IMPROVING BREEDING SELECTION EFFICIENCY: ADVANCED POPULATION DESIGNS AND *IN VITRO* TECHNOLOGY

A Thesis

by

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ABSTRACT

Cultivar progression requires years of development prior to performance trials; reducing development time requirements as well as introgression of favorable alleles is crucial to the rapid improvement of cultivars. Multi-parental advance generation intercrossing (MAGIC) can provide improved genetic mapping resolution through increased allelic diversity and higher effective recombination frequencies. The Four Parent Maize (FPM; *Zea mays L.*) population implements a series of the strategies used in MAGIC and bi-parental populations, creating a mapping population comprised of 1,149 individuals with 118,509 markers for comparison of effects on genetic mapping resolution and accuracy of quantitative trait locus (QTL) allelic estimates. Measurements were recorded for plant height (PH), ear height (EH), days to anthesis (DTA) and silking (DTS) in seven environments spanning three years. While increasing the generations of intermating prior to selection does not increase the phenotypic distribution among the dihybrid subpopulations, it does increase the mapping resolution of QTL for EH, DTA and DTS. Using association mapping software we have identified an allele from Tx903 on chromosome 3 which decreased plant and ear height, by 4.2 and 3.7 cm, respectively. Additionally, an allele that decreases flowering time by one day was donated by Tx903 and Tx772. The detection of these QTL have previously been reported in the same region, but the allelic effect has yet to be validated. Although a single QTL was found for each quantitative trait, it is expected that many additional QTL are present; but were undiscovered due to the conservative nature of the Bonferroni multiple test correction criteria. Linkage map construction will improve estimates of the effects of multiple founders and advance generation intermating on increased effective recombination and resulting accuracy in QTL estimation and mapping resolution.

Cycling of plant cells *in vitro* could reduce generation times required for new cultivar development. Carrot (*Daucus carota)* and tobacco (*Nicotiana tabacum)* species were selected for their extensive tissue culture history and high tolerance toward *in vitro* manipulation. Isolation of parental protoplasts from cell suspensions was followed by sorting of individual cells through fluorescence activated cell sorting (FACs); expectantly allowing for production of totipotent single cell derived colonies. Supposed colonies could be designated, with marker assisted selection for further *in vitro* cycling or regeneration and advancement to performance trials. Demonstrating that single cells can be isolated, can divide to form cell colonies, and can be genotyped and regenerated is central to testing the proposed hypothesis of Cycling of Gametes *in Vitro (CoGiV)* as conceivable. This will warrant further testing towards development of procedures intended for *in vitro* gametogenesis induction.

DEDICATION

To my girlfriend Lauren for showing me love, support and understanding while I follow my passion. Also to my parents for supporting me through all life’s endeavors and giving me encouragement to follow my dreams.

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NOMENCLATURE

BC	Backcross
BLUP	Best linear unbiased predictor
CoGiV	Cycling of gametes *in vitro*
DH	Doubled haploid
FACs	Florescence activated cell sorting
FPM	Four parent maize
GEI	Genetic environmental interaction
LOD	Logarithm of odds
MAGIC	Multi-parental advance generation intercrossing
MAS	Marker assisted selection
PCV	Packed cell volume
RIL	Recombinant inbred line
SI	Support interval
SNP	Single nucleotide polymorphism
QTL	Quantitative trait locus/loci

TABLE OF CONTENTS

Page

LIST OF FIGURES

LIST OF TABLES

Page

1. INTRODUCTION

World population size is projected to expand by greater that nine billion people by the year 2050 (FAO, 2013), resulting in a necessity to produce improved cultivars at a faster, and more efficient rate to meet the demands of the growing population. Quantitative trait locus (QTL) are frequently used by breeders to select and introgress favorable loci into their breeding populations while reducing the evaluation of unwanted entries. Traditionally, QTL are estimated using bi-parental mating designs, in which, a single cross is made between two selected parental lines and individuals are selfed down to recombinant inbred lines for phenotypic evaluation. Such mating designs require less labor and resources to produce a mapping population than more advanced mating designs, but result in QTL with low precision and reduced confidence in effect estimates.

