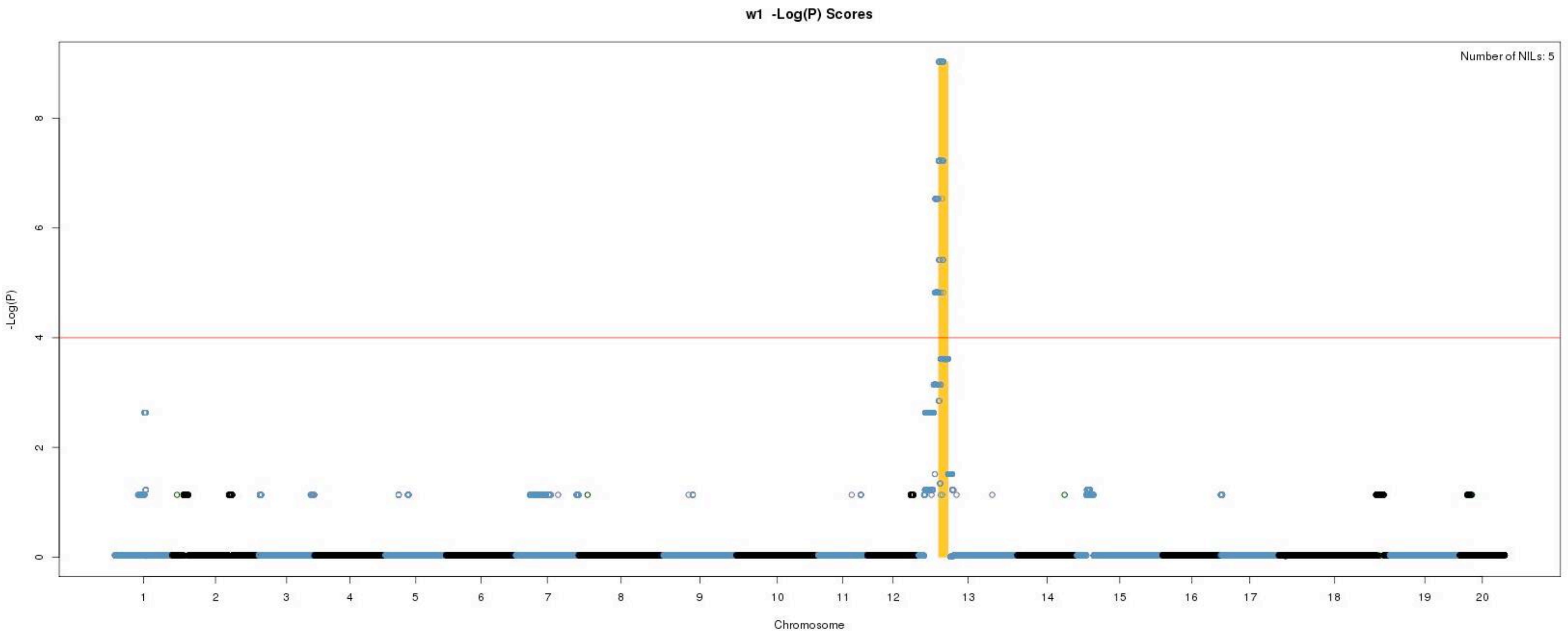
Supplementary Figure 1. 34 - log(P) scores for polymorphic markers in NILs with the trait t (Grey pubescence). The final interval selected is on chromosome 6.



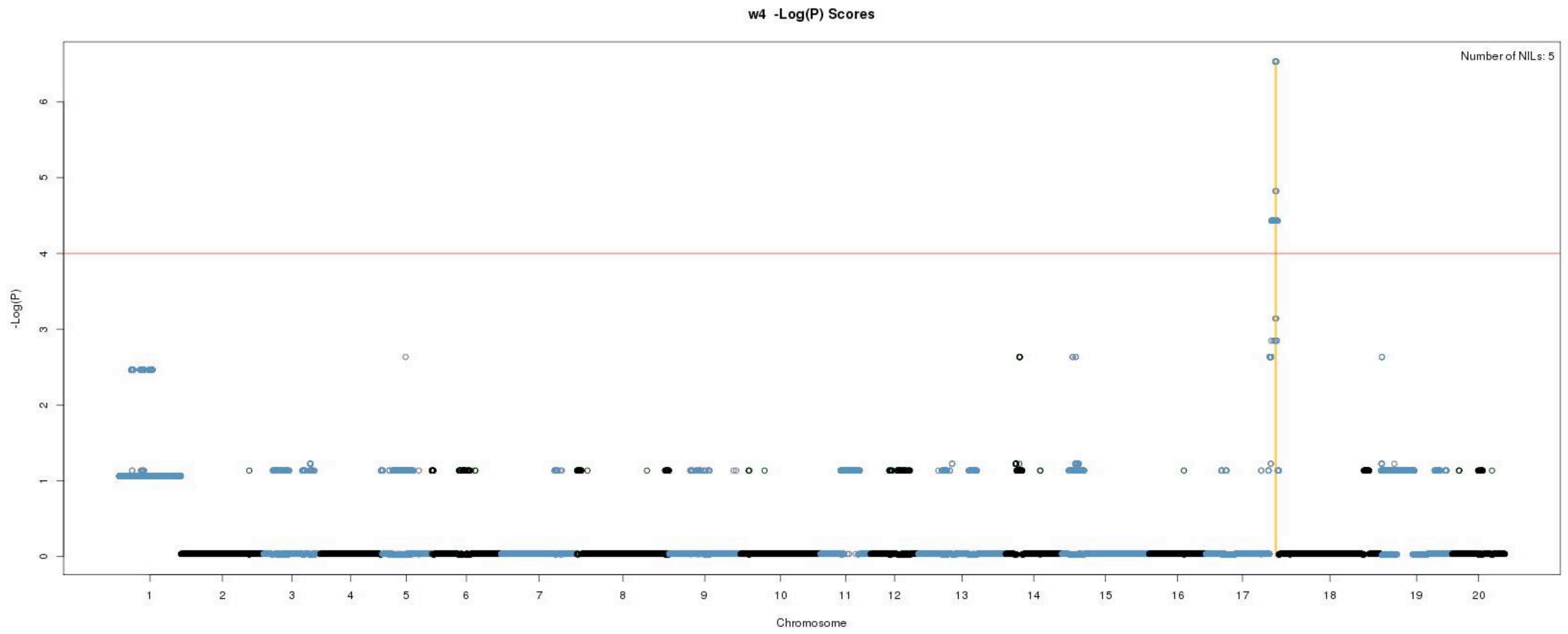
Supplementary Figure 1. 35 - log(P) scores for polymorphic markers in NILs with the trait td (Light tawny to near-grey pubescence with T). The final interval selected is on chromosome 3.



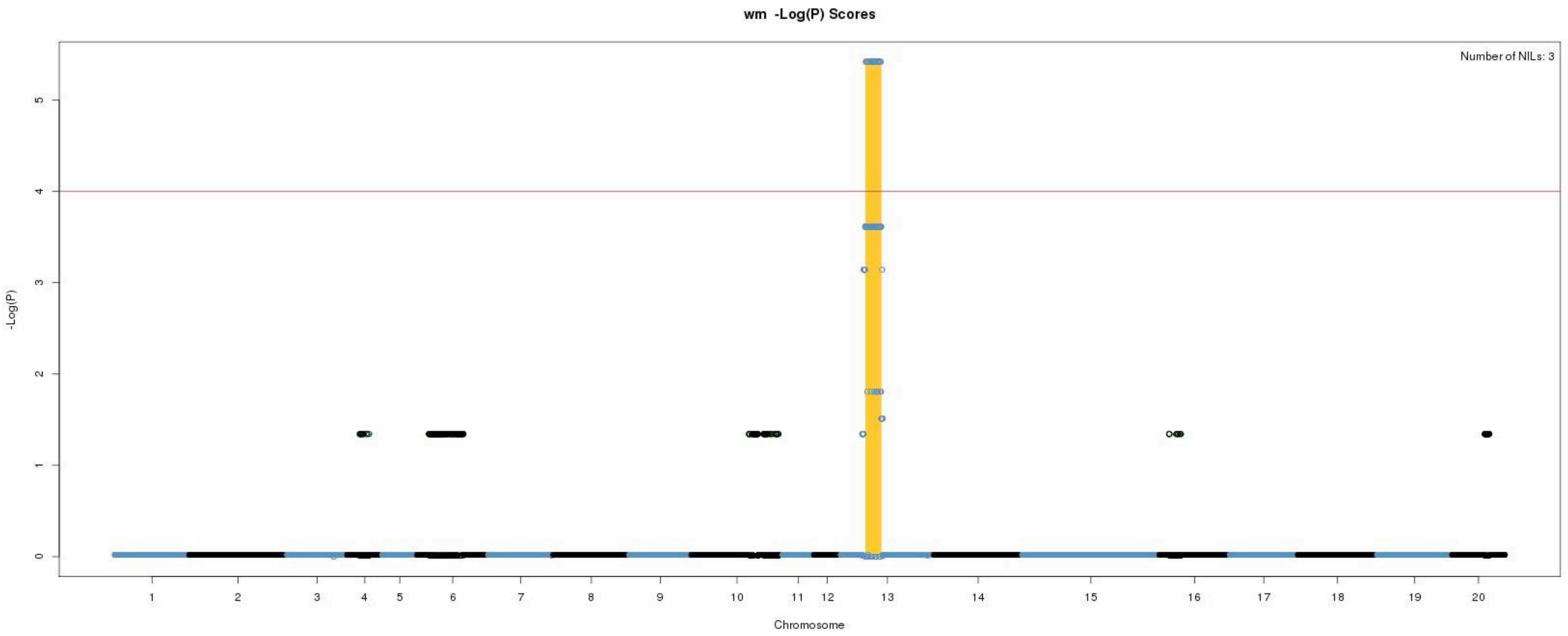
Supplementary Figure 1. 36 - log(P) scores for polymorphic markers in NILs with the trait ti (Kunitz trypsin inhibitor absent). The final interval selected is on chromosome 8.



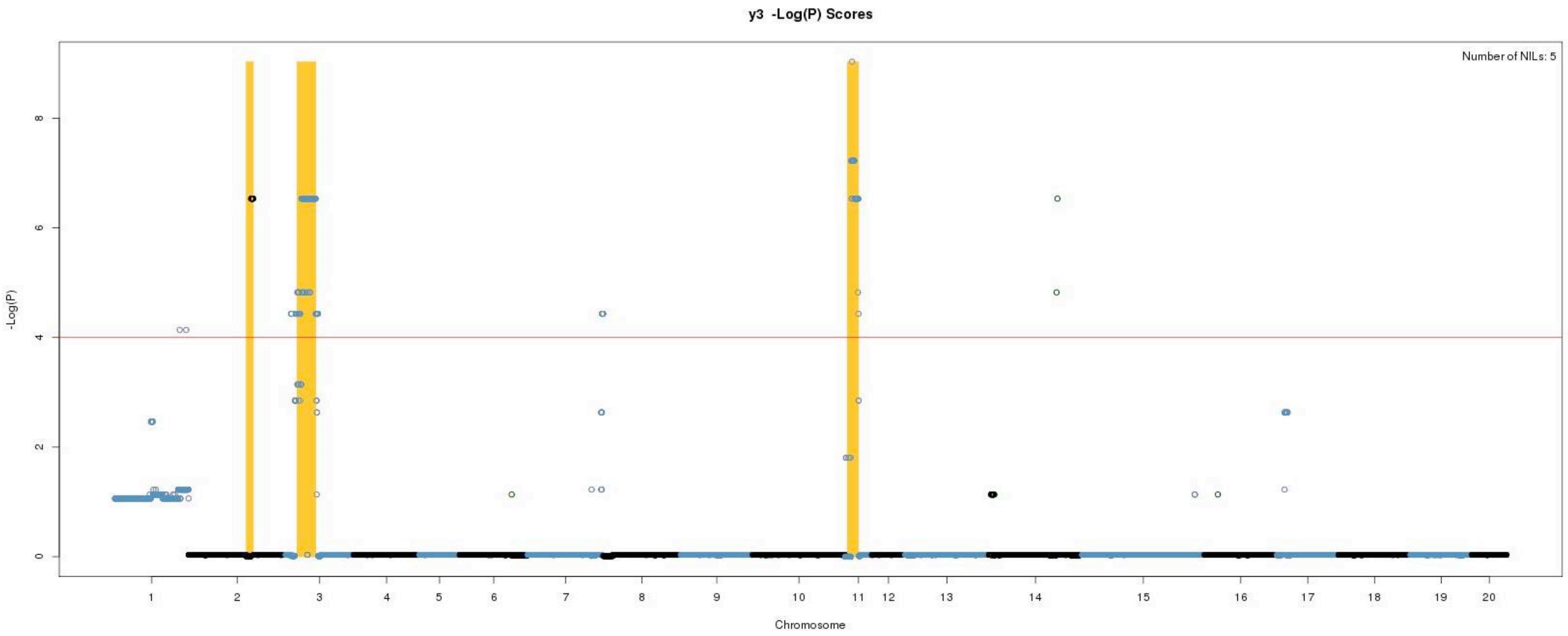
Supplementary Figure 1. 37 - log(P) scores for polymorphic markers in NILs with the trait w1 (White flower). The final interval selected is on chromosome 13.



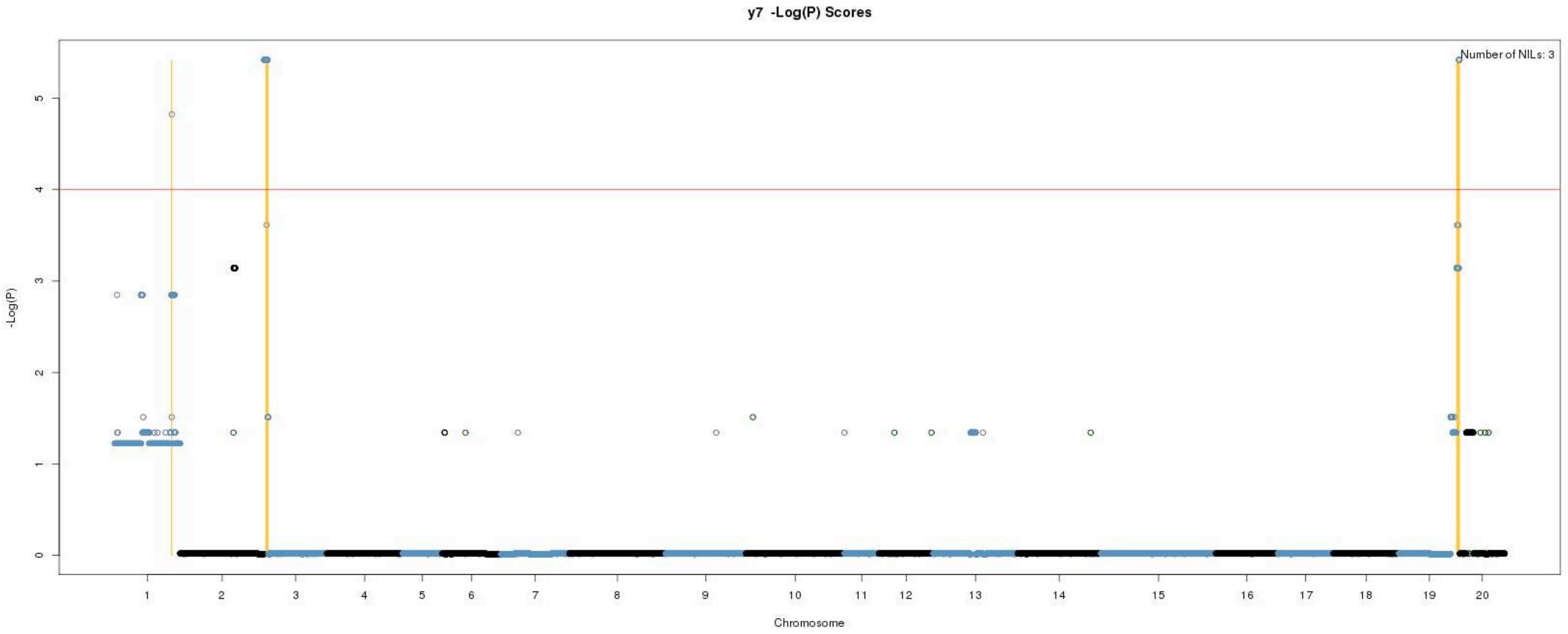
Supplementary Figure 1. 38 - log(P) scores for polymorphic markers in NILs with the trait w4 (Near-white flower). The final interval selected is on chromosome 17.



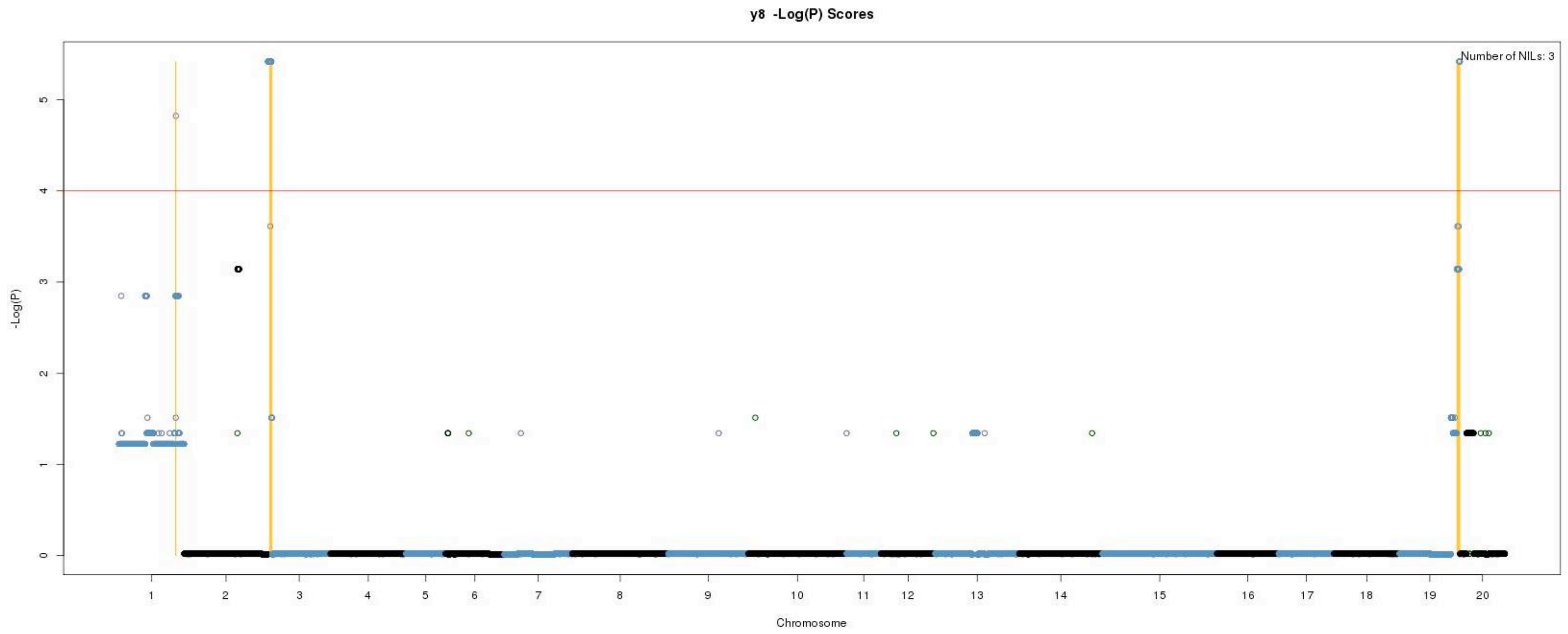
Supplementary Figure 1. 39 - log(P) scores for polymorphic markers in NILs with the trait wm (Magenta flower). The final interval selected is on chromosome 13.



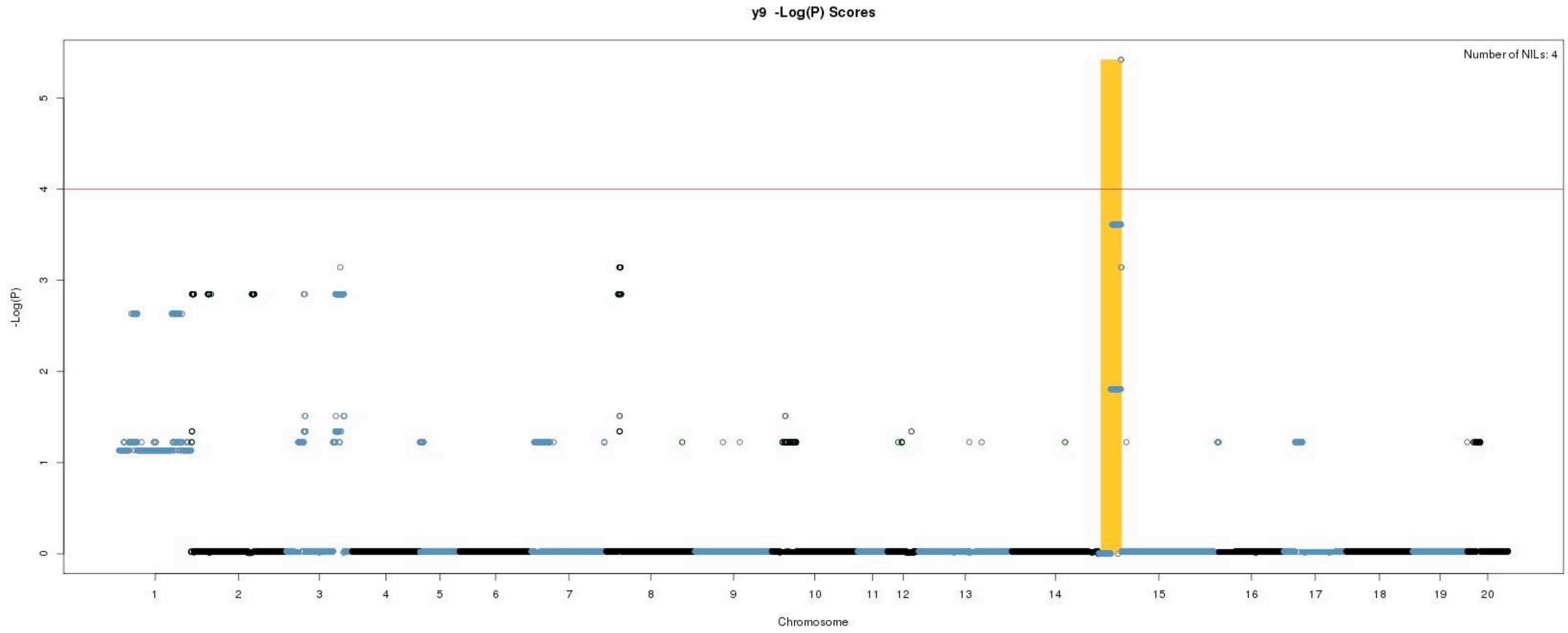
Supplementary Figure 1. 40 - log(P) scores for polymorphic markers in NILs with the trait y3 (Leaves turn rusty yellow with g). The final interval selected is on chromosome 11.



Supplementary Figure 1. 41 - log(P) scores for polymorphic markers in NILs with the trait y7/y8 (New leaves very light green in cool weather with y8). The final interval selected is on chromosome 3.