Development of mapping populations utilizing greater than two founder lines increases allelic diversity within the population broadening the level of the genome that can be evaluated due to increased polymorphisms within the population (Huang, et al., 2015; Mott, et al., 2000). Additionally, advanced generations of intermating increases the frequency of effective recombination events that can be captured within the population increasing the resolution of QTL mapping (Darvasi and Soller, 1995; Lee, et al., 2002). The combination of these mating methodologies results in the production of multi-parent advance generation intercrossed (MAGIC) populations to improve the resolution and precision of mapping QTL allowing greater opportunities to analyze the underlying alleles/genes that controlling complex, quantitative traits in many species

(Bandillo, et al., 2013; Dell'Acqua, et al., 2015; Huang, et al., 2012; Kover, et al., 2009; Sannemann, et al., 2015). The four parent maize (FPM) population provides a unique opportunity to evaluate elements of advanced mating designs (increased founder numbers, degree of intermating prior to inbreeding), as well as population size on mapping QTL to important agronomic traits.

Furthermore, breeders must develop new varieties capable of competing with genetic gains equivalent to the standard 10 to 20 years in the future (Shimelis and Laing, 2012). Implementation of marker assisted selection, genomic selection, gene introgression, off season nurseries, grafting and clonal propagation have allowed breeders to complete several generations of improvement within one calendar year, as well as decrease time intervals required to complete generation advancements (Harfouche, et al., 2012; Lee and Tracy, 2009). Development of new technologies, such as *in vitro* cell cycling (De La Fuente, et al., 2013; Murray, et al., 2013), utilizing fluorescence activated cell sorting will allow the selection and growth of varieties through generations advancement and selection under cultured conditions. Refinement of cell cycling protocols, successful *de novo* gametogenesis and application of marker assisted selection will provide a novel technology in rapid acceleration of generation time requirements in cultivar development.

2. QUANTIFICATION OF AGRONOMIC TRAITS CHARACTERIZED IN THE FOUR-PARENT MAIZE MAGIC POPULATION

2.1 Introduction

Since the advent of agriculture, breeders have progressively developed plants to satisfy humanities requirements through artificial selection of advantageous traits. Until the last quarter century, such advances in crop production were based on visible phenotypic analysis methods, leading to fixation of favorable alleles for highly heritable traits through selection. Consequently, present-day breeders are now faced with the challenges of selecting for complex traits with small effects in order to make gains in crop improvement. Statistical estimations of loci which correlate to phenotypic variation of a trait and the effects of such loci, known as quantitative trait loci (QTL), are now achievable due to advances in genotype-by-sequencing technologies and statistical analysis software. Complex traits are thought to be quantitative in nature, that is, the overall trait phenotype is due to multiple QTL of varying effect magnitude that collectively produce the overall phenotype. Thus, breeders have developed several population designs in order to achieve high resolution mapping of molecular markers and the statistical power necessary to detect true QTL with accurate estimates.

To identify QTL, linkage mapping populations are constructed generally following a bi-parental mating scheme in which two parental lines are crossed to produce offspring (F_2; backcross, BC; and recombinant inbred line, RIL) segregating for the traits of interest. Though effective at detecting QTL, bi-parental based populations are restricted in allelic diversity and recombination events. Advance generation intermating and multi-parental designs have been implemented to overcome the limitations of traditional mapping populations.

Intermating before inbreeding, demonstrated in the intermated B73 x Mo17 maize population (IBM), can increase recombination frequency by a magnitude of 2.7 within 3 generations, causing an increase in genetic resolution and map distance (Lee, et al., 2002). Additionally, population development with greater than two founders broadens the allelic diversity available for any given trait while increasing recombination events and decreasing linkage disequilibrium (Huang, et al., 2012). Multi-parental advanced generation intercross (MAGIC) populations have been developed to eliminate the drawback of bi-parental designs through the incorporation of multiple founder mating followed by subsequent intermating before inbreeding. A maize MAGIC population is expected to result in higher mapping resolution, greater power in detecting minor QTL and the ability to dissect several minor QTL disguised as a major QTL as compared to a traditional bi-parental population structure in mapping.

The Four Parent Maize (FPM) MAGIC RIL population was developed via four founders through one "funnel path", producing four multi-parental subpopulations of varying generations of intermating and two bi-parental subpopulations. The goals in development of this FPM population resource within this thesis include: (i) evaluation of quantitative traits in the FPM population; (ii) a genome wide association study (GWAS) approach to detecting QTL conditioning quantitative traits; (iii) detection and estimation of QTL effects correlated to quantitative agronomic traits (plant height, ear height, flowering time, leaf rolling); and (iv) evaluation of the mapping resolution across subpopulations and the effects of intermating on mapping resolution.

2.2 Literature Review

2.2.1 Effects of Intermating within RIL Populations on QTL Mapping

A recombinant inbred line is the result of a bi-parental cross of two inbreds followed by several generations of selfing, resulting in near-completely homozygous progeny whose genome is a combination of the parental alleles. RIL populations have several advantages; the ability to obtain a broad range of phenotypic variation among individuals, fixation of alleles resulting in individuals being genotyped once, and proper partitioning of error due to individual, environment, and measurement variability by phenotyping multiple individuals (Broman, 2005). Unfortunately, QTL mapping of traditional biparental RIL and F_2 populations are limited in the amount of allelic diversity and effective/detectable recombination that can be achieved from the parental lines (Korte and Farlow, 2013) necessary to detect the small effect QTL involved in quantitative agronomic traits.

Several populations have been designed to combat such issues by incorporating multi-parent, as well as, successive generations of intermating before inbreeding. The intermated B73 x Mo17 (IBM) population displayed a 2.7-fold increase in recombination frequency after five successive generations of intermating, leading to a 91% increase in genetic resolution (Lee, et al., 2002). Additionally, advanced intercrossed RILs (AI-RILs) have increased recombination events, resulting in reduced QTL support intervals, increasing the power to detect multiple small effect QTL that would routinely appear as one large effect QTL (Balasubramanian, et al., 2009). An extension of AI-RILs, integration of multiple parental lines have led to the development of multi-parental advanced generation inter-cross (MAGIC) populations with improved mapping resolution and greater genetic diversity in Arabidopsis (Kover, et al., 2009), rice (Bandillo, et al., 2013), wheat (Huang, et al. 2012; Mackay, et al. 2014), mice (Consortium, 2012) and very recently maize (Dell'Acqua, et al., 2015). Currently MAGIC populations have provided a basis for precision fine-mapping through high density maps.

2.2.2 Association Mapping

Association mapping is a statistical approach based on linkage disequilibrium between markers and QTL through correlations between genetic and phenotypic variation (Mackay and Powell, 2007). Unlike linkage mapping, association mapping follows the identical-by-state approach to define genetic marker data (Würschum, 2012) allowing the exploitation of historical recombination events through the utilization of a diverse population (Yu and Buckler, 2006). Although association studies can also be a helpful approach in analyzing multi-parent populations that do not follow the traditional methods of linkage population construction, population structure, false discovery rate and QTL support interval cannot be overlooked.

Population structure can result in varying allele frequencies between unidentified subpopulations, due to genetic drift, domestication or background selection, resulting in LD between unlinked loci (Ersoz, et al., 2009). Population structure must be accounted for within association studies as it can create false positives (type I error) in marker-trait associations (Zhao, et al., 2007). Population structure can also arise within a MAGIC population if the development of the population is done using limited funnel paths (>1) and deriving progeny from a small sample of individuals across a limited funnel structure (Huang, et al., 2015). Several methods have been widely used to overcome population stratification: genomic control (Devlin, et al., 2001), case control structural association (SA-model) (Pritchard, et al., 2000), quantitative trait structural association (Q-model) (Camus-Kulandaivelu, et al., 2006; Thornsberry, et al., 2001), and unified mixed model approach (Q+K) (Yu, et al., 2006).

Once associations are found, a significance threshold must be determined to reduce the false-positive (type I error) discovery rate of QTL accounting for the multiple testing issues. Historically, the highly conservative Bonferroni significance thresholds have been used in association studies which results in increased type II errors and loss of detection power if markers are in LD (Johnson, et al., 2010). Permutation tests (Churchill and Doerge, 1994), which are non-parametric, are one preferred avenue for setting significance p-values, unfortunately they are computationally demanding and time consuming. Consensus has not been made on alternative methods of setting the false discovery threshold and many other methods are currently being explored including false discovery rate (FDR) procedure (Benjamini and Hochberg, 1995; Verhoeven, et al., 2005), Bayesian approach (Efron and Tibshirani, 2002; Wakefield, 2007), underlying LD structure (Duggal, et al., 2008), and effective number of tests (M_{eff}) approach (Cheverud, 2001; Galwey, 2009; Gao, et al., 2008).