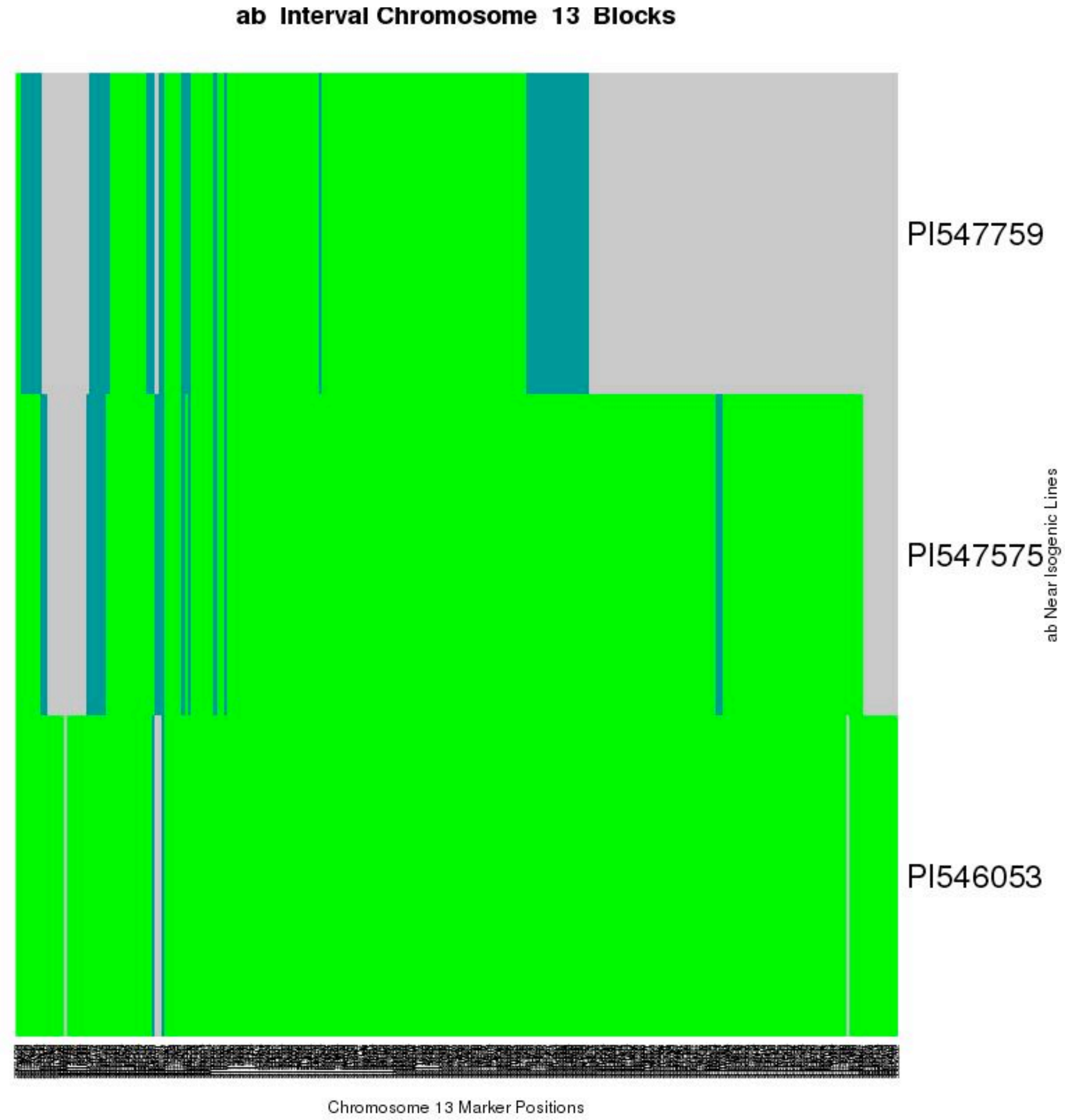
Supplementary Figure 1. 42 - log(P) scores for polymorphic markers in NILs with the trait y7/y8 (New leaves very light green in cool weather with y7). The final interval selected is on chromosome 19.



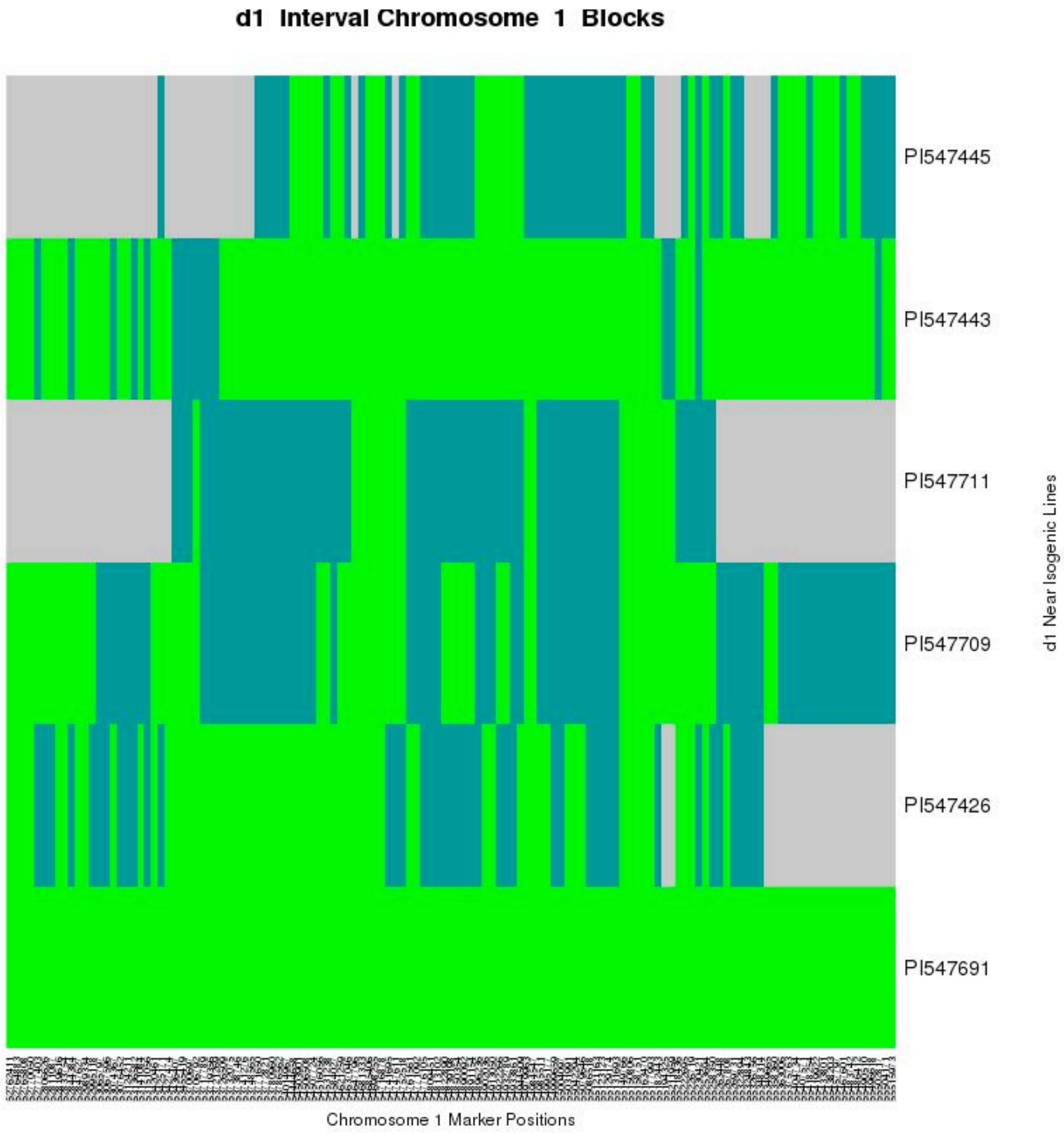
Supplementary Figure 1. 43 - log(P) scores for polymorphic markers in NILs with the trait y9 (Yellow-green plant). The final interval selected is on chromosome 15.

Supplementary Figures 2

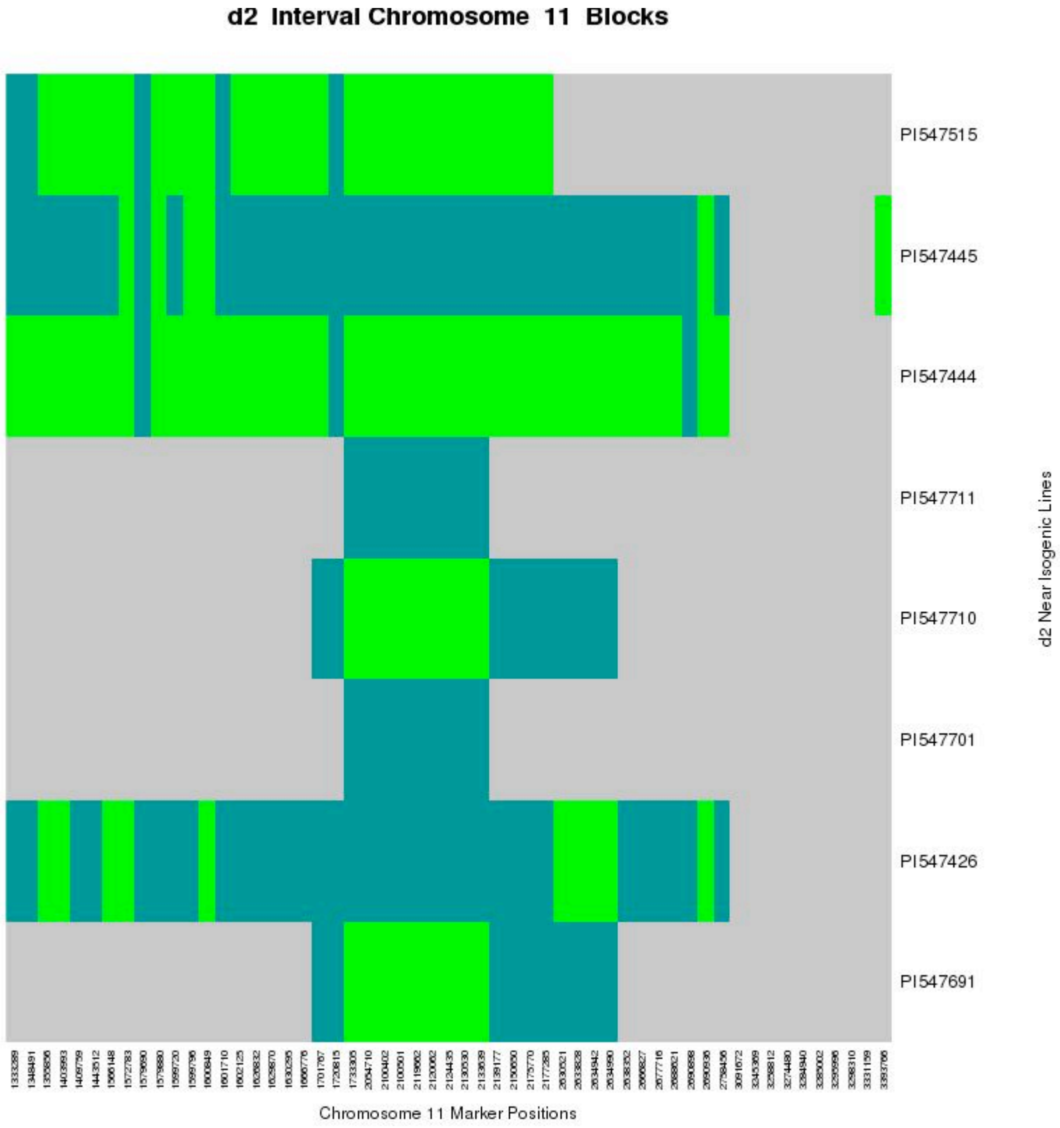
These figures show the values of scores in intervals predicted by computational comparative mapping that were chosen as final candidate intervals. Green indicates a polymorphic locus matching a donor, while grey indicates a polymorphic locus matching the recurrent parent. Blue indicates a locus polymorphic between parents, but a heterozygous read in the NIL.



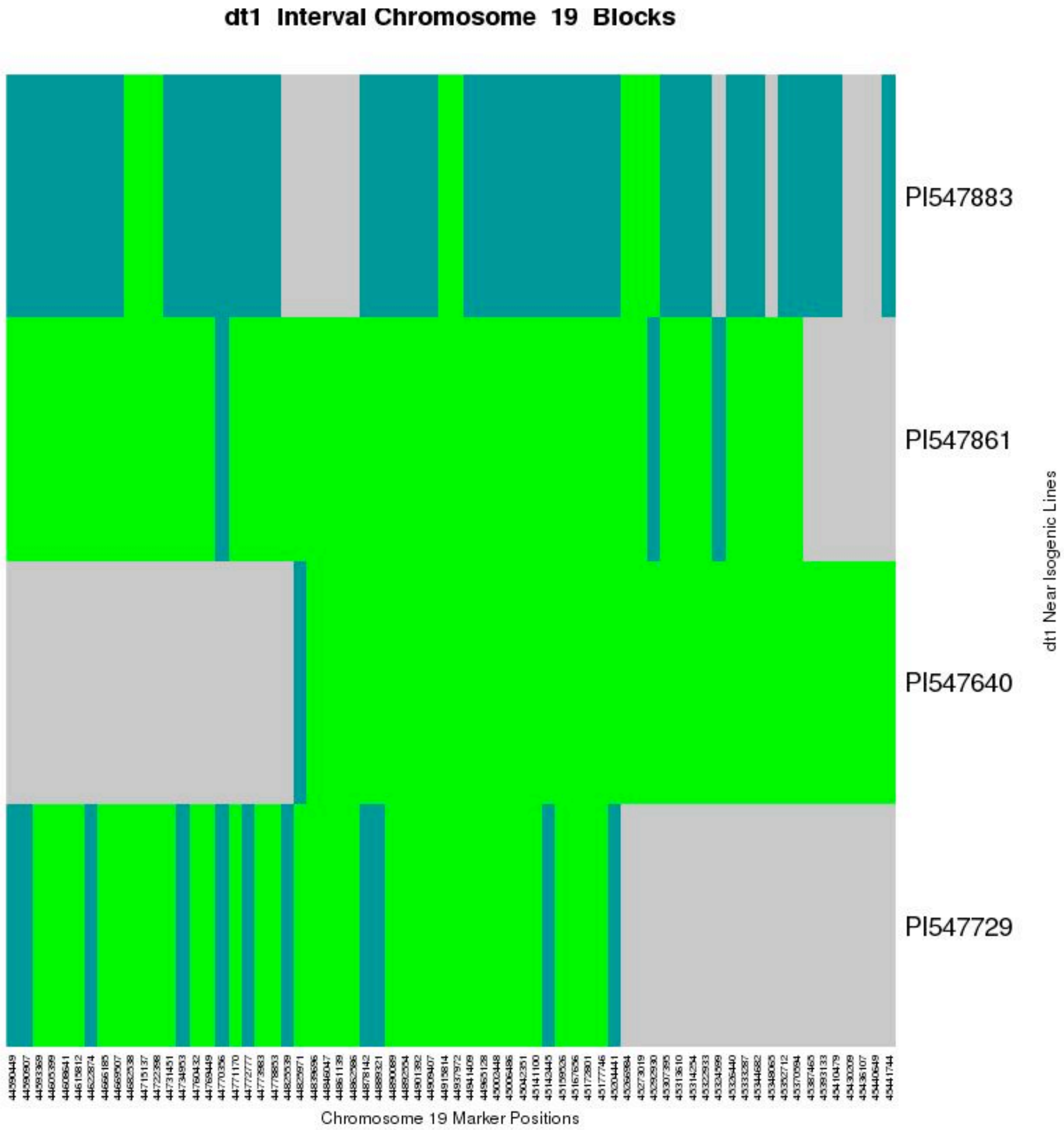
Supplementary Figure 2. 1 Interval visualization for ab (Delayed leaf abscission). The final interval selected is on chromosome 13 at positions 30086805-34775605.



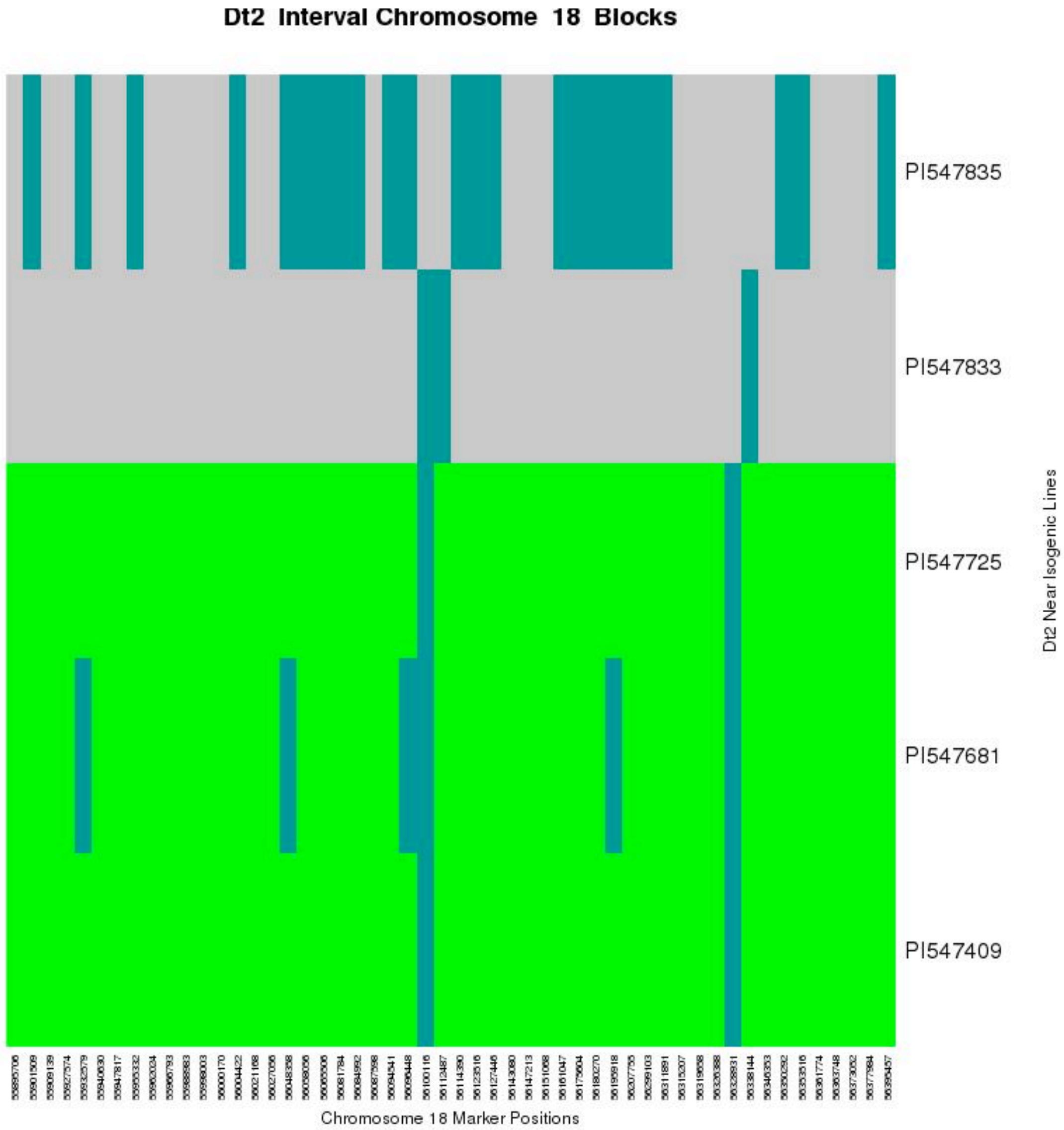
Supplementary Figure 2. 2 Interval visualization for d1 (Nuclear "stay green” chlorophyll presence after senescence). The final interval selected is on chromosome 1 at positions 53786562-55086518.



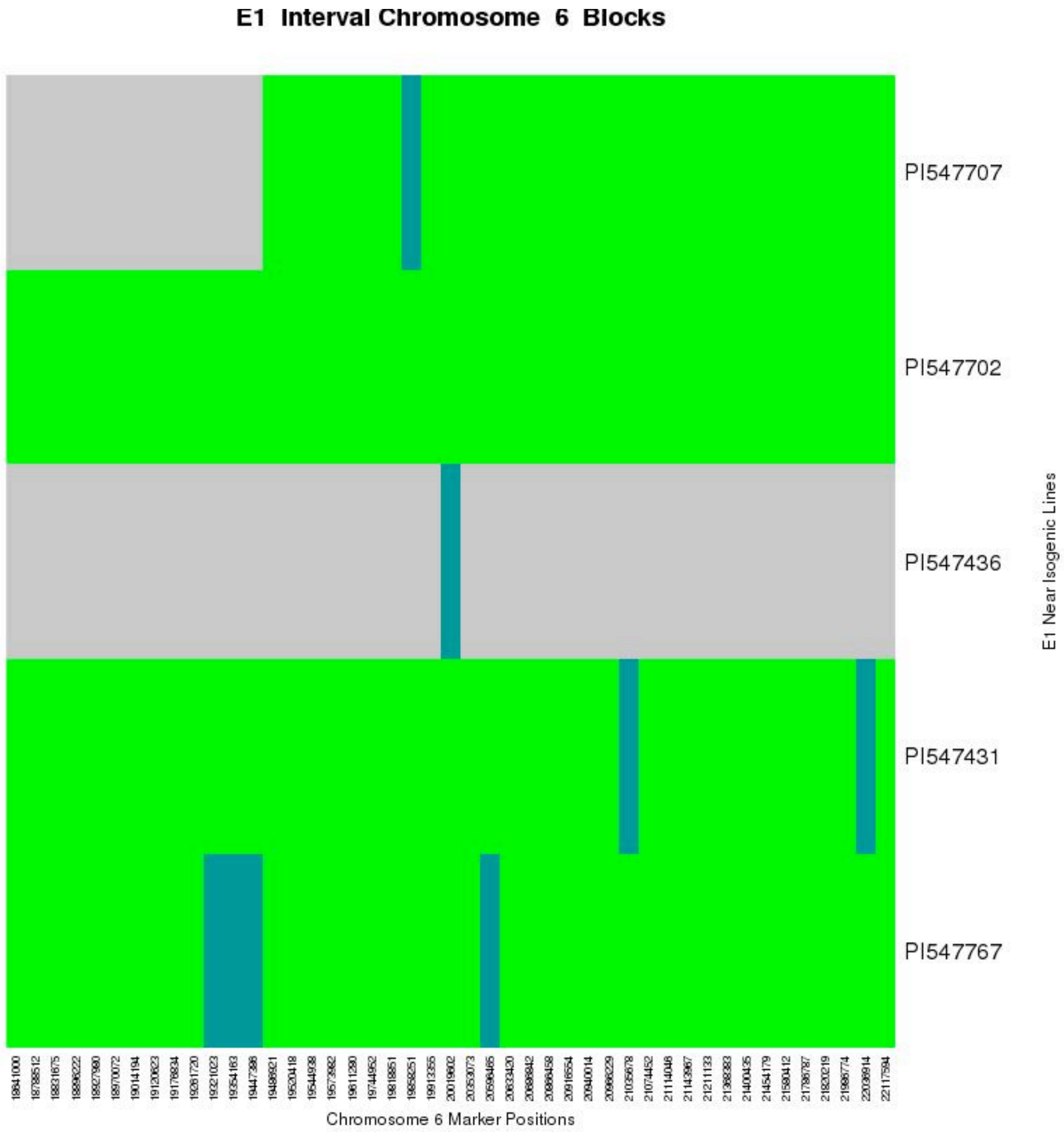
Supplementary Figure 2. 3 Imtervals visualization for d2 (Nuclear "stay green” chlorophyll presence after senescence). The final interval selected is on chromosome 11 at positions 1629870-2633828.



Supplementary Figure 2. 4 Interval visualization for dt1 (Determinate stem). The final interval selected is on chromosome 19 at positions 43882137-45273019.



Supplementary Figure 2. 5 Interval visualization for Dt2 (Semi-determinate stem). The final interval selected is on chromosome 18 at positions 54576800-56430921.



Supplementary Figure 2. 6 Interval visualization for E1 (Late maturity). The final interval selected is on chromosome 6 at positions 19354163-20353073.