Once QTL are detected, a support interval (SI) is needed to estimate location and genomic coverage of the QTL. Similar to defining QTL significance thresholds, support interval (SI) estimation methods vary. Likelihood (likelihood of odds ratio, LOD) support intervals (Dupuis and Siegmund, 1999; Lander and Botstein, 1989; Ott, 1999) define the genetic location of the furthest marker on either side of a QTL peak that is within a specified LOD difference of the peak, and are most commonly used. Although the standard likelihood SI is 1-LOD, simulations have shown that as marker density increases, greater LOD intervals are necessary to attain 95% coverage of QTL (Manichaikul, et al., 2006). Additionally, there is interest in using the logarithm of posterior distribution (LPD) to construct the Bayes credible interval, as it does not need to be adjusted for samples size, marker density or QTL effect size (Sen and Churchill, 2001). Most recently, the linear model method is being used in association panels, in which markers flanking QTL are added to a linear model one at a time until the QTL regains significance, defining the boundary of one side of the SI (Kump, et al., 2011; Tian, et al., 2011).

2.2.3 Genetic Architecture of Quantitative Traits in Maize

Maize is an outcrossing species that has adapted to a wide range of climates from the tropics to temperate regions, allowing it yo be grown across the world. Maize experienced a duplication of a paleopolyploid ancestor 70 million years ago (Paterson, et al., 2004) followed by a separation from its closest relative Sorghum (Paterson, et al., 2009) five to twelve million years ago through tetraploidization (Blanc and Wolfe, 2004; Swigonova, et al., 2004), resulting in an estimated one third of all maize genes being present in multiple locations throughout the genome (Gaut, 2001). Furthermore, the sequenced B73 maize genome is composed of ~85% transposable elements and at 2.3 Gb in size, it is more than twice as large as its' relative sorghum (Schnable, et al., 2009). Roughly 10,000 years ago, maize was domesticated from its wild ancestor teosinte (*Zea mays* subsp. parviglumis) (Hufford, et al., 2012). Such gene duplication and high non-collinearity (Fu and Dooner, 2002; Springer and Stupar, 2007) across maize lines has resulted in abundant genetic diversity within the available germplasm for quantitative traits.

Maize flowering time (FT) genetic architecture is a highly heritable adaptive trait. Unlike sorghum, in which flowering time is controlled by a few large effect photoperiod-sensitivity loci (Lin, et al., 1995; Mullet and Rooney, 2013; Mullet, et al., 2012); maize FT genetic architecture consists of many small effect additive QTL that are stable across environments (Buckler, et al., 2009). Several FT QTL have been identified that co-localize with known genes (ZmCCT (Hung, et al., 2012), DLF-1 (Salvi, et al., 2007), ZCN8 (Muszynski, et al., 2006), zmm22 (Kaeppler, et al., 2014), Vgt1 and ZmRap2.7 (Salvi, et al., 2007)) explaining variation in maize vegetative to reproductive transition. Although high haplotype diversity and rapid LD decay within regions make identifying causative polymorphisms for maize FT challenging (Romay, et al., 2013).

Plant height is another of the highly heritable traits in maize, with variation explained by a very large number of small additive effect QTL; although large effect height genes exist, they have likely been fixed during domestication and early selection (Peiffer, et al., 2014). Plant height is an important trait in many agronomic crops (wheat, rice, etc.) for increasing yield potential through selection for reduced overall height, which increases harvest index and reduces losses to lodging (Khush, 2001). This practical variability combined with the ease of phenotyping and high-heritability has made identification of causative polymorphisms for height important. Over 40 genes have been shown to have large effects on plant height when mutated, many of which are involved in biosynthetic pathways of auxin (Multani, et al., 2003), gibberellin (Hartwig, et al., 2011; Lawit, et al., 2010; Winkler and Helentjaris, 1995) and brassinosteriods (Hartwig, et al., 2011). Additionally, plant (61%) and ear (56%) heights have significant positive correlations to maize grain yield in commercial varieties when grown in semi-tropical Texas environments (Farfan, et al., 2013) and where little research has been conducted on identification of maize QTL.