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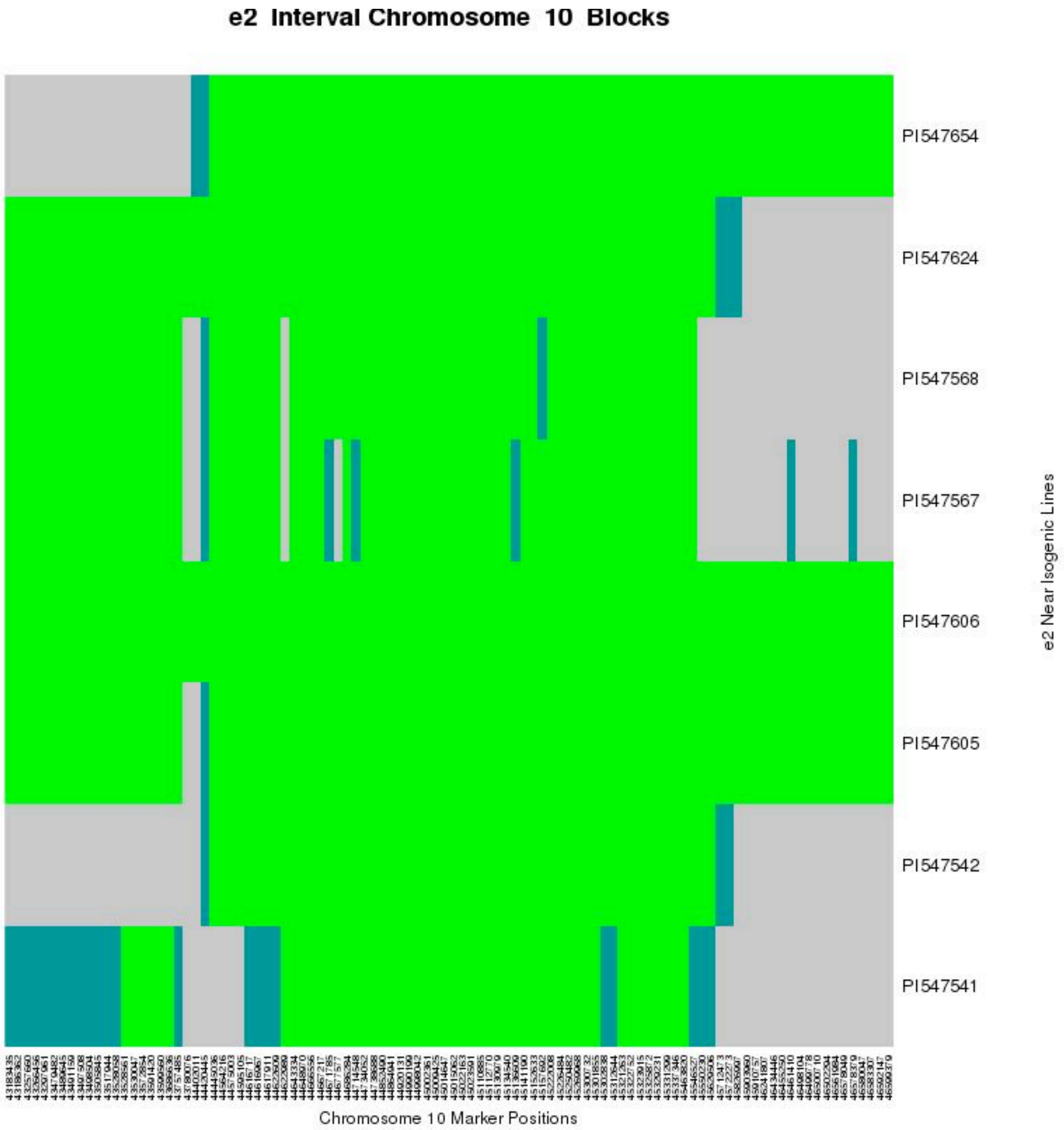
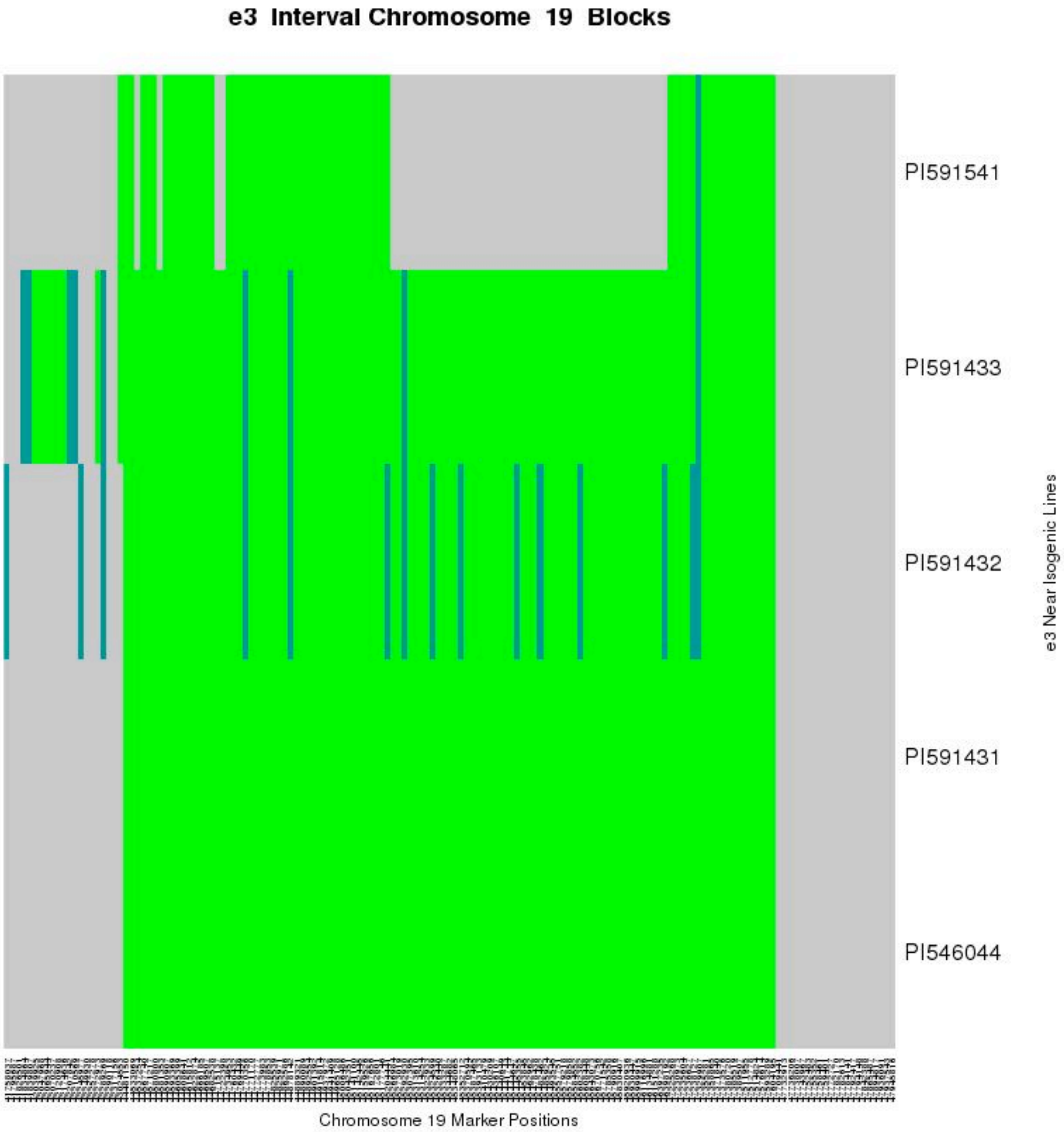
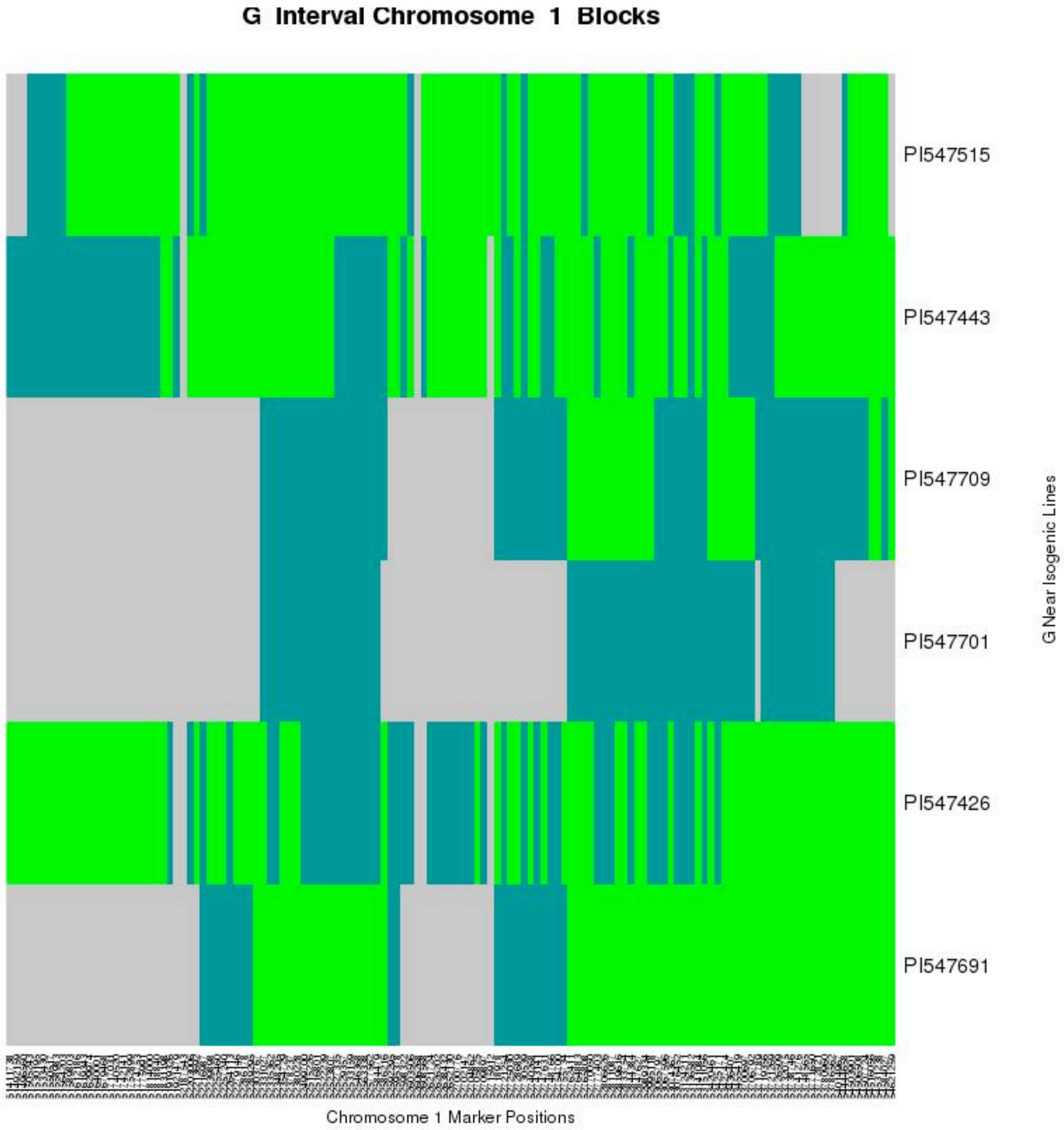


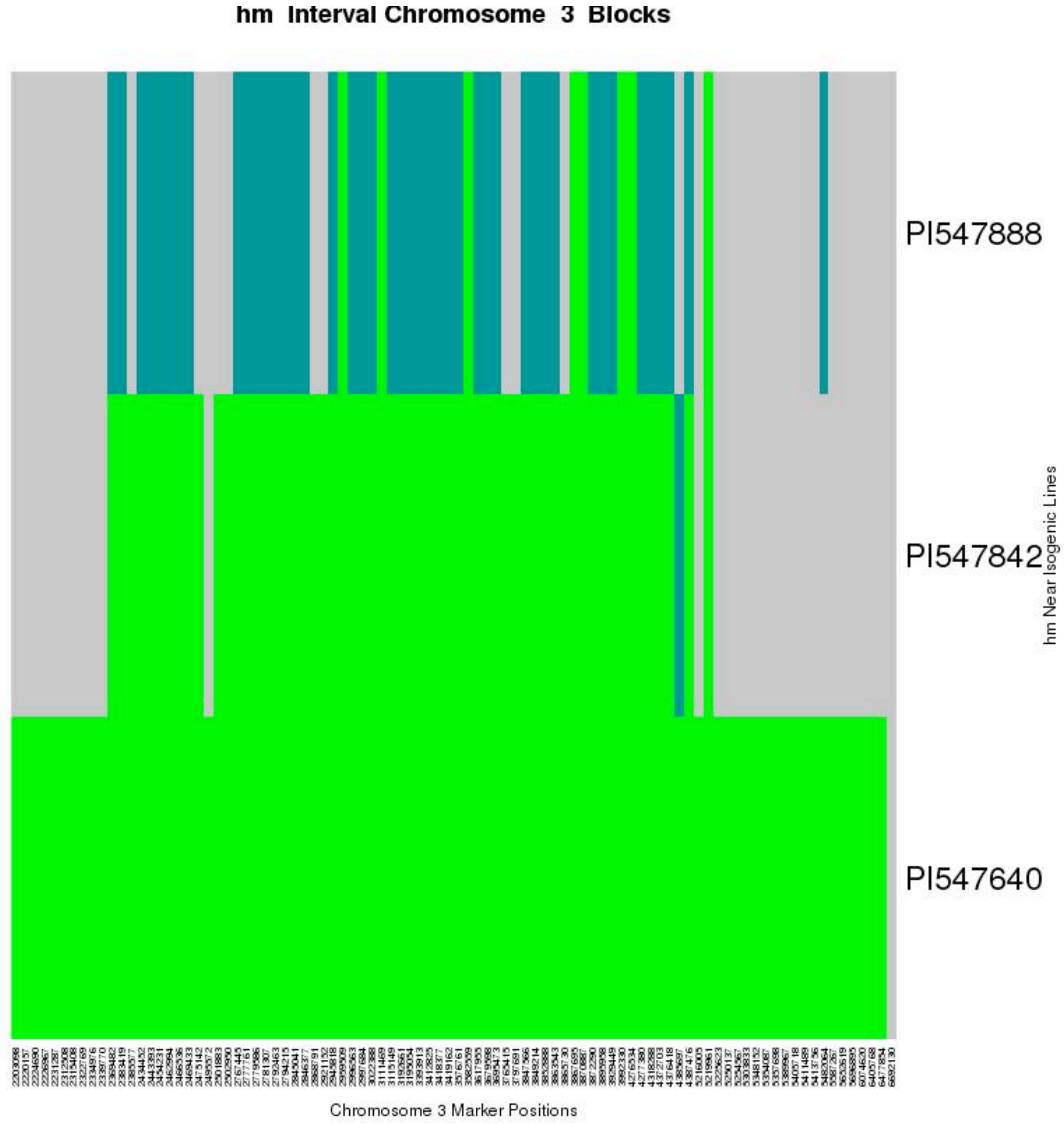
Supplementary Figure 2. 7 Interval visualization for e2 (Early maturity). The final interval selected is on chromosome 10 at positions 43780076-45629506.



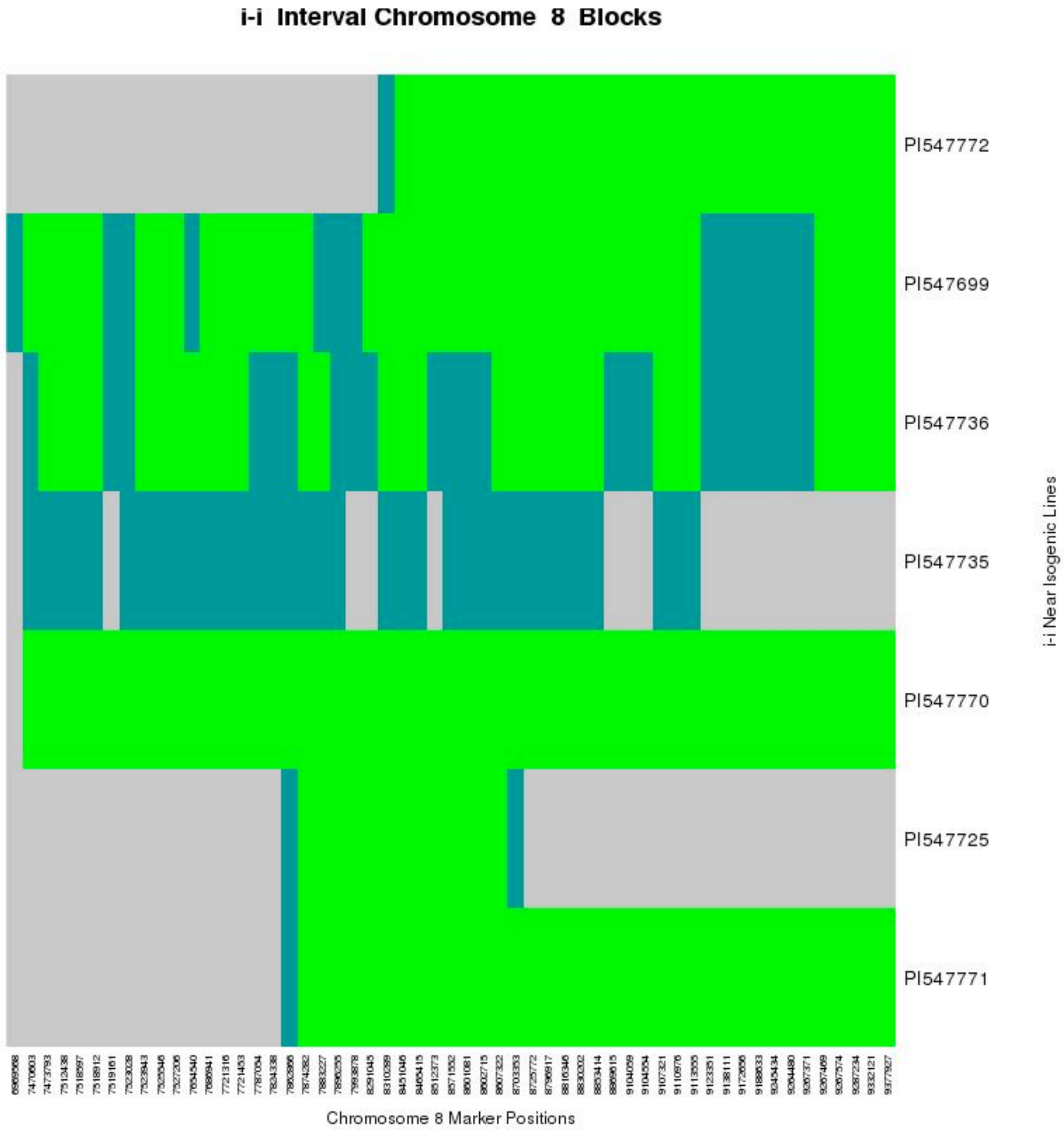
Supplementary Figure 2. 8 Interval visualization for e3 (Early maturity and low photoperiod sensitivity to incandescent light). The final interval selected is on chromosome 19 at positions 45920936-48259684.



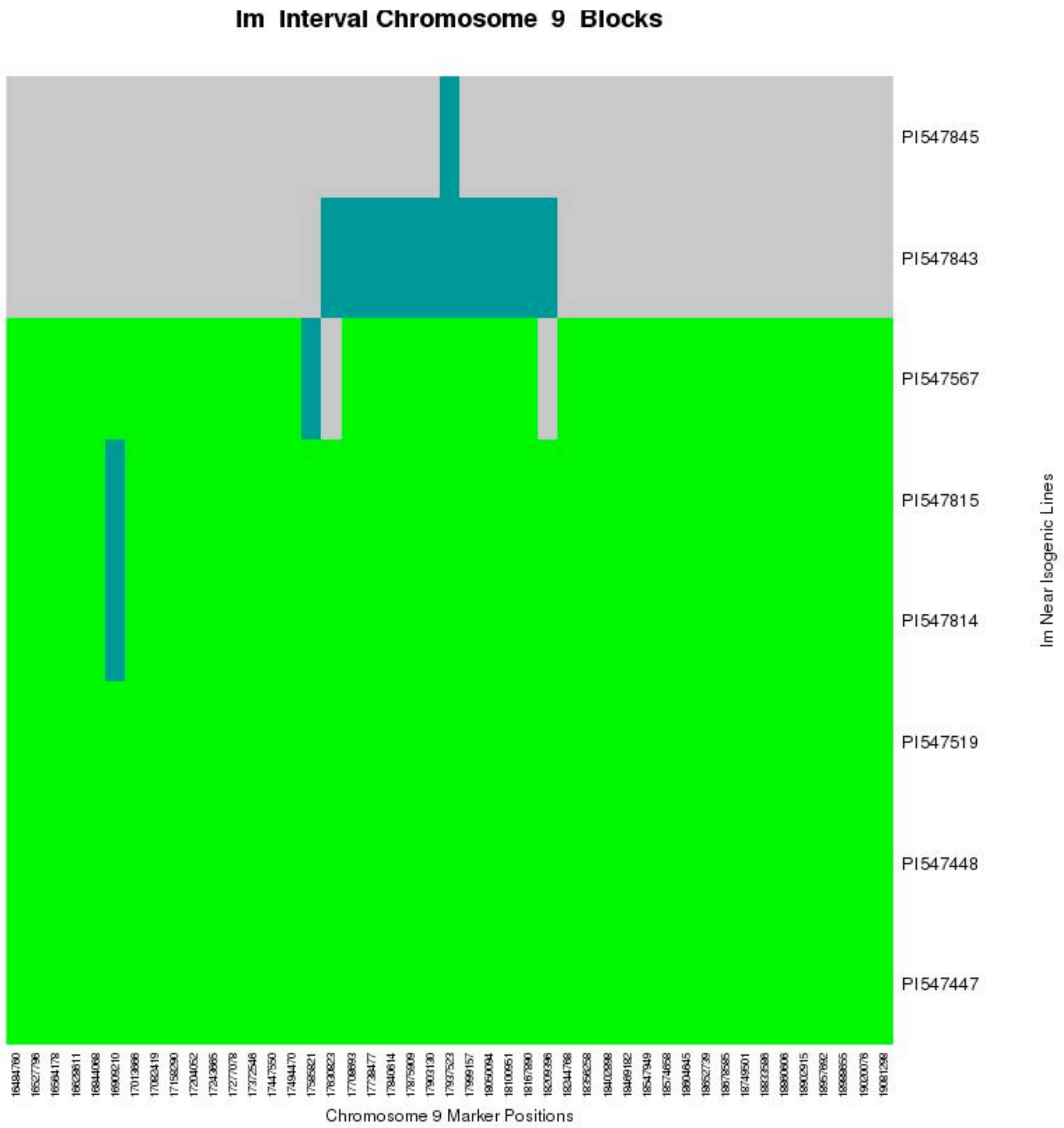
Supplementary Figure 2. 9 Interval visualization for G (Green seed coat). The final interval selected is on chromosome 1 at positions 51775991-55375763.



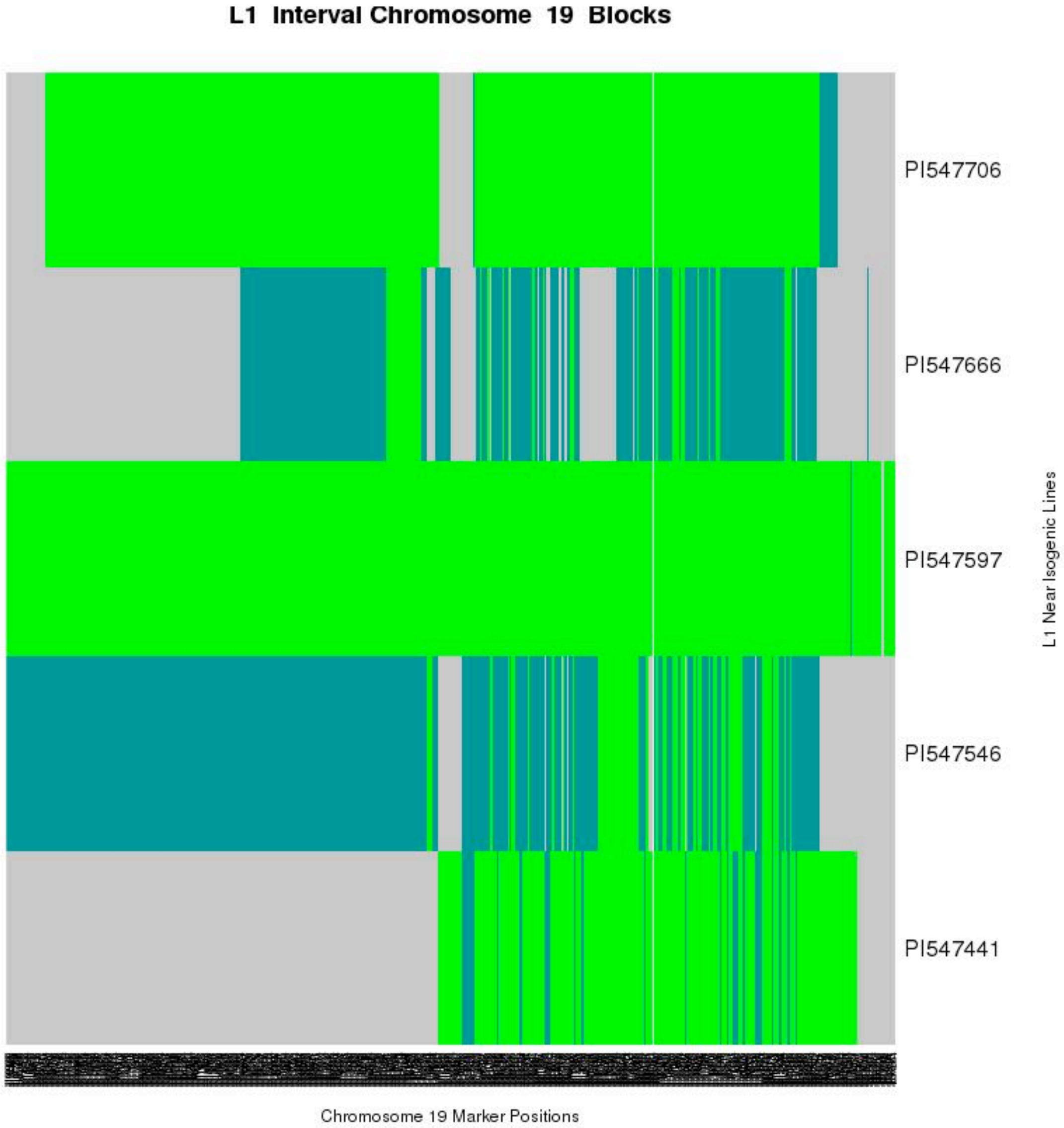
Supplementary Figure 2. 10 Interval visualization for hm (Metribuzin sensitive). The final interval selected is on chromosome 3 at positions 2495572-5216005.



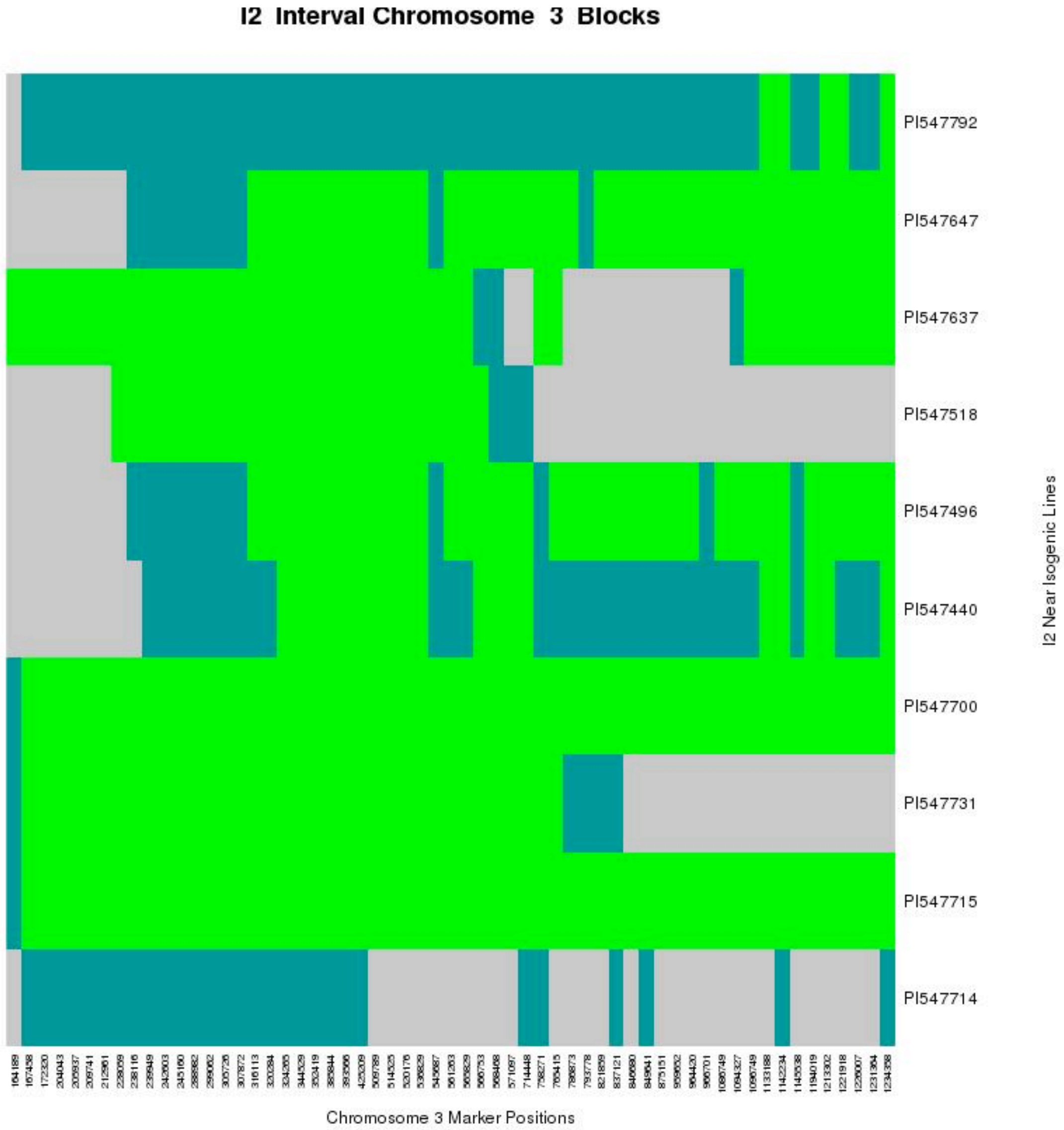
Supplementary Figure 2. 11 Interval visualization for i-i, an allele of I that aided in mapping.



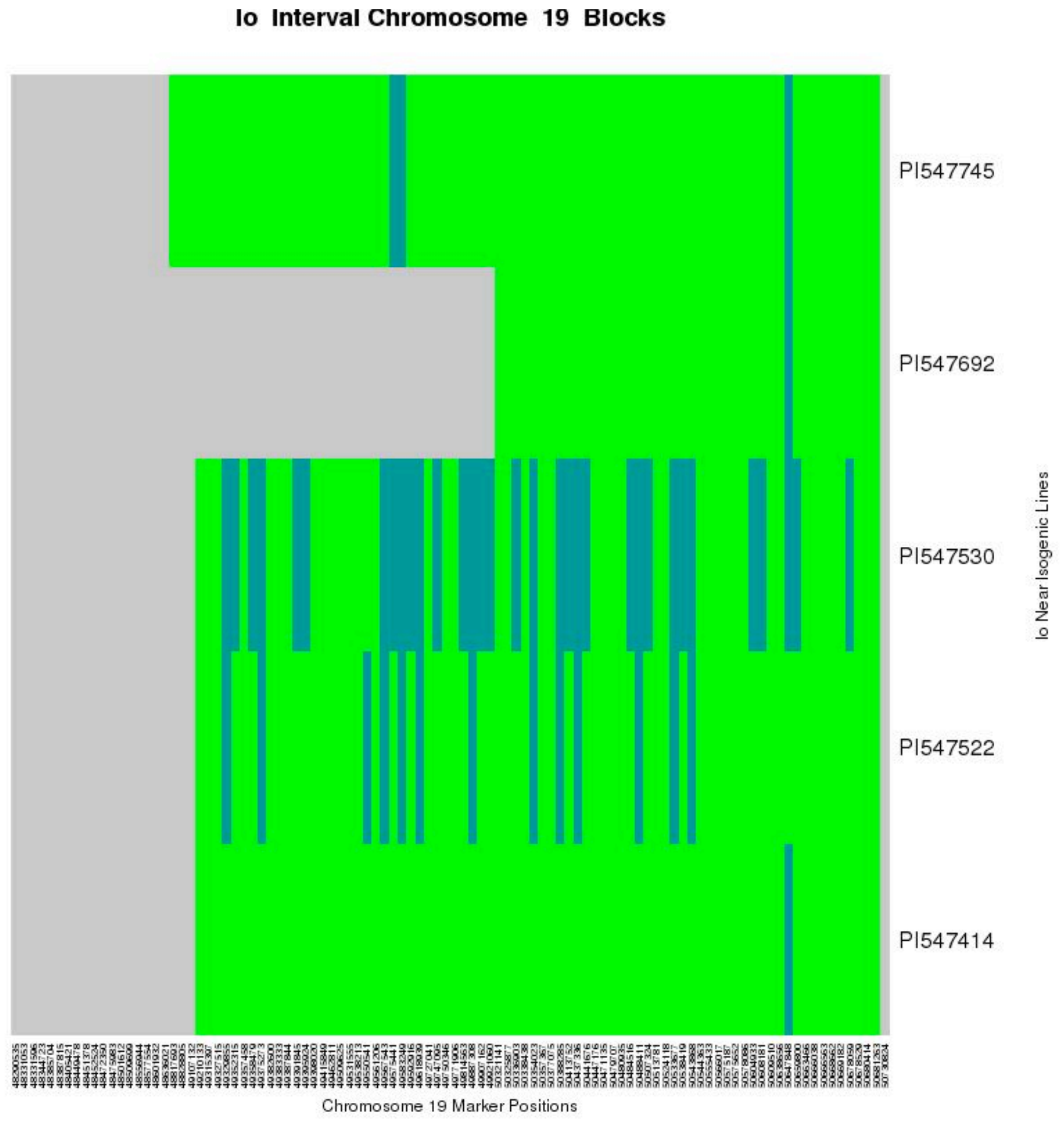
Supplementary Figure 2. 12 Interval visualization for Im (Non-mottling (Non-mottling under SMV infection)). The final interval selected is on chromosome 9 at positions 12809350-21080454.



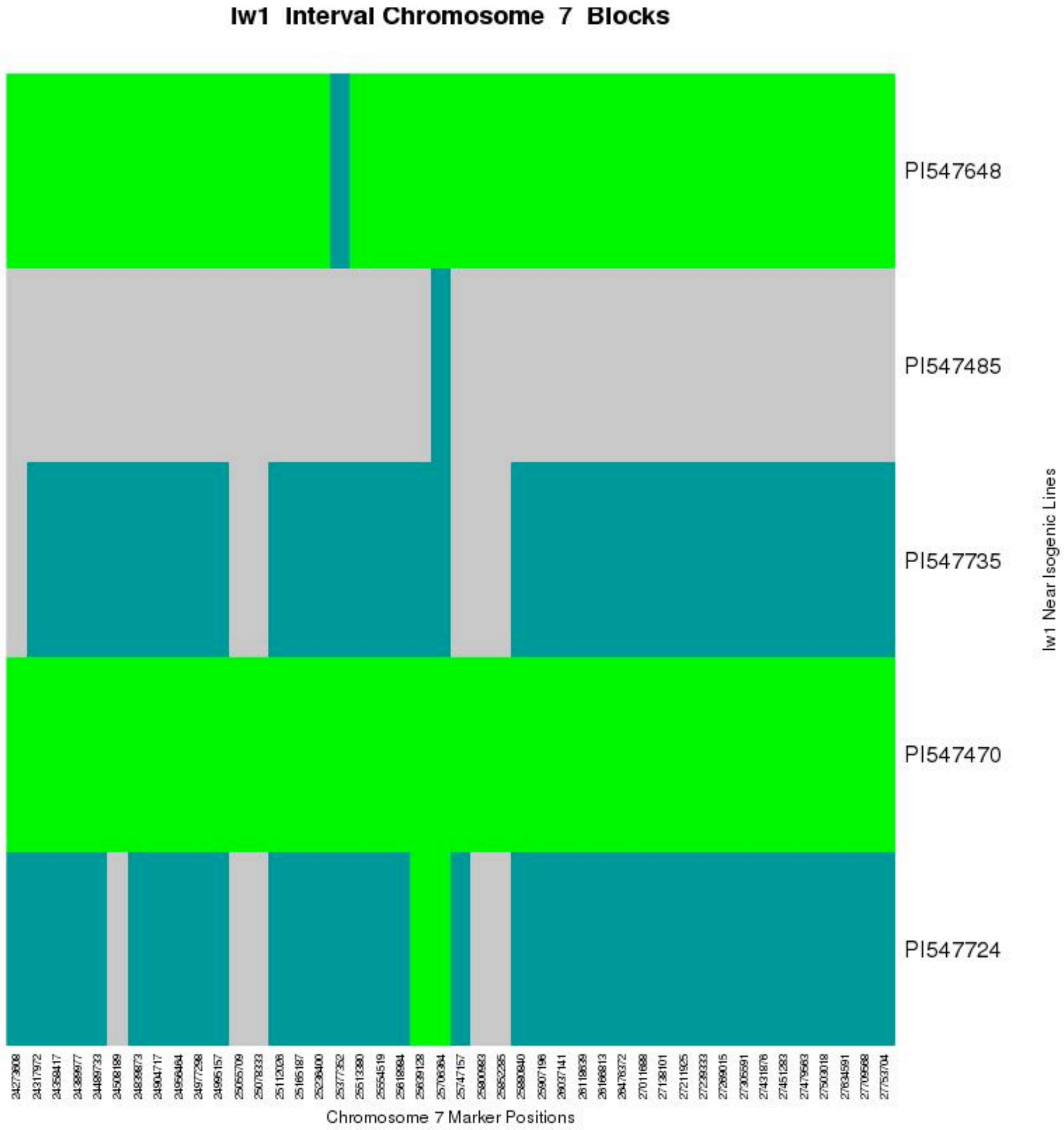
Supplementary Figure 2. 13 Interval visualization for L1 (Black pod). The final interval selected is on chromosome 19 at positions 32245731-39929607.



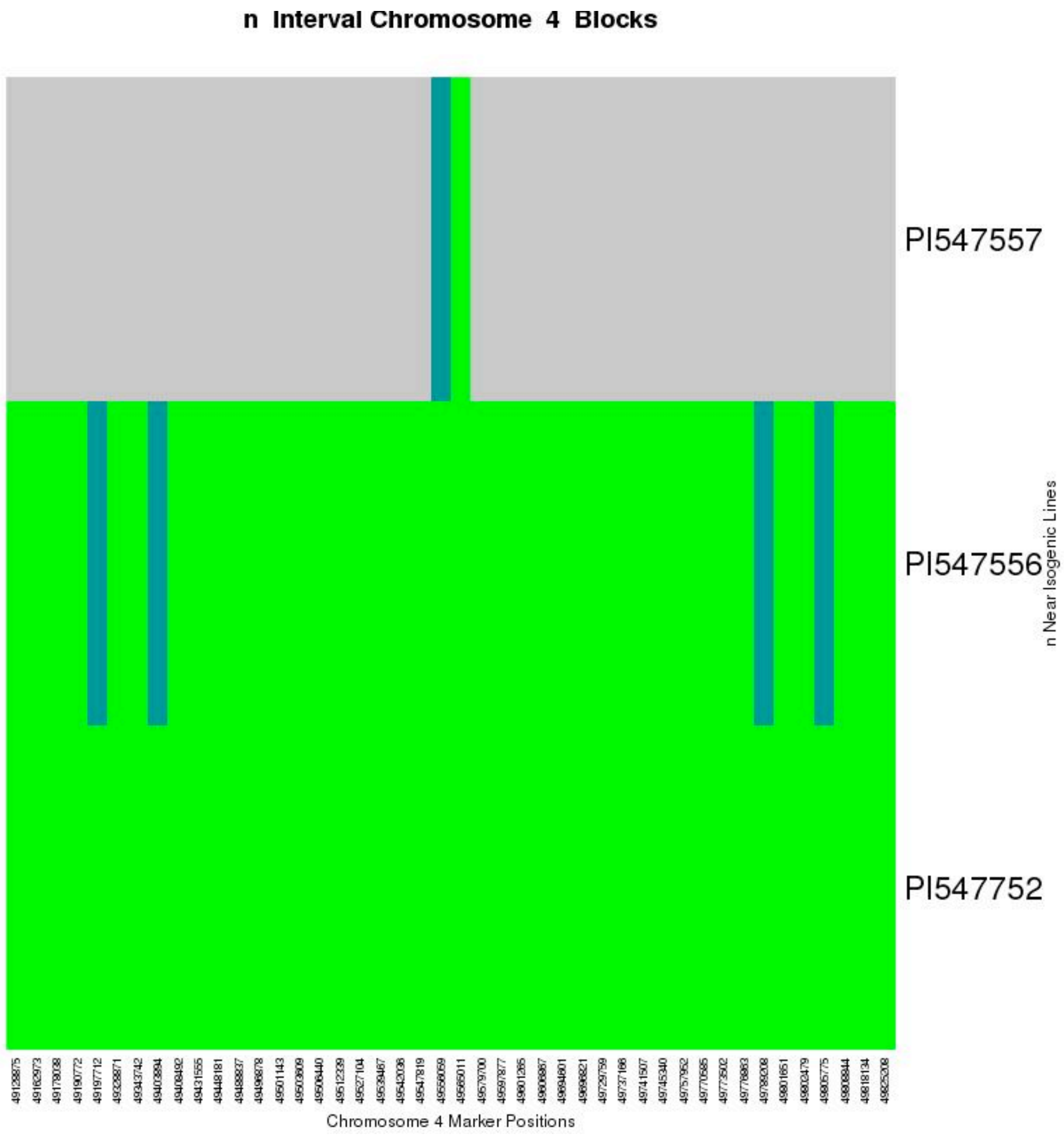
Supplementary Figure 2. 14 Interval visualization for l2 (Tan pod). The final interval selected is on chromosome 3 at positions 385844-793778.



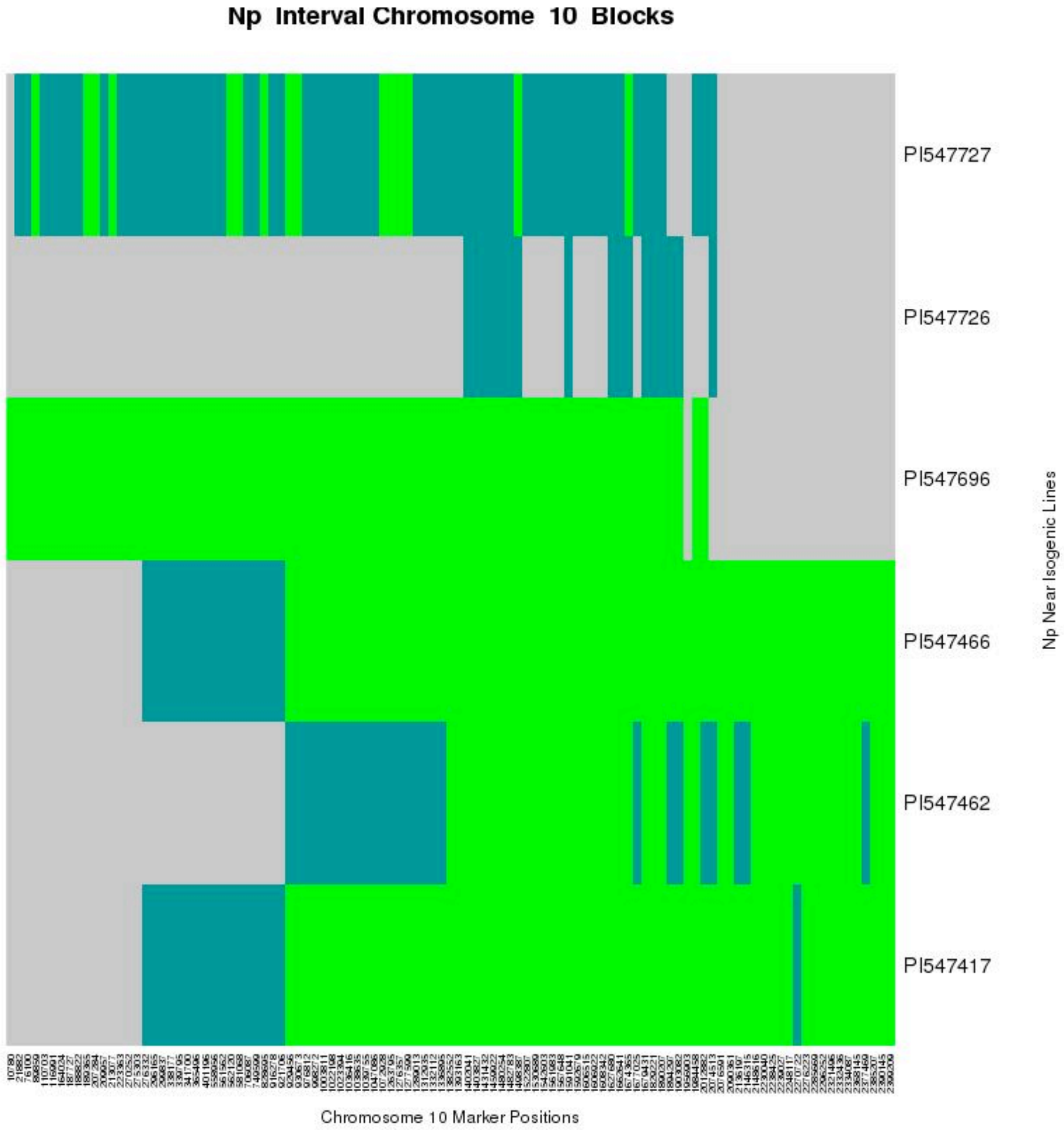
Supplementary Figure 2. 15 Interval visualization for lo (Oval leaflet few-seeded pod). The final interval selected is on chromosome 19 at positions 49107132-50555433.