Leaf rolling has been observed in a number of cereal species (wheat, rice, barely, sorghum and maize) in response to water deficits, high air temperature and photo intensity of the sun (Kadioglu and Terzi, 2007). Leaf rolling benefits the plant by either reducing the “effective” leaf area (Begg, et al., 1980) or by creating a humid boundary layer limiting transpiration (Oppenheimer, 1960). Leaf rolling in maize is associated with higher air temperatures and positively correlated to leaf water potential (Ψ_w), in which leaf rolling is initiated when leaf water potential drops below Ψ_w= -0.480 MPA (Fernandez and Castrillo, 1999). Leaf rolling QTL have been mapped in rice (Price, et al., 1997), indicating a leaf rolling scaling system (O'Toole and Cruz, 1980) can effectively explain leaf roll variation and should be adaptable to mapping QTL in maize.

2.3 Materials and Methods

2.3.1 Four-Parent Maize Population

The Four-Parent Maize (FPM) population is comprised of 1291 individual recombinant inbred lines (RIL), derived from a variety of mating schemes involving four parental inbred lines (Figure 1). Tx903 and Tx906 were selected for their independent sources of blue aleurone trait. Tx772 was incorporated for decreased susceptibility to aflatoxin.

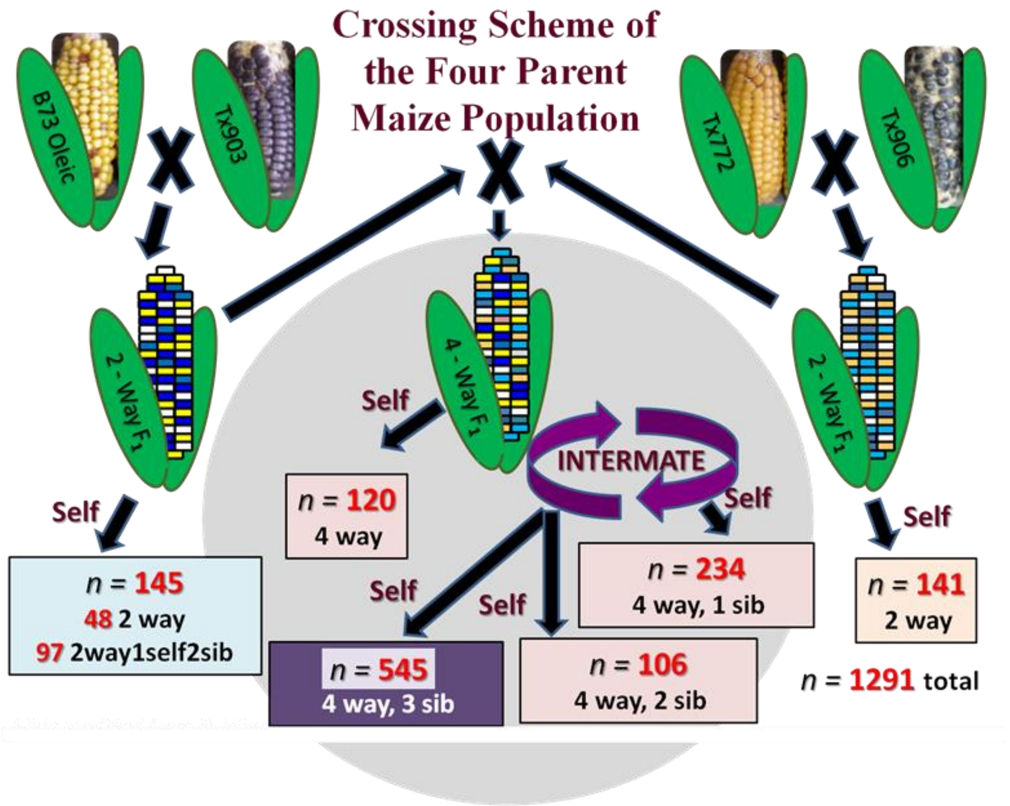


Figure 1. Mating design, creation of subpopulations, and number of phenotyped individuals (Mahan, 2015).