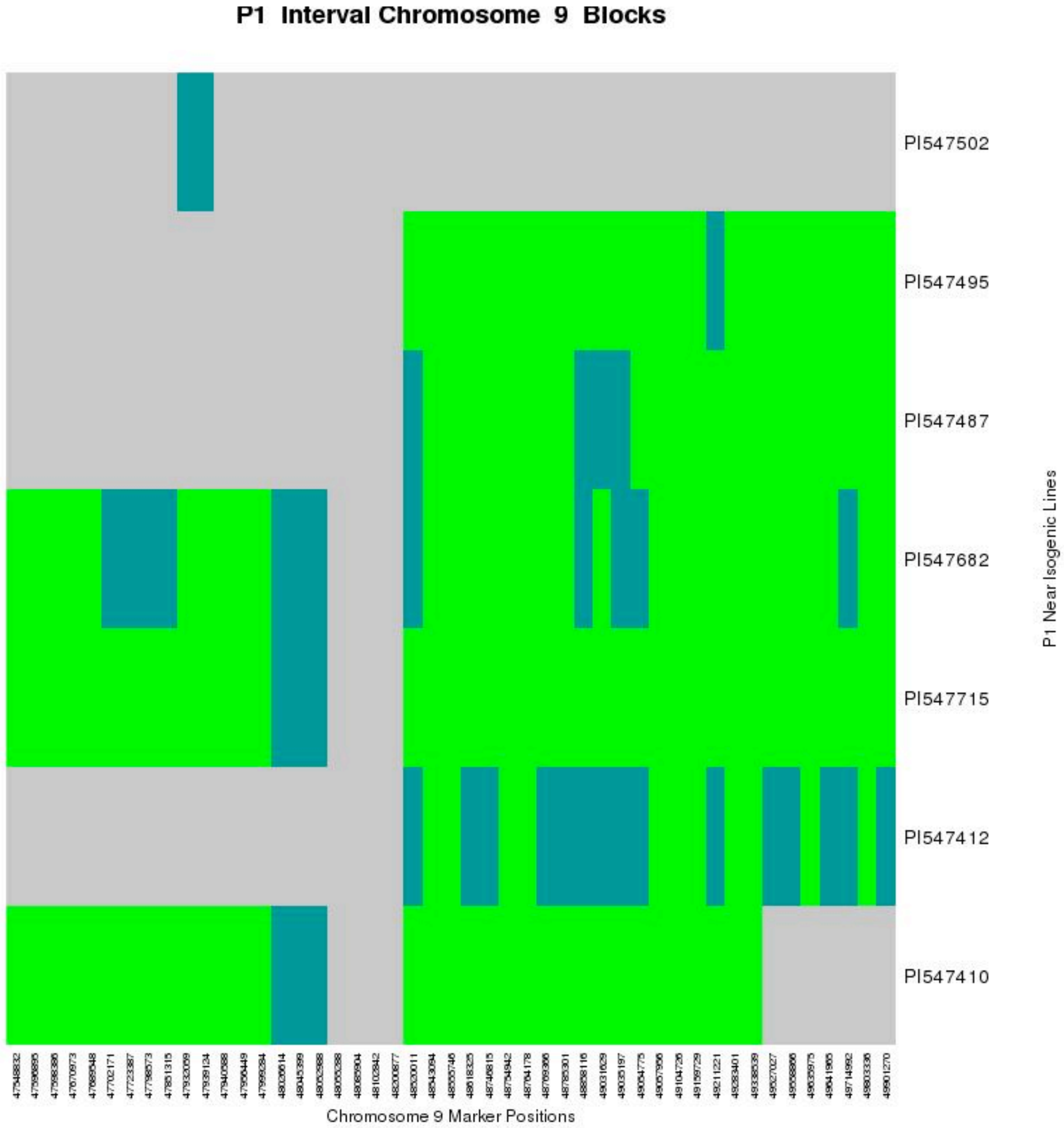
Supplementary Figure 2. 16 Interval visualization for lw1 (Wavy leaf (Requires lw2 no effect with T or individually)). The final interval selected is on chromosome 7 at positions 19017836-25800983.



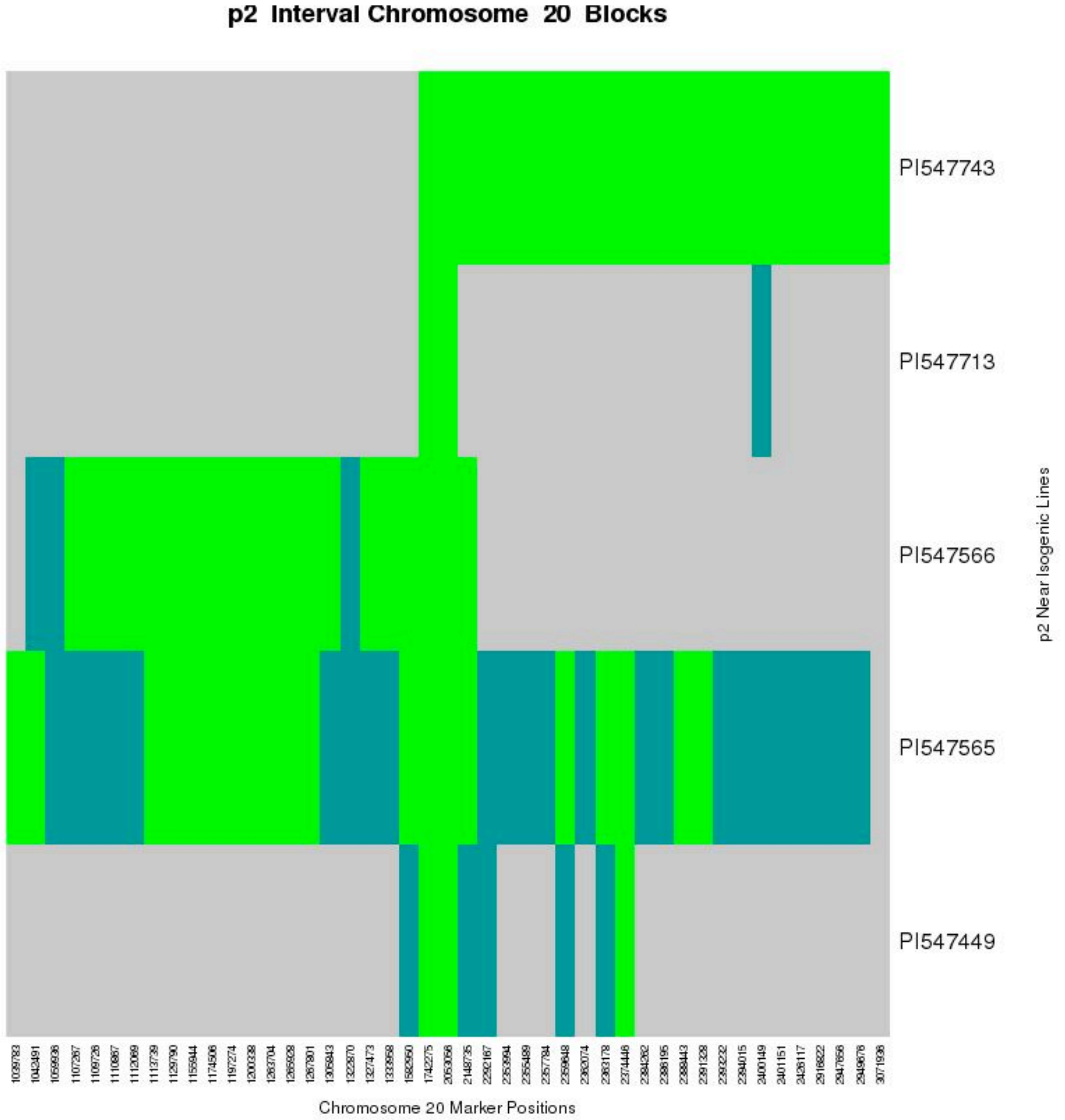
Supplementary Figure 2. 17 Interval visualization for lw1 (Wavy leaf (Requires lw2 no effect with T or individually)). The final interval selected is on chromosome 7 at positions 19017836-25800983.



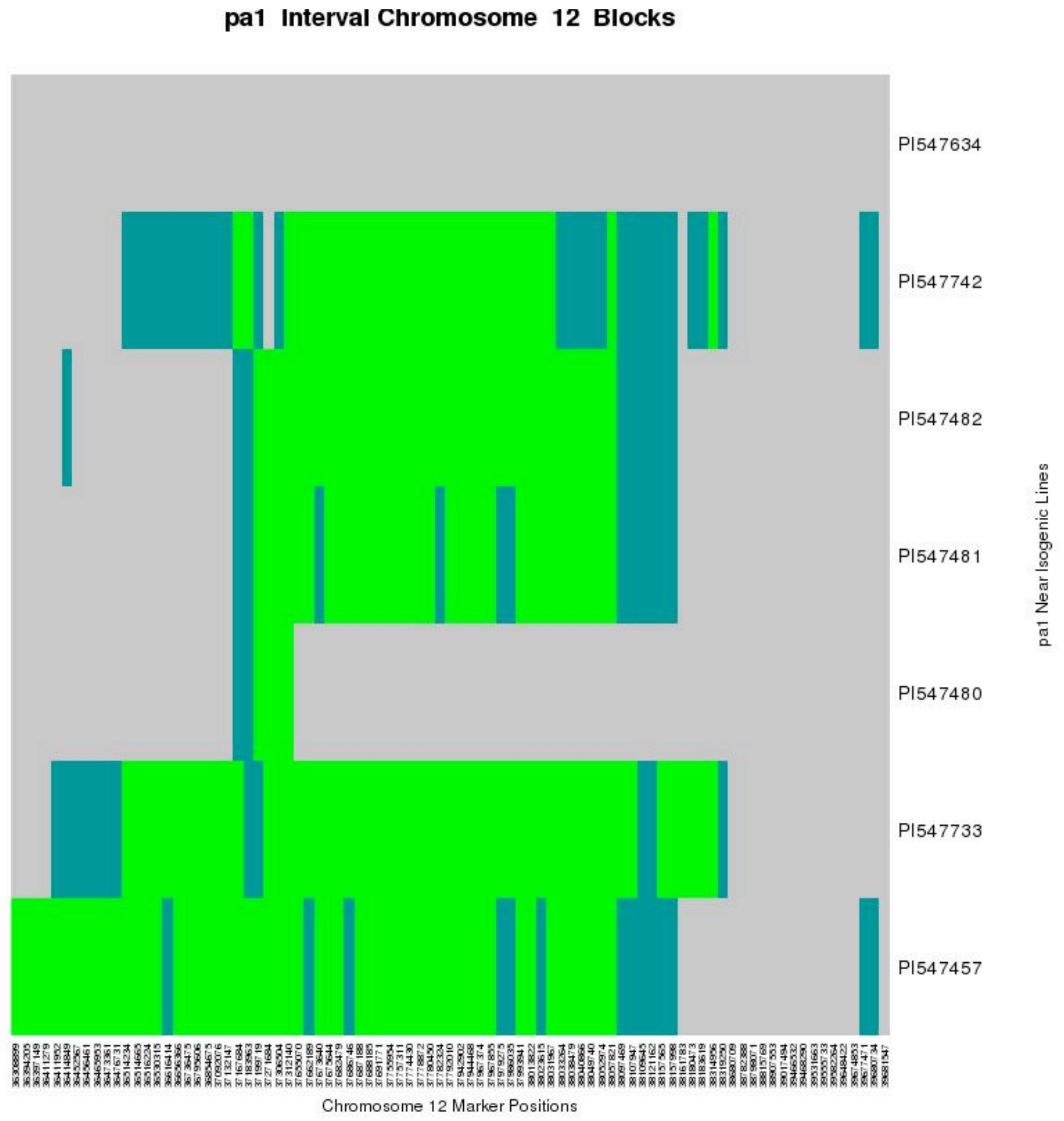
Supplementary Figure 2. 18 Interval visualization for Np (Phosphorous tolerant). The final interval selected is on chromosome 10 at positions 339795-2076591.



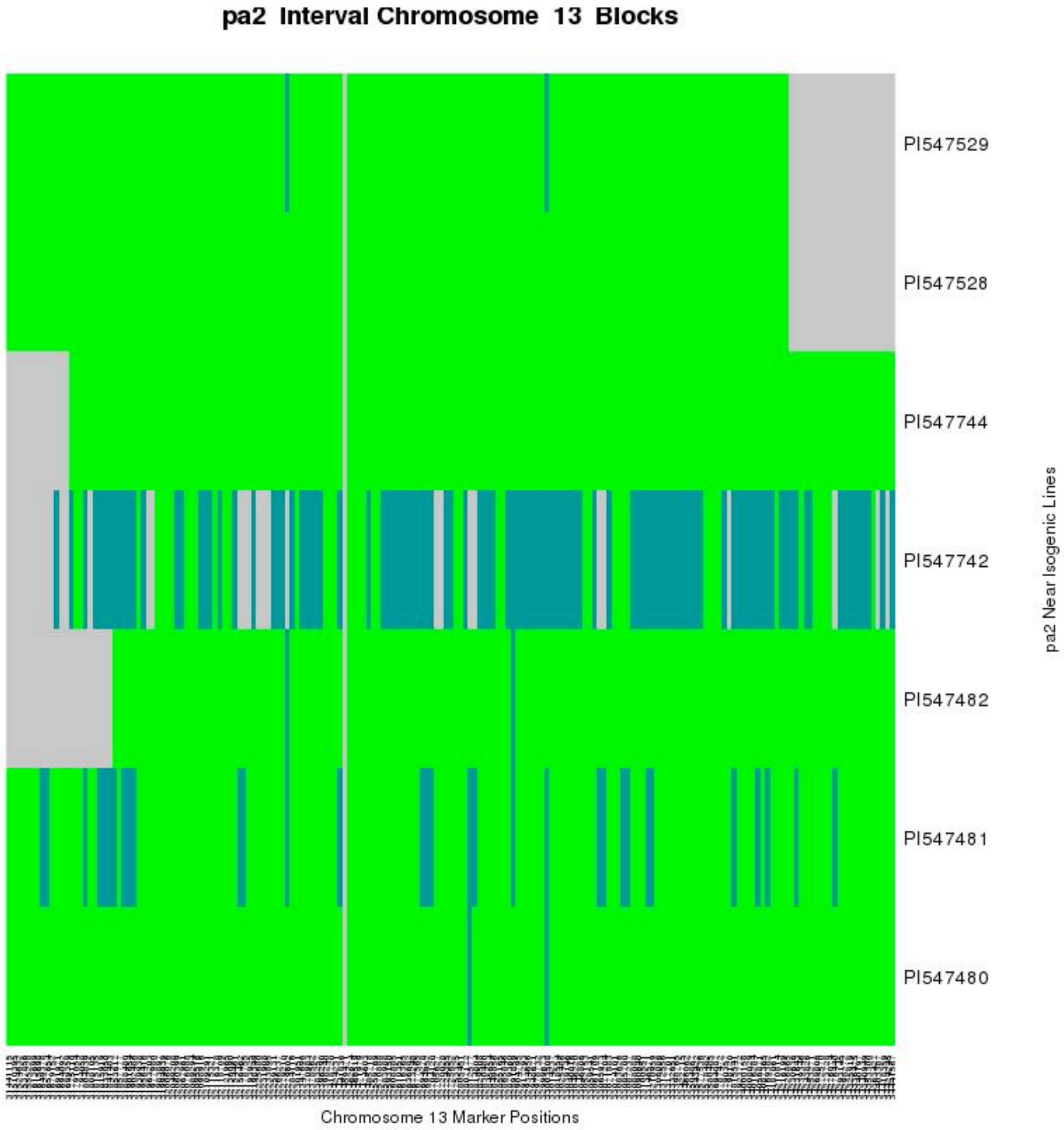
Supplementary Figure 2. 19 Interval visualization for P1 (Glabrous (Pubescence density)). The final interval selected is on chromosome 9 at positions 48200877-49558866.



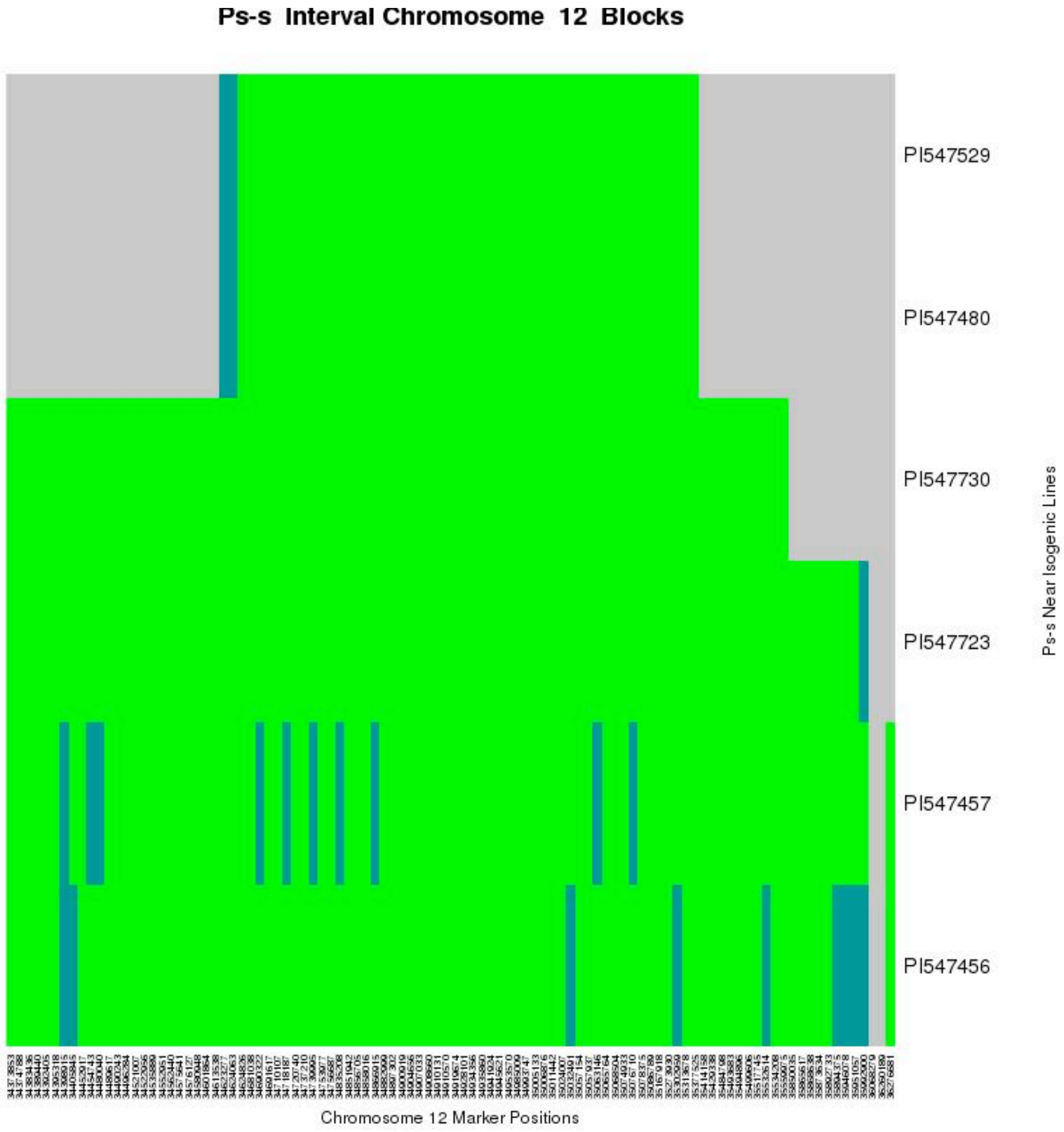
Supplementary Figure 2. 20 Interval visualization for p2 (Puberulent (Pubescence Density) dwarf seed coat cracks partly male sterile). The final interval selected is on chromosome 20 at positions 1582950-2292167.



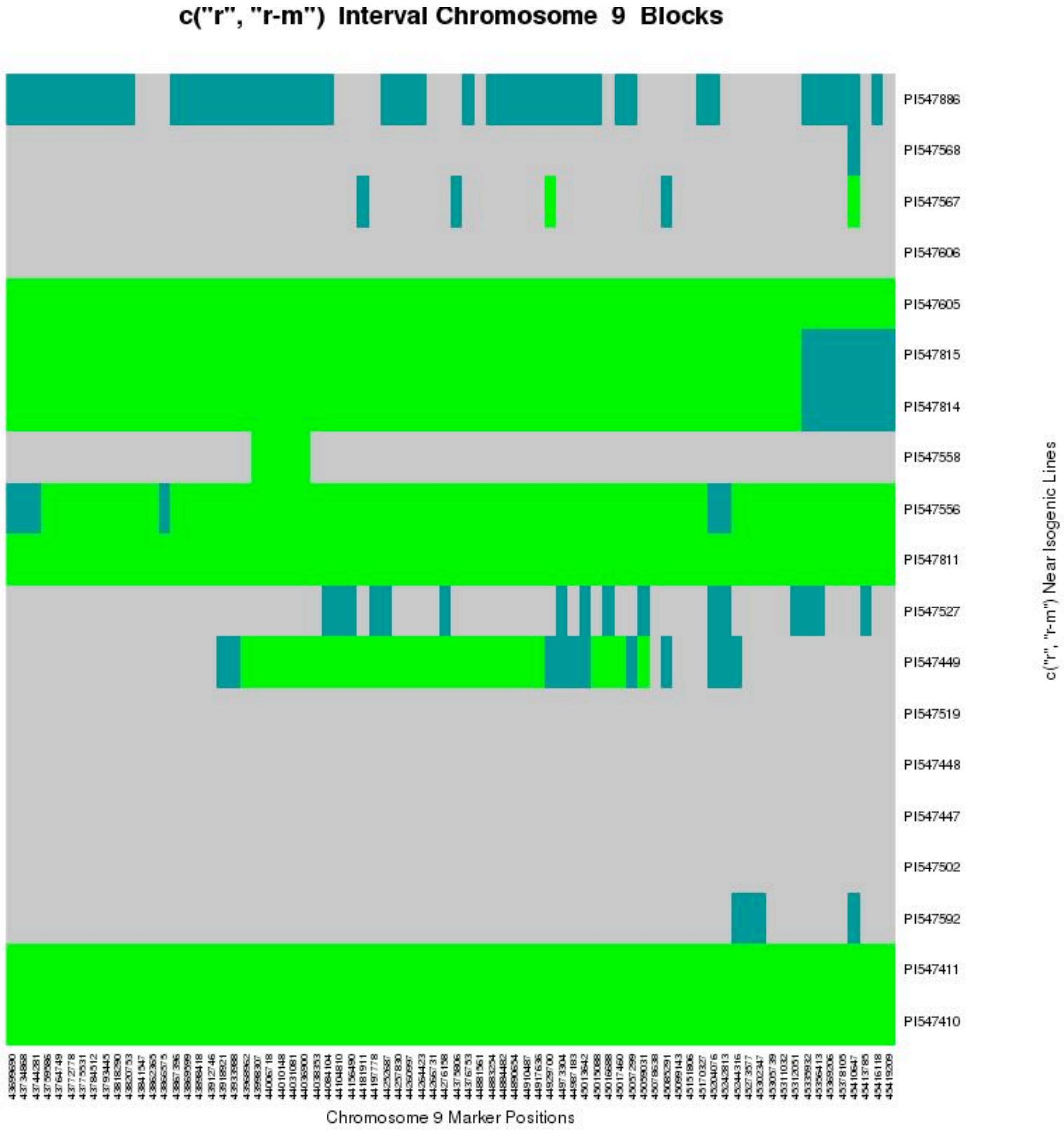
Supplementary Figure 2. 21 Interval visualization for pa1 (Semi-appressed pubescence (upper leaf surface)). The final interval selected is on chromosome 12 at positions 37092076-37662189.



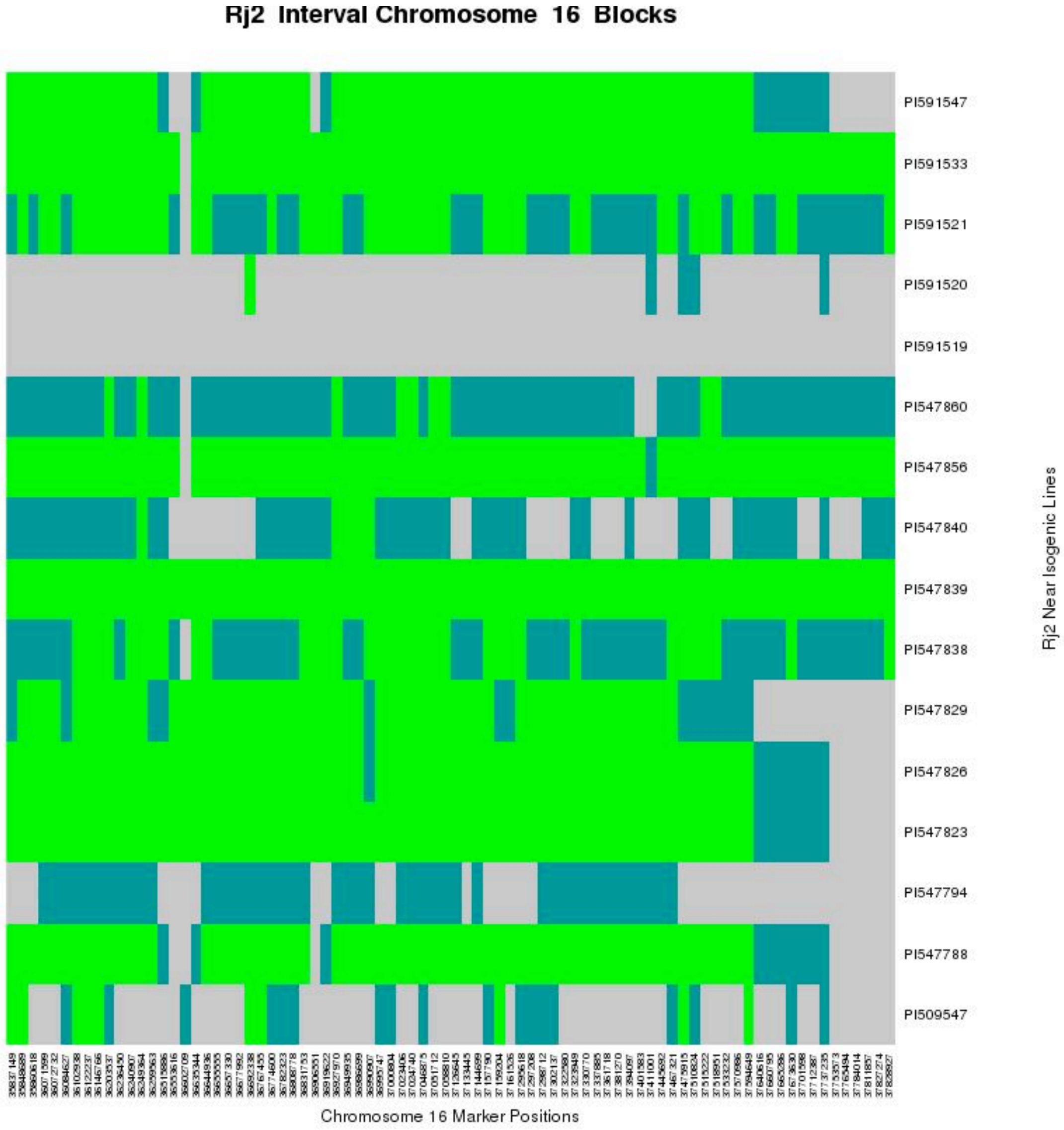
Supplementary Figure 2. 22 Interval visualization for pa2 (Appressed pubescence with pa1). The final interval selected is on chromosome 13 at positions 31833050-34231643.



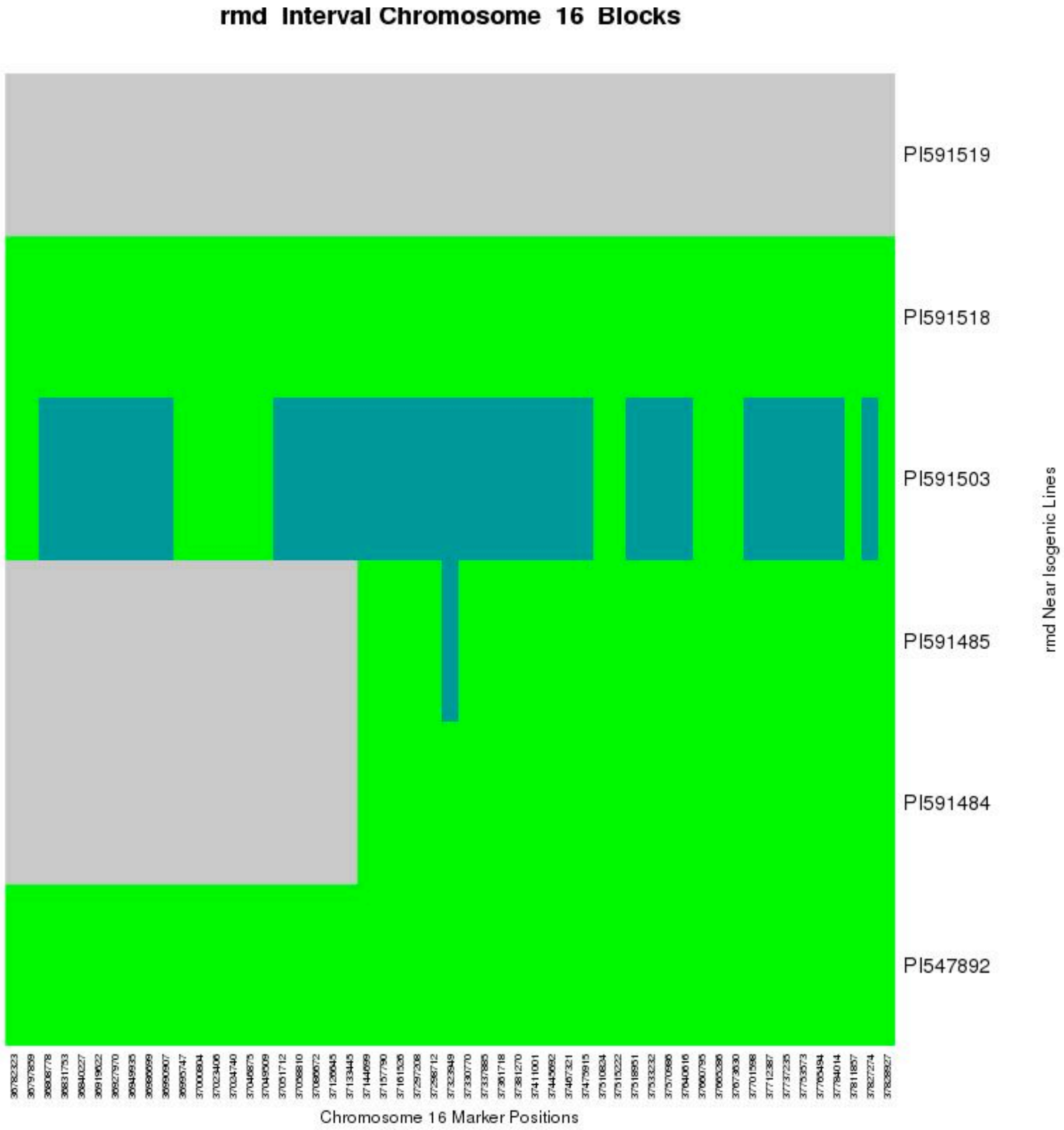
Supplementary Figure 2. 23 Interval visualization for Ps/Ps-s (Sparse pubescence). The final interval selected is on chromosome 12 at positions 34718187-34756687.



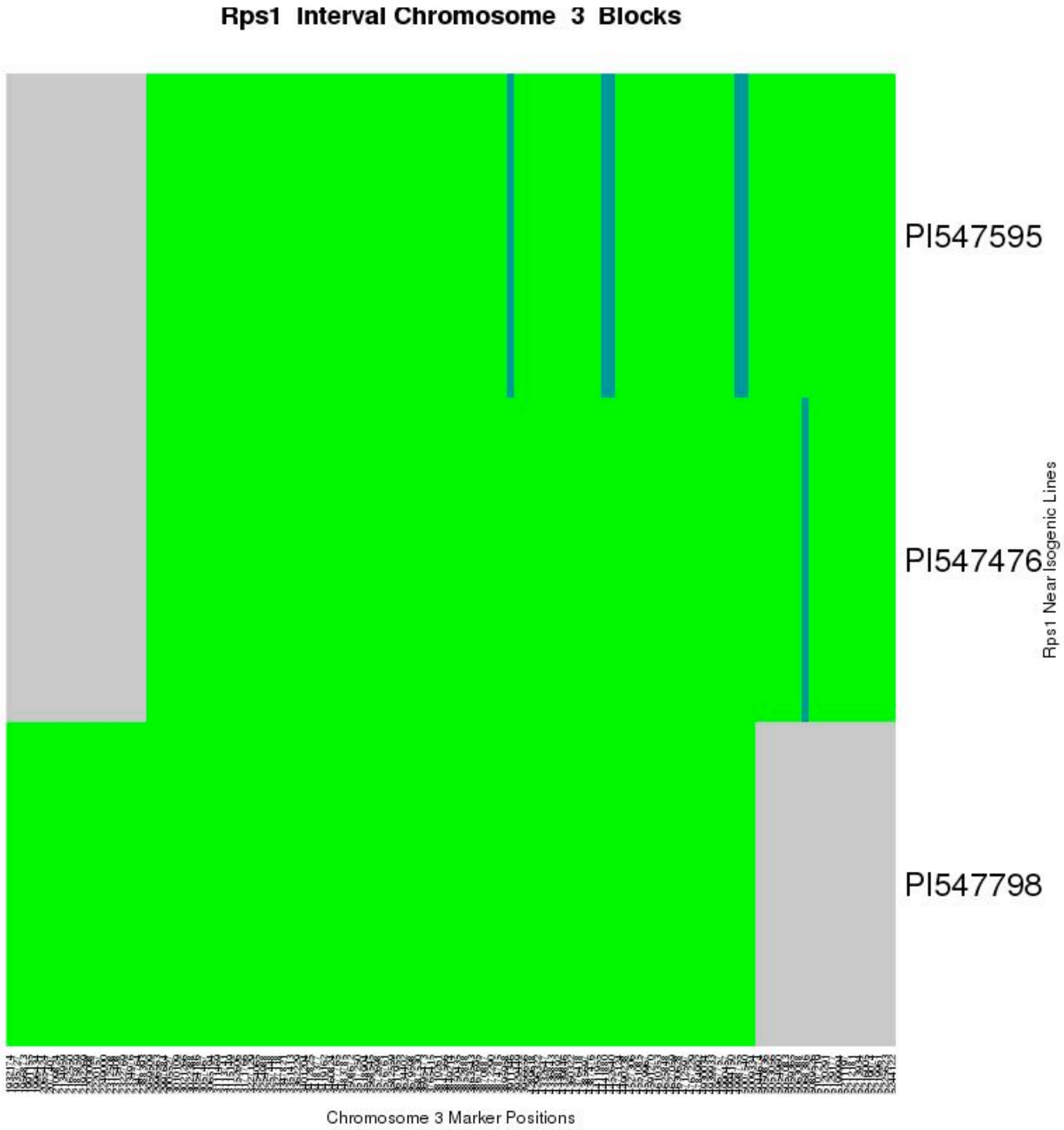
Supplementary Figure 2. 24 Interval visualization for R (Black seed pigment with T imperfect black with t W1 or buff with t w1). The final interval selected is on chromosome 9 at positions 43968962-45078638.



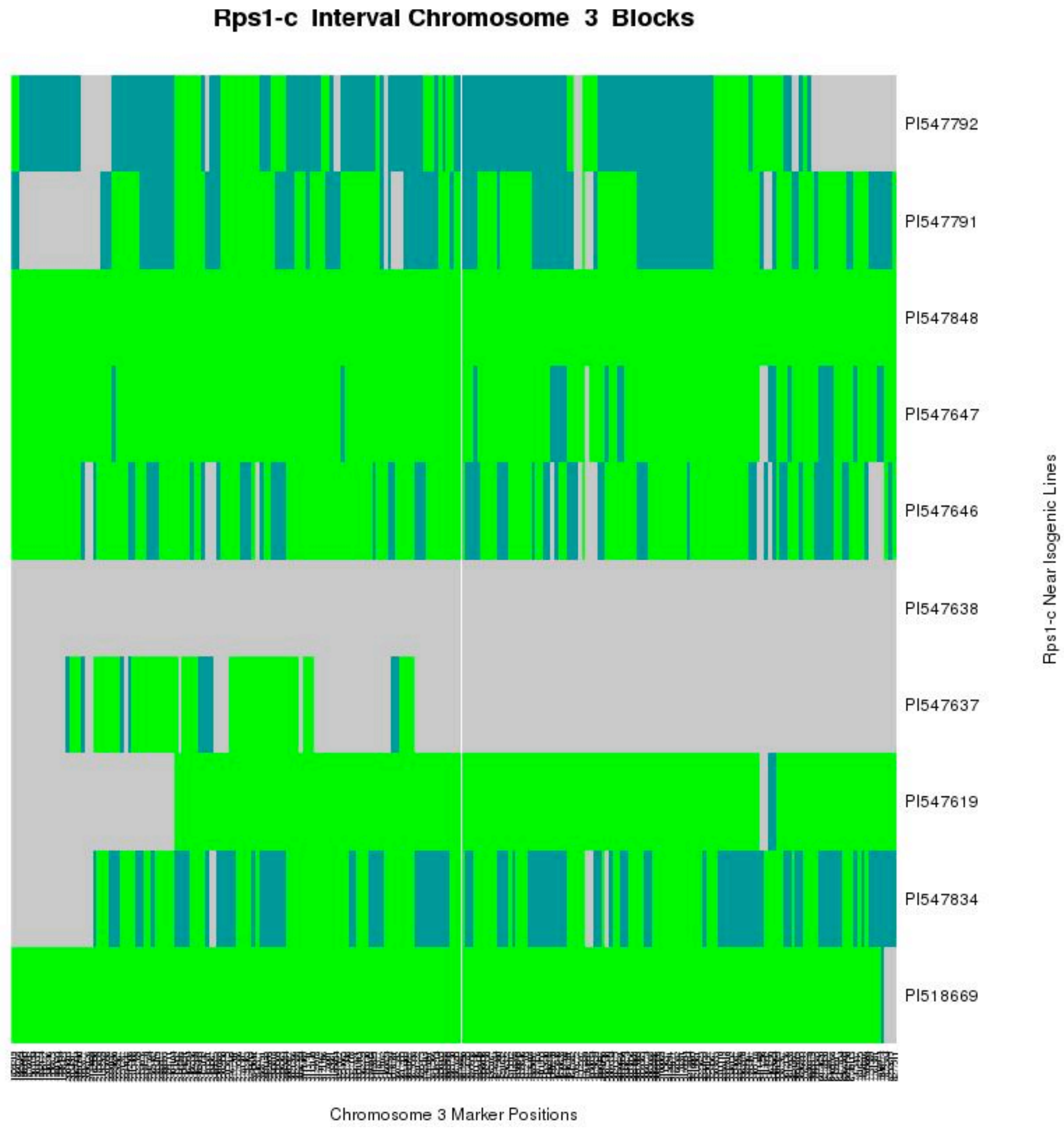
Supplementary Figure 2. 25 Interval visualization for Rj2 (Ineffective nodulation with Rhizobium strains b7 b14 and b122.). The final interval selected is on chromosome 16 at positions 36657330-37510824.



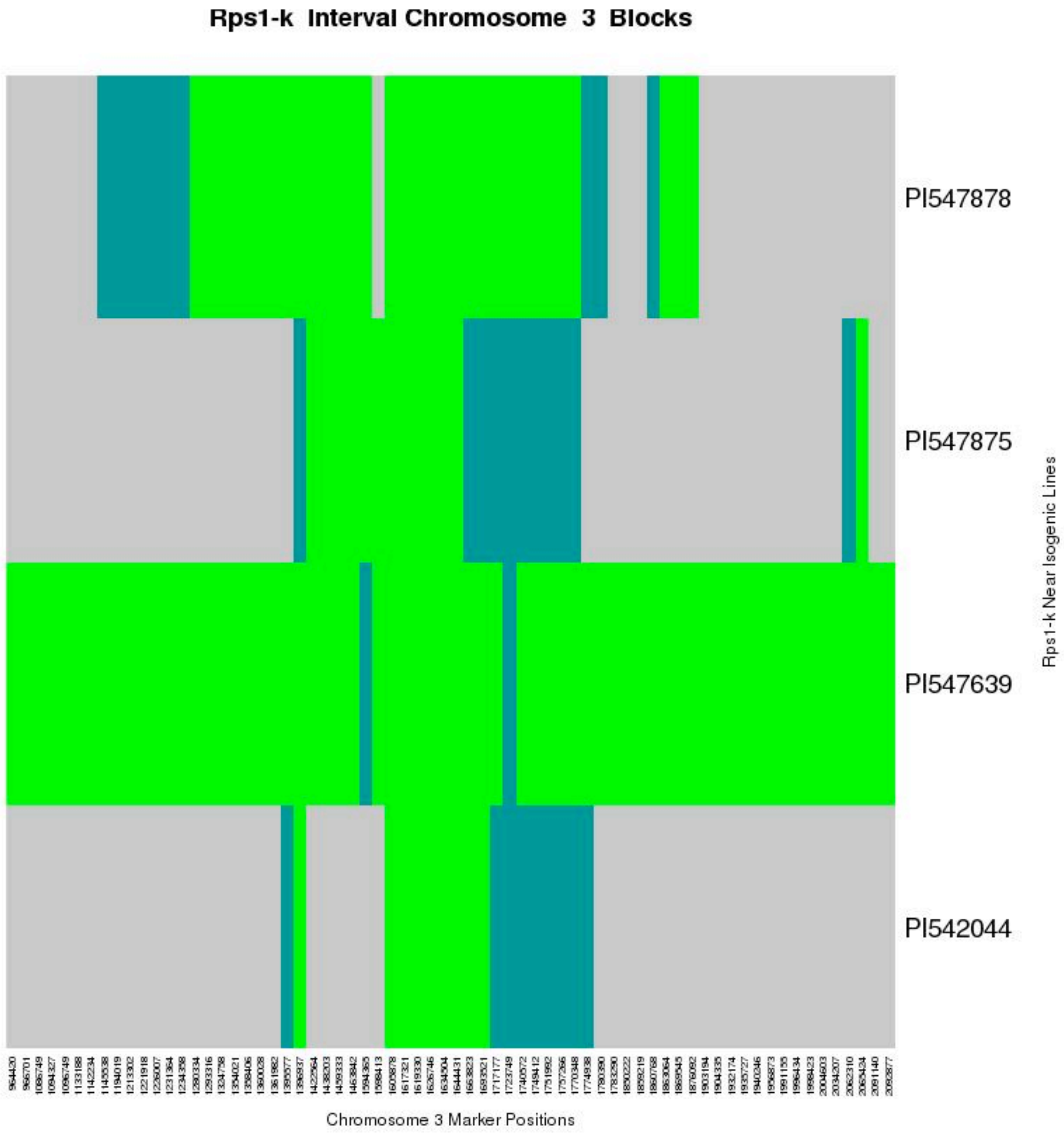
Supplementary Figure 2. 26 Interval visualization for rmd (Susceptible to powdery mildew). The final interval selected is on chromosome 16 at positions 37133445-37445692.



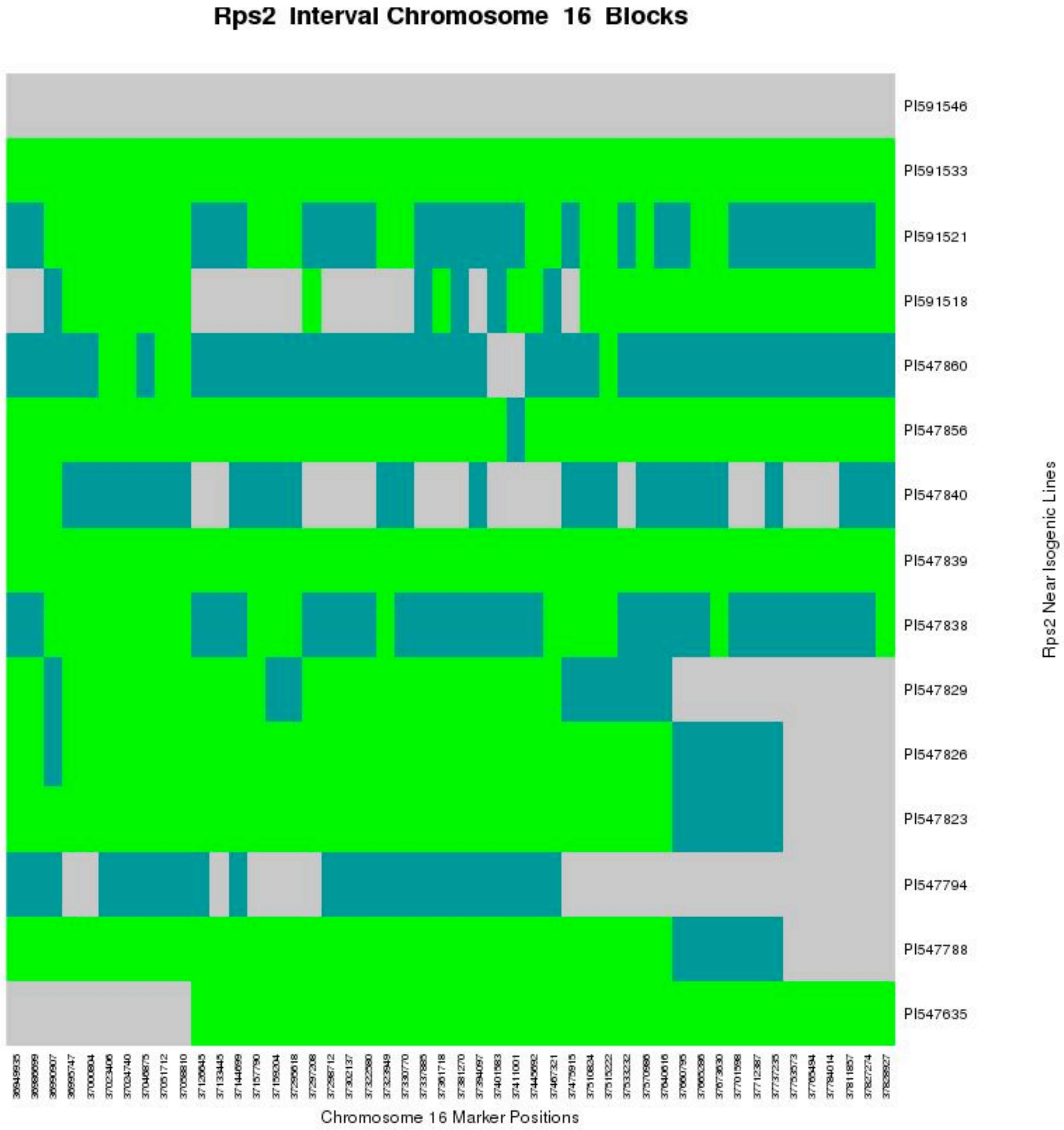
Supplementary Figure 2. 27 Interval visualization for Rps1 (Resistant to Phytophthora rot races 1 2 10 13 16.). The final interval selected is on chromosome 3 at positions 2388393-5044674.



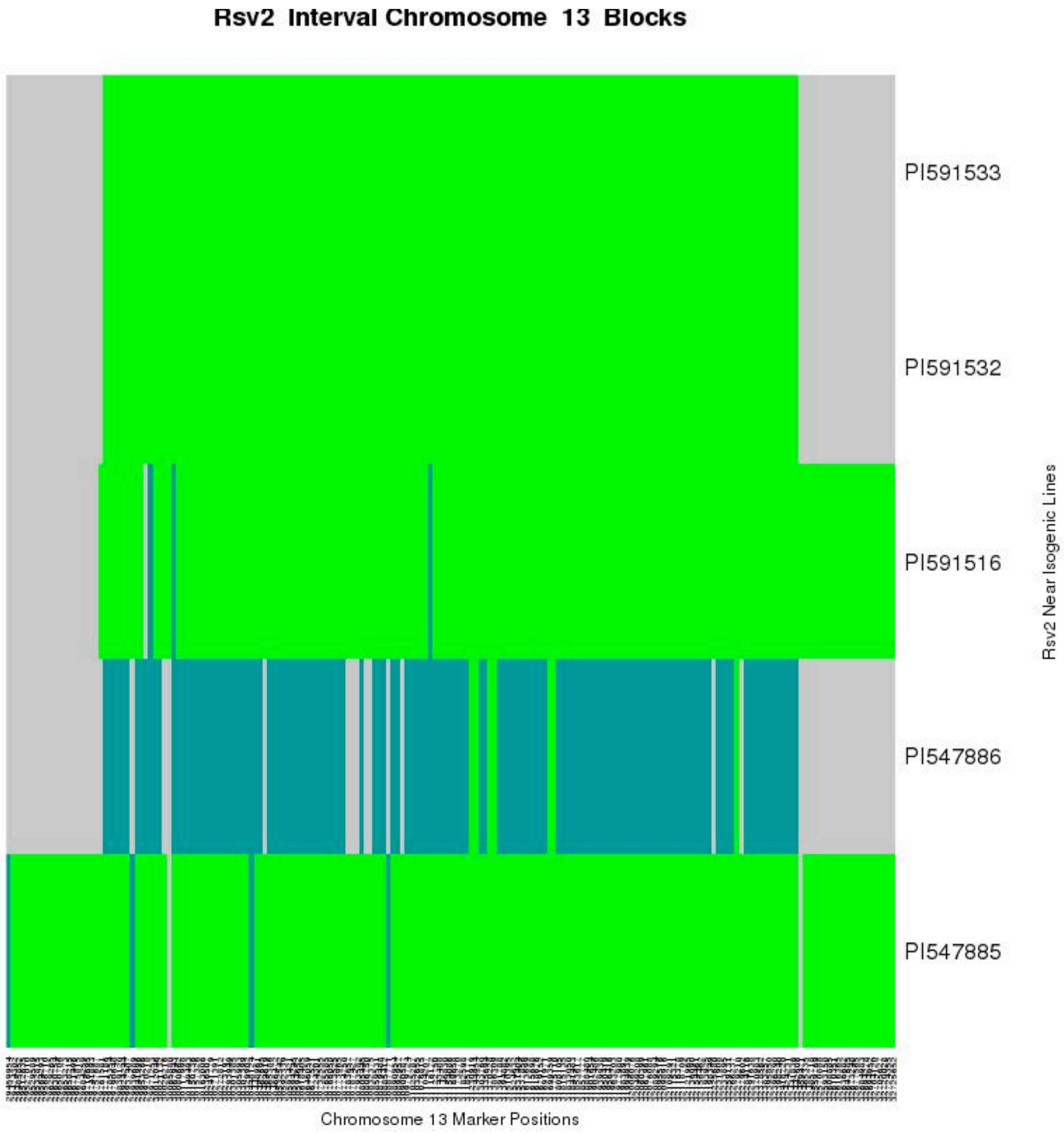
Supplementary Figure 2. 28 Interval visualization for Rps1-c, an allele of Rsp1 that aided in mapping.