B73*Olc1* was anticipated to be nearly isogenic to the maize reference genome except for a mutant allele that increased oleic acid concentrations (Wright, 1995). Tx903 was crossed to B73*Olc1* and Tx906 was crossed to Tx772, creating two bi-parental F_1 hybrids. From these F_1 hybrids, six subpopulations were developed: the bi-parental populations Tx772 x Tx906, B73*Olc1* x Tx903, B73*Olc1* x Tx903 1self2sib (where two generations of sibling intermating were performed after one generation of selfing, 4way0sib (no sibling intermating), and 4way1sib, 4way2sib and 4way3sib with one, two and three generations of sibling intermating before selfing, respectively.

A complete description on the steps taken in creating the population and its subpopulations can be found in Table 1. In brief, to construct the population, the original bi-parental F_1 hybrids were developed in College Station, TX (CS) in 2009, and the 4-way F_1 hybrids were made in the following 2009 winter nursery located in Weslaco, TX (WE).

Individuals derived from the 4-way cross, underwent subsequent levels of intermating until three generations of intermating were achieved in CS 2011. Additionally in CS 2011, all of the subpopulations (except the 4way3sib) were selfed for the first time. During the WE 2011 nursery, in some sub-populations two random individuals were selected from their respective plots for the purposes of increasing the size of the subpopulation (Table 2). For every generation of intermating and successive inbreeding a random ear was selected for the corresponding plot and planted ear-to-row. During the CS 2012, WE 2012, CS 2013 and WE 2013 nurseries all individuals were planted and selfed.

Table 1. Sequence of events during the development of the four-parent maize population and resulting subpopulations (Mahan, 2015).

Subpopulation	College Station 2009	Weslaco 2009	College Station 2010	Weslaco 2010	College Station 2011
4way3sib		Di-hybrid cross	Intermated, harvested 95 ears	Bulked 3 kernels from each CS-10 ear, planted 8 plots and intermated within and between plots, harvested 78 ears	Intermated between 79 plots, harvested 430 ears
4way2sib					114 selfed ears harvested
4way1sib					Selfed 89 plots, harvested 295 ears
4way0sib					Selfed 6 plots, harvested 49 ears
B73*Olc1* x Tx903	hybrid cross				Selfed 3 plots, harvested 15 ears
Tx772 x Tx906	hybrid cross				Selfed 6 plots, harvested 40 ears
B73*Olc1* x Tx9031self2sib			1 plot selfed	1 plot intermated, 8 ears harvested	Intermated 8 plots, harvested 41 ears
Total					984 individuals

Table 1. Continued

	Weslaco 2011	College Station 2012	Weslaco 2012	College Station 2013
4way3sib	Planted 428 plots, selfed, harvested 575 ears.	Planted 575 plots, selfed, harvested 575 ears.	Planted 575 plots, selfed, harvested 545 ears.	Planted 545 nursery plots, selfed, harvested 527 ears. Planted 502 yield trial plots.
4way2sib	Planted 112 plots, selfed, harvested 173 ears.	Planted 133 plots, selfed, harvested 133 ears.	Planted 133 plots, selfed, harvested 106 ears.	Planted 106 nursery plots, selfed, harvested 101 ears. Planted 89 yield trial plots.
4way1sib	Planted 295 plots, selfed, harvested 253 ears.	Planted 253 plots, selfed, harvested 253 ears.	Planted 253 plots, selfed, harvested 235 ears	Planted 235 nursery plots, selfed, harvested 228 ears. Planted 205 yield trial plots.
4way0sib	Planted 49 plots, selfed, harvested 133 ears.	Planted 133 plots, selfed, harvested 133 ears.	Planted 133 plots, selfed, harvested 120 ears.	Planted 120 nursery plots, selfed, harvested 116 ears. Planted 110 yield trial plots.
B73*Olc1* x Tx903-F_5	Planted 15 plots, selfed, harvested 55 ears.	Planted 55 plots, selfed, harvested 53 ears.	Planted 53 plots, selfed, harvested 52 ears.	Planted 52 nursery plots, selfed, harvested 49 ears. Planted 49 yield trial plots.
Tx772 x Tx906-F_5	Planted 39 plots, selfed, harvested 140 ears.	Planted 140 plots, selfed, harvested 140 ears.	Planted 140 plots, selfed, harvested 137 ears.	Planted 137 nursery plots, selfed, harvested 134 ears. Planted 124 yield trial plots.
B73*Olc1* x Tx9031self2sib	Planted 41 plots, selfed, 103 ears.	Planted 103 plots, selfed, harvested 103 ears.	Planted 103 plots, selfed, harvested 97 ears.	Planted 97 nursery plots, selfed, harvested 91 ears. Planted 86 yield trial plots.
Total	1432 individuals	1430 individuals	1291 individuals	1246 individuals

Table 2. Number of plots with two randomly selected ears during WE 2011 nursery for increasing individuals in respective subpopulation.