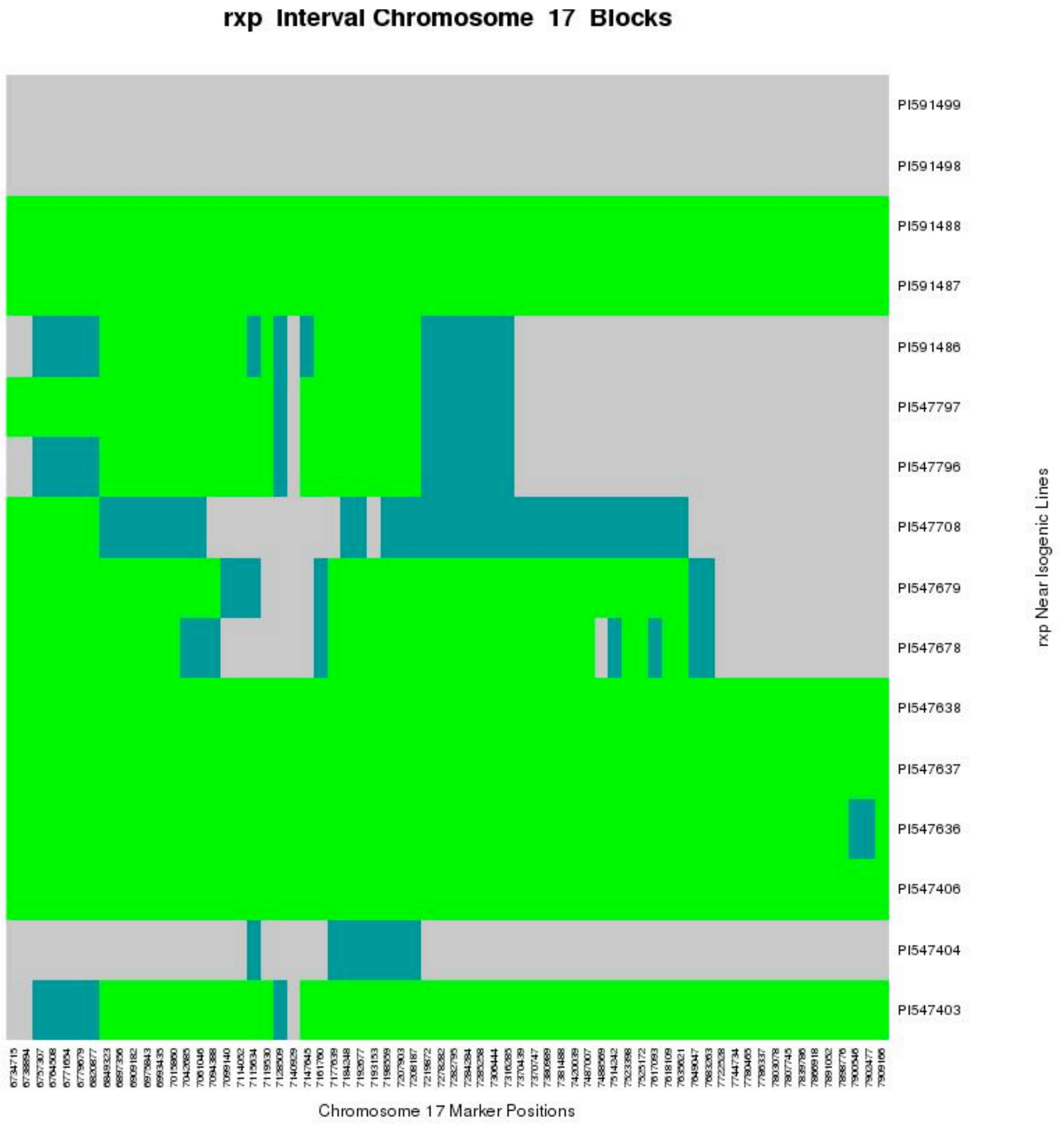
Supplementary Figure 2. 29 Interval visualization for Rps1-k, an allele of Rps1 that aided in mapping.



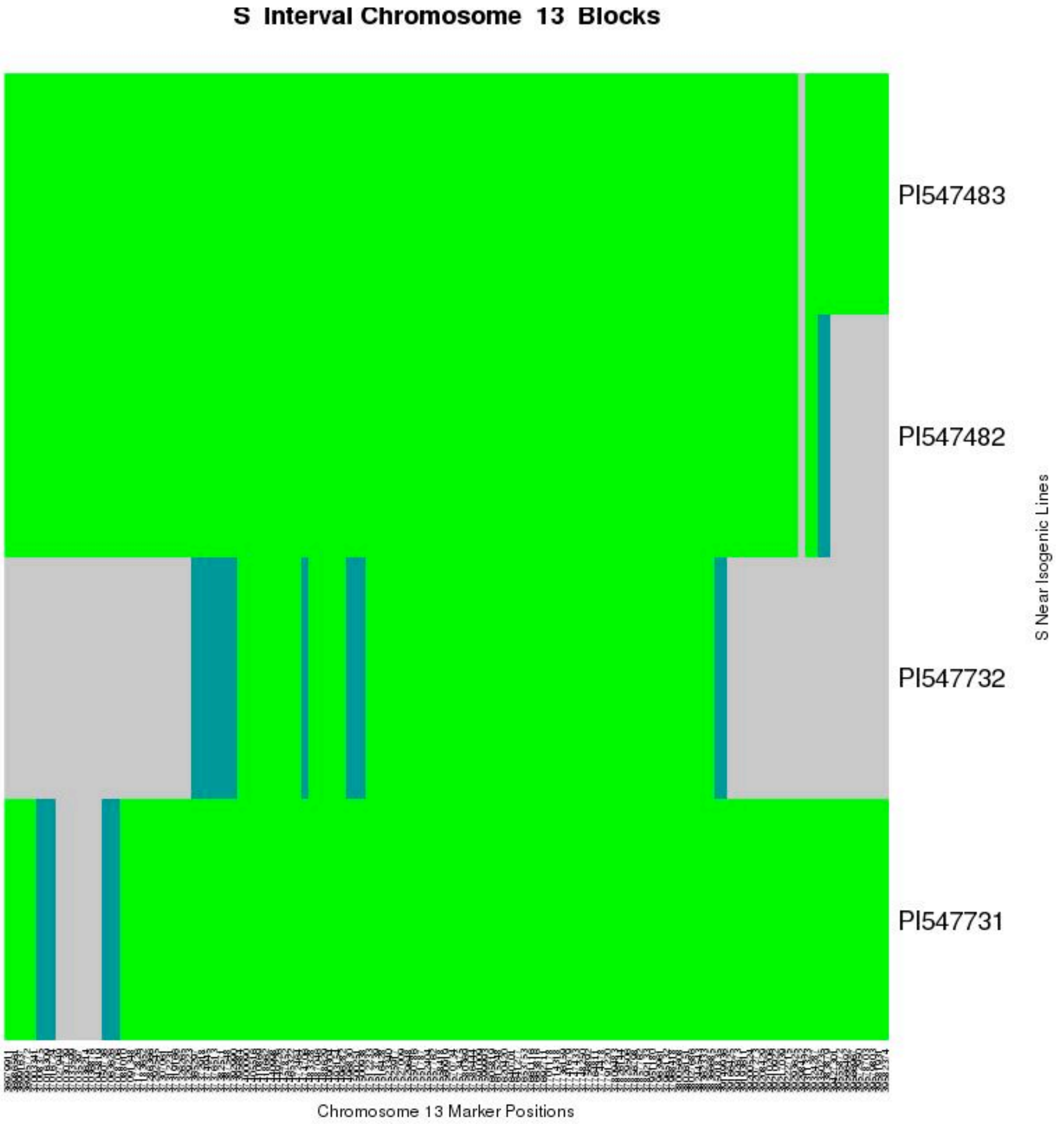
Supplementary Figure 2. 30 Interval visualization for Rps2 (Resistant to Phytophthora rot races 1-2.). The final interval selected is on chromosome 16 at positions 37323949-37510824.



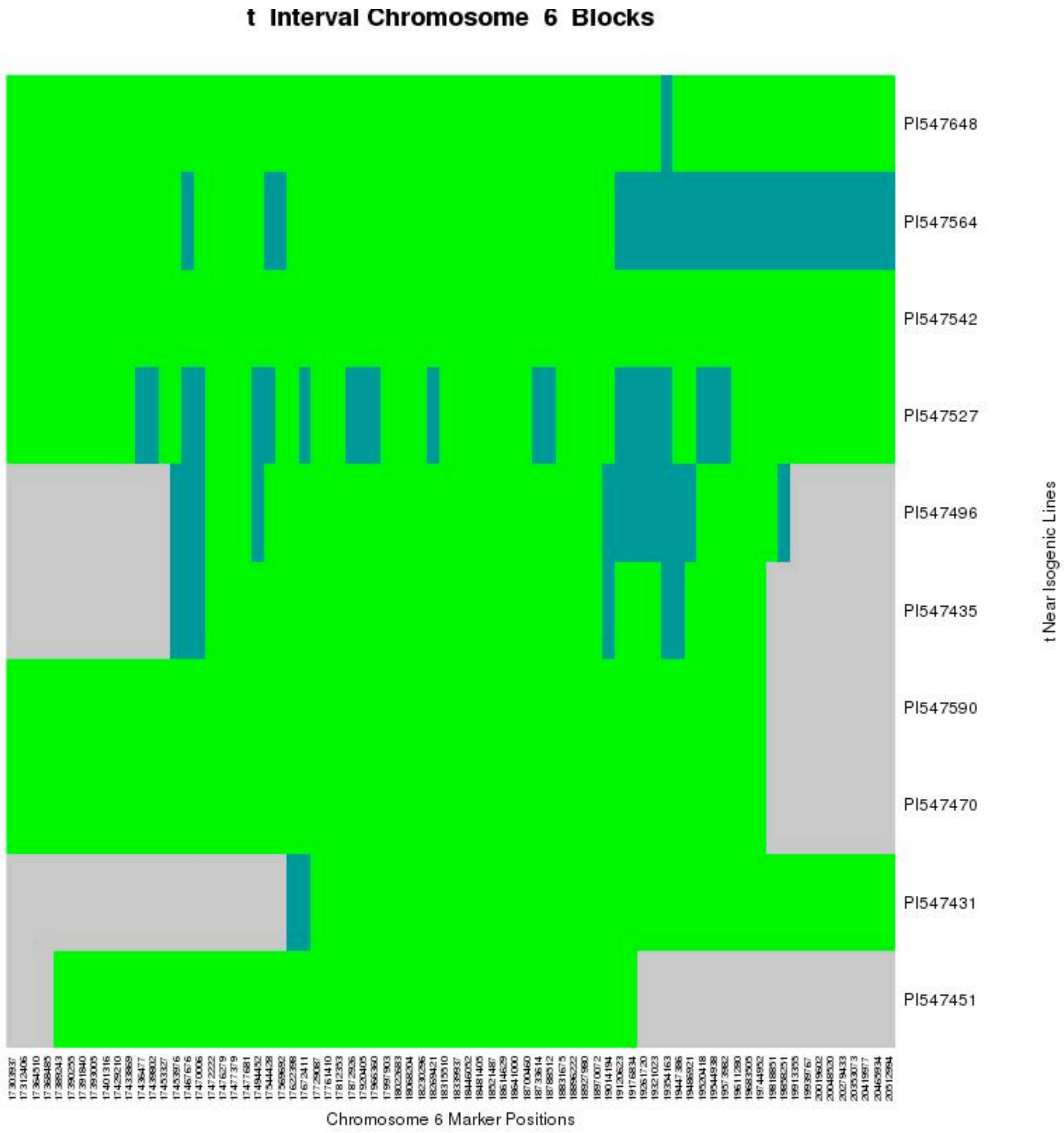
Supplementary Figure 2. 31 Interval visualization for Rsv2 (Resistant to Soybean Mosaic potyvirus Infection). The final interval selected is on chromosome 13 at positions 29761581-32459471.



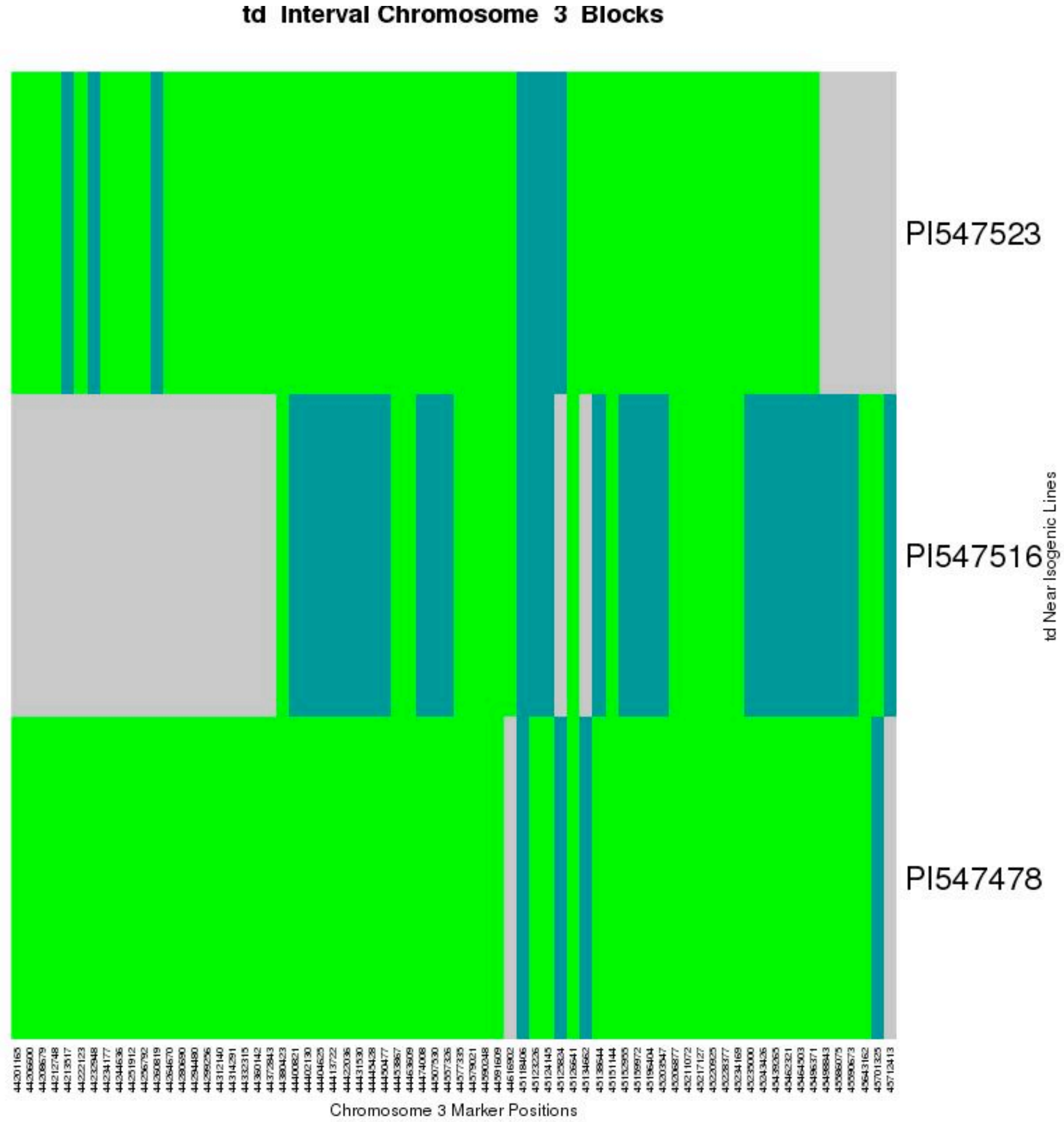
Supplementary Figure 2. 32 Interval visualization for rxp (Resistant to bacterial pustule.). The final interval selected is on chromosome 17 at positions 7128509-7514242.



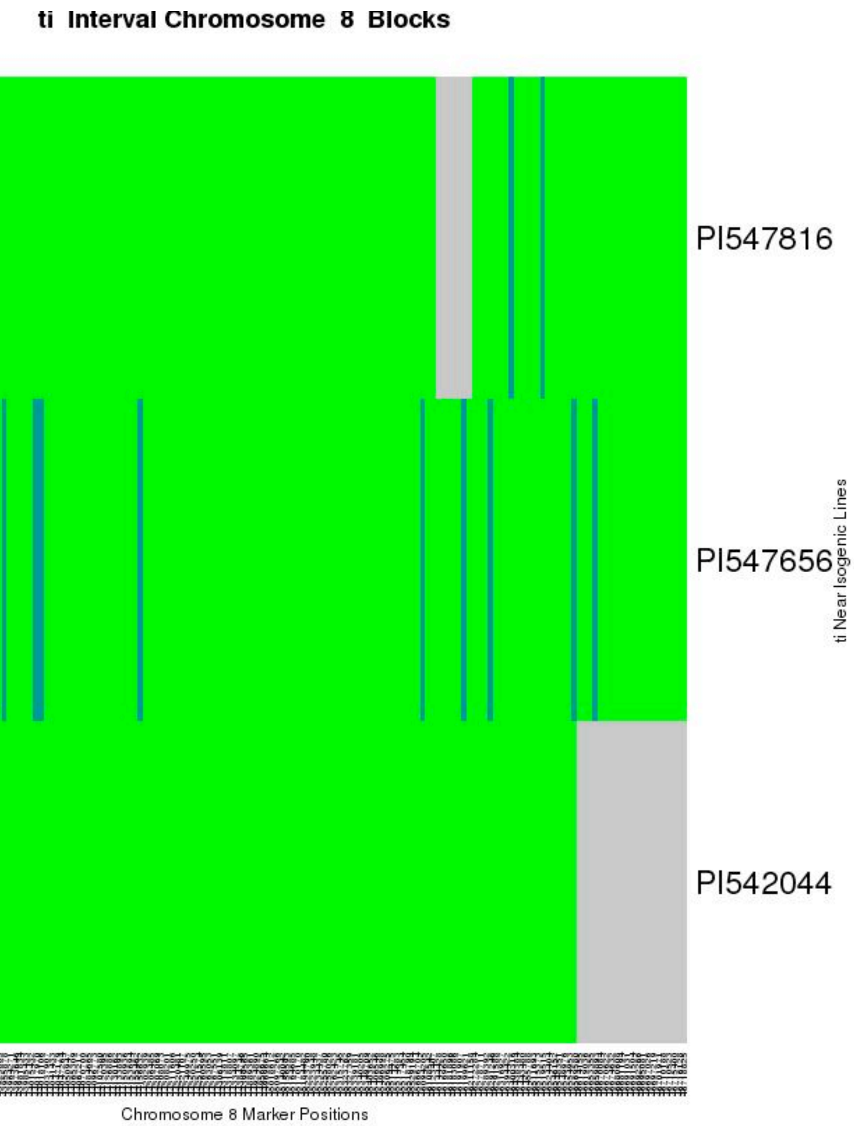
Supplementary Figure 2. 33 Interval visualization for S (Short internode length). The final interval selected is on chromosome 13 at positions 38027686-39207273.



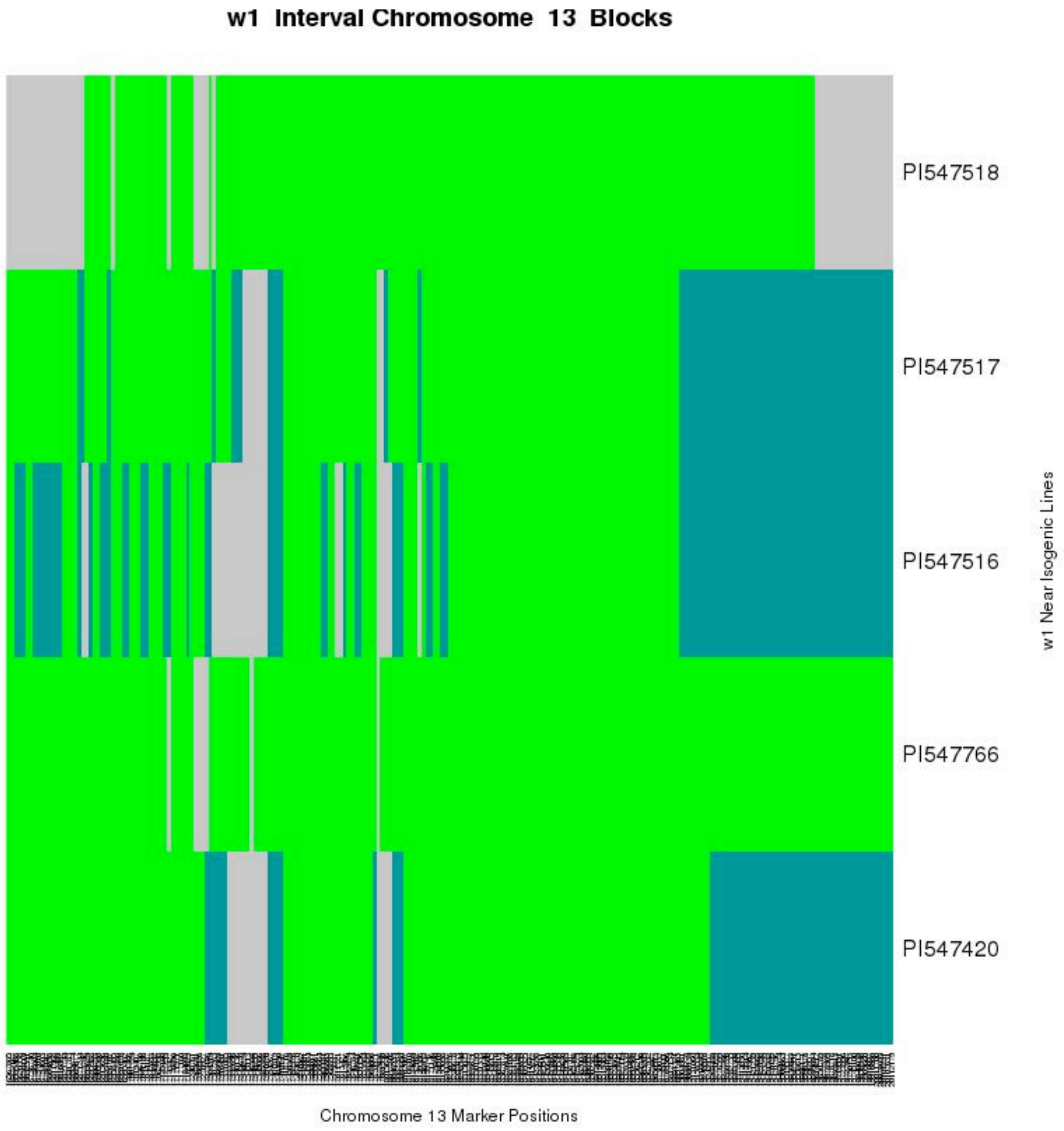
Supplementary Figure 2. 34 Interval visualization for t (Grey pubescence). The final interval selected is on chromosome 6 at positions 18481405-19120623.



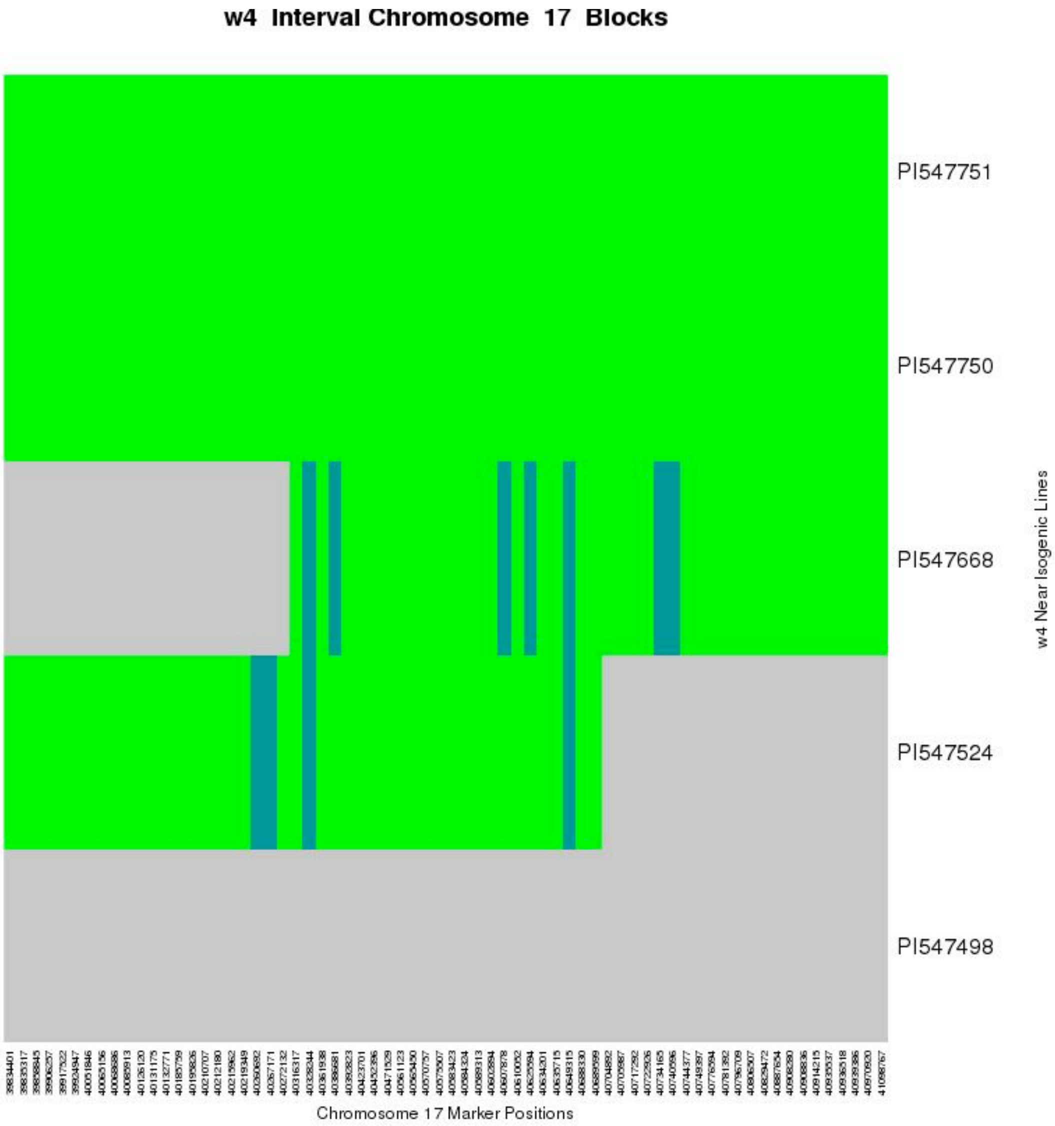
Supplementary Figure 2. 35 Interval visualization for td (Light tawny to near-grey pubescence with T). The final interval selected is on chromosome 3 at positions 43513124-45643162.



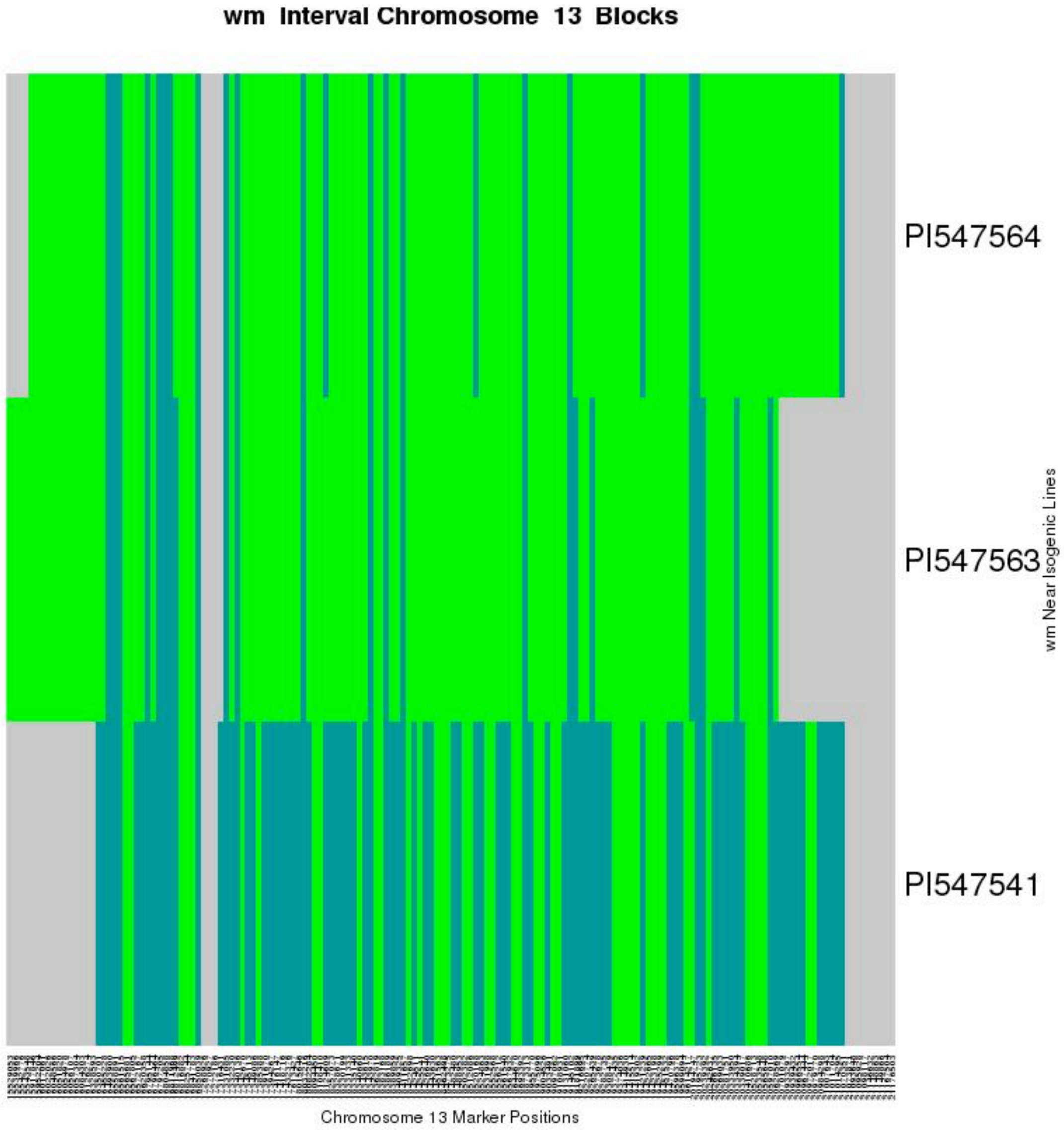
Supplementary Figure 2. 36 Interval visualization for ti (Kunitz trypsin inhibitor absent). The final interval selected is on chromosome 8 at positions 43763761-46569580.



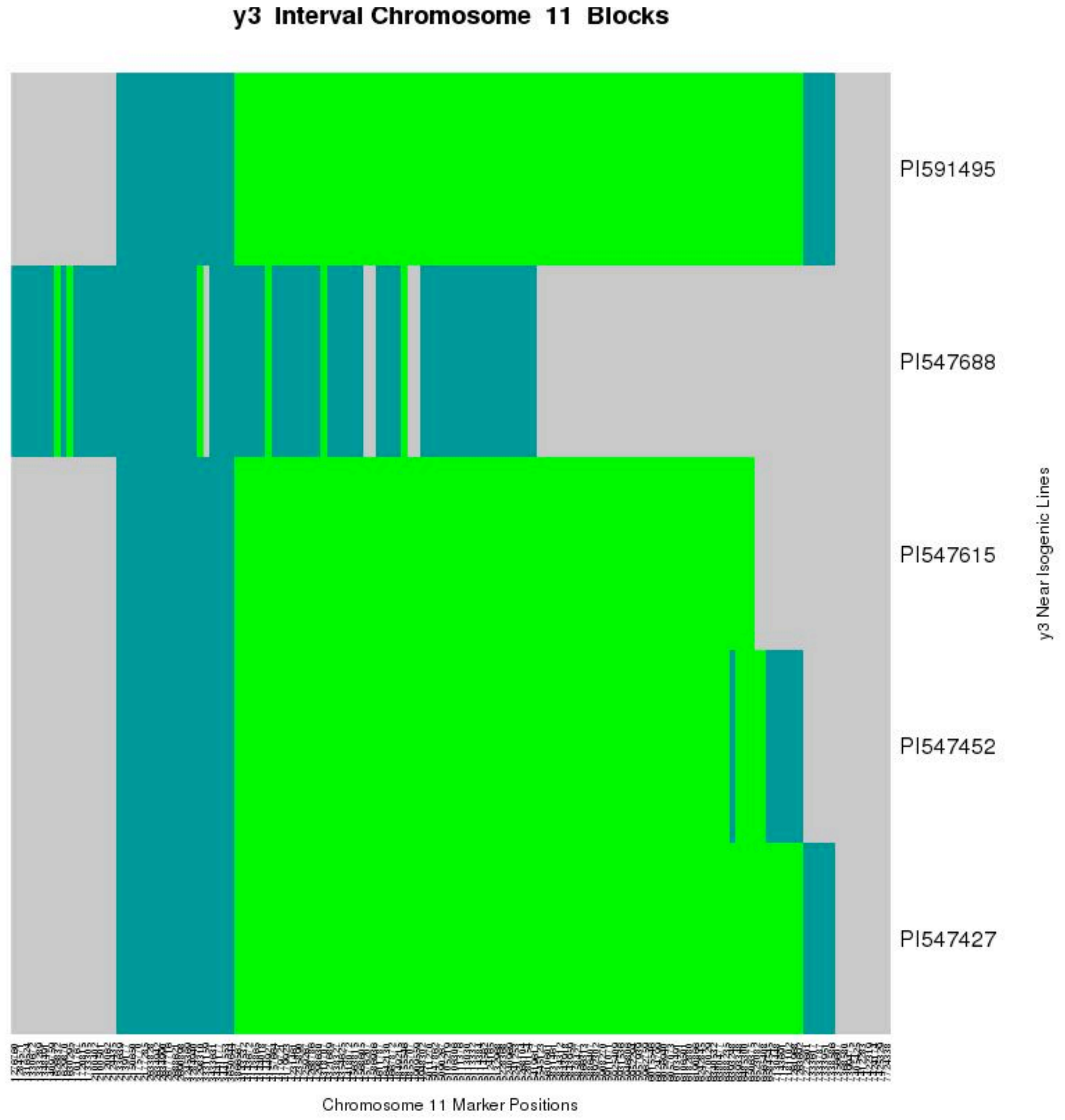
Supplementary Figure 2. 37 Interval visualization for w1 (White flower). The final interval selected is on chromosome 13 at positions 17048632-18248678.



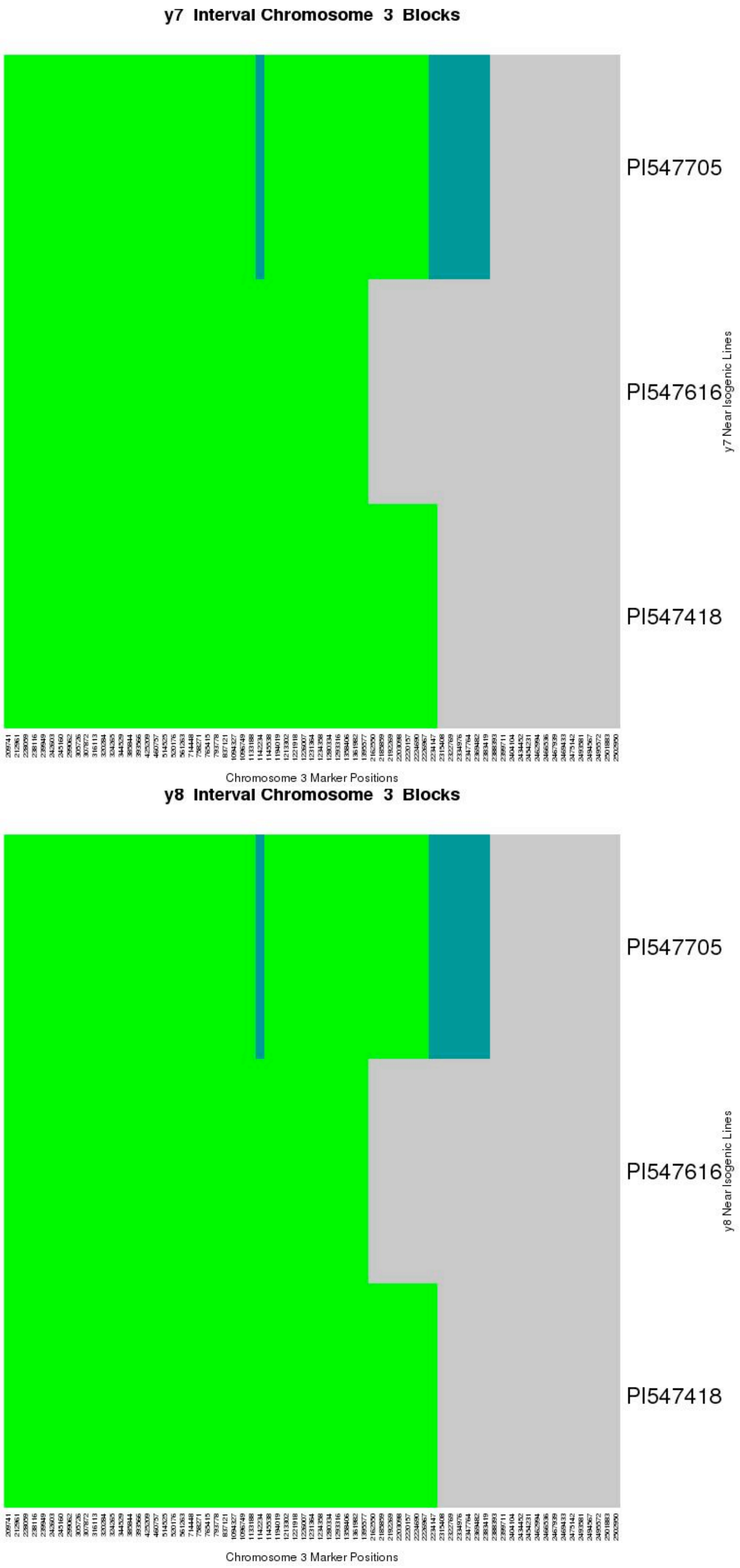
Supplementary Figure 2. 38 Interval visualization for w4 (Near-white flower). The final interval selected is on chromosome 17 at positions 40267171-40705987.



Supplementary Figure 2. 39 Interval visualization for wm (Magenta flower). The final interval selected is on chromosome 13 at positions 15543548-21073871.

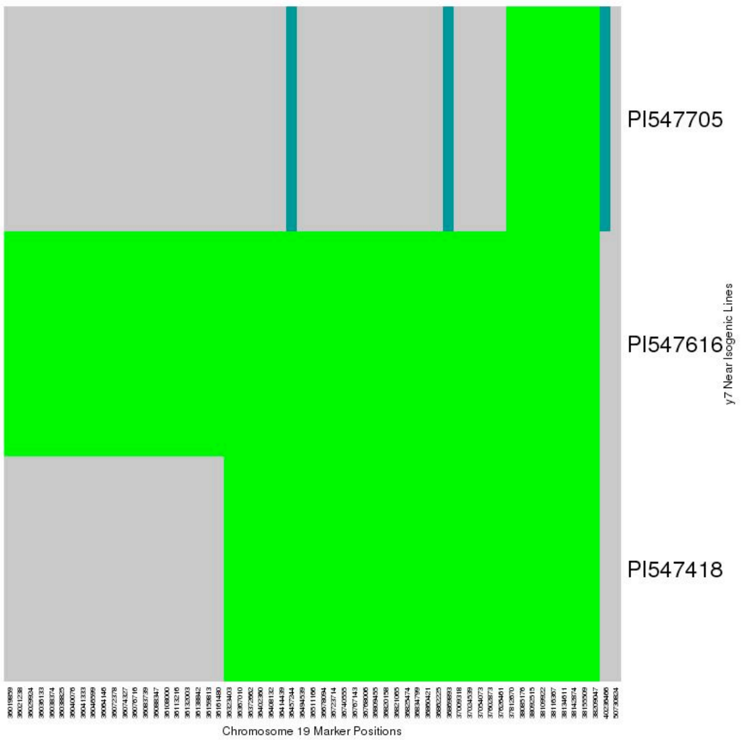


Supplementary Figure 2. 40 Interval visualization for y3 (Leaves turn rusty yellow with g). The final interval selected is on chromosome 11 at positions 2175770-6565408.

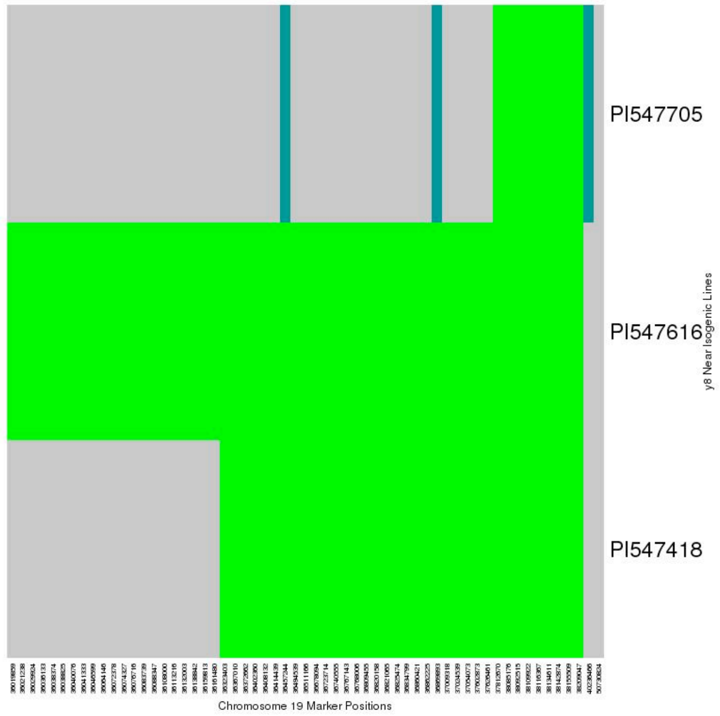


Supplementary Figure 2. 41 Interval visualization for y7/y8 (New leaves very light green in cool weather with y8). The final interval selected is on chromosome 3 at positions 561263-2315408.

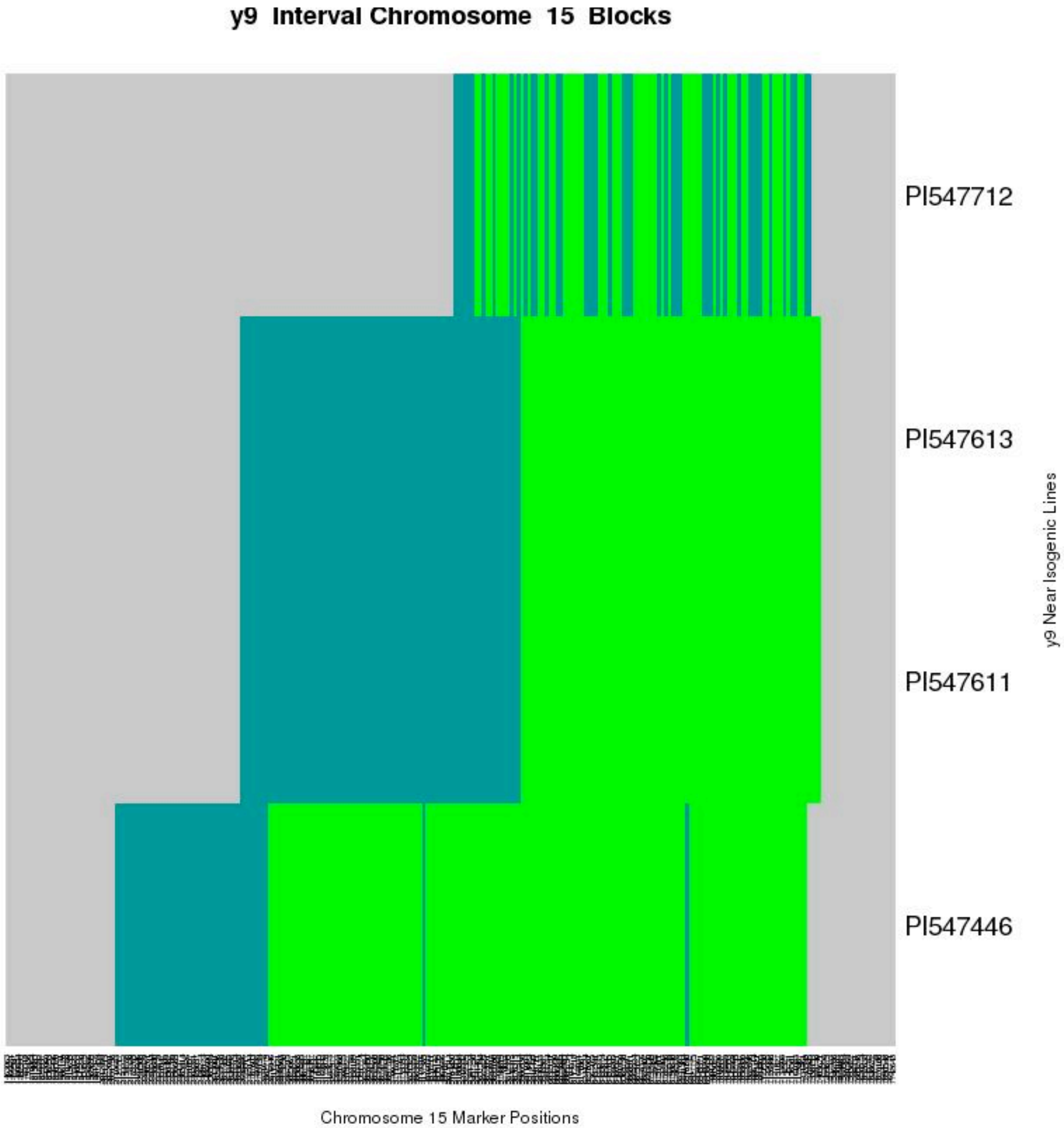
y7 Interval Chromosome 19 Blocks



y8 Interval Chromosome 19 Blocks



Supplementary Figure 2. 42 Interval visualization for y7/y8 (New leaves very light green in cool weather with y7). The final interval selected is on chromosome 19 at positions 36161480-40236466.



Supplementary Figure 2. 43 Interval visualization for y9 (Yellow-green plant). The final interval selected is on chromosome 15 at positions 1940853-7473258.