Subpopulations	Number of plots
4way3sib	147
4way2sib	21
4way1sib	0
4way0sib	84
B73Olc1 x Tx903-F $_5$	40
Tx772 x Tx906-F $_5$	0
B73Olc1 x Tx9031self2sib	62

2.3.2 Experimental Design of Field Trials

Agronomic trait phenotypes were collected in seven different trials of the population each using an augmented design. Early and late nursery plantings, separated by nine days, in CS 2013 had no significant differences for flowering time and therefore these two plantings were combined and treated as one environment for analysis. Detailed information on the size of each trial, including the number of entries, parental lines and commercial checks are included in Table 3.

The augmented design allowed for non-replicated entries within a trial by using replicated checks throughout the blocks. Each of the seven trials were evenly blocked to account for field variation with three expired plant variety protection (ex-PVP) inbreds, replicated twice within each block during CS 2013 and 2014, followed by one replicate per block in CS 2015. During CS 2013, LH82 (Holden's Foundation Seeds, 1985), LH195 (Holden's Foundation Seeds, 1991) and PHV63 (Pioneer Hi-Bred International, 1998) were used as the commercial checks. In subsequent years LH82 was switched for

PB80 (DeKalb-Pfizer Genetics, 1988) because LH82 was much earlier than the lines in the population, while LH195 and PHV63 remained as checks. The nursery trials were single row plots 3.05 m in length and row spacing of 0.76 m. The observation trials were single row plots 6.40 m in length and row spacing of 0.76 m, except for CS 2015 in which the observation trials were 3.05 m in length.

Table 3. Total number of entry, parent, and check plots for seven environments in College Station 2013, 2014 and 2015. Modified from Mahan (2015).

Trial	Trial code	Entries	Parent plots	Check plots	Total plots	Planting date
CS 2013 nursery early planted	CS13N	646	4 (1 per parent)	54 (18 per check)	704	March 4, 2013
CS 2013 nursery late planted		646	4 (1 per parent)	54 (18 per check)	704	March 13, 2013
CS 2013 observation trials late planted	CS13T	1290	8 (2 per parent)	108 (36 per check)	1406	March 20, 2013
CS 2014 nursery	CS14N	654	16 (4 per parent)	48 (16 per check)	718	March 14, 2014
CS 2014 observation trials early late planted	CS14I	1173	16 (4 per parent)	78 (26 per check)	1267	March 14, 2014
CS 2014 observation trials late planted	CS14D	1142	16 (4 per parent)	72 (24 per check)	1230	March 28, 2014
CS 2015 observation trials	CS15T	1223	12 (3 per parent)	64 (16 per check)	1298	March 9, 2015
CS 2015 observation trials extremes	CS15TP	385	28 (7 per parent)	28 (7 per check)	468	March 9, 2015
Total		7159	104	506	7795	

2.3.3 Phenotypic Measurements

Nursery trials were used to produce RILs from the original parental crosses. Additionally, plant height and ear height were recorded in both the 2013 and 2014 nursery, while flowering times were only recorded in 2013. Nursery entries were hand harvested and notes were taken on cob and seed color during seed processing (as reported in Mahan (2015)). Furthermore, flowering times, plant height and ear height were collected on all observation trials during each year. Flowering time was measured as the point in which 50% of the individuals within a plot were shedding pollen (days to anthesis) or displaying silks (days to silk). Days to anthesis/silk were calculated by subtracting the planting date from the recorded flowering date of the respective trait. Plant height was measured in the field as the average height of the plants within the plot from the base of the plant to the tip of the tassel. Ear heights were measured similarly as the average ear height from the base of the plant to the node of the top ear. Starting in 2013, leaf rolling severity was noted on a scale of 0-3; 0- no observable leaf rolling, 1- slight leaf rolling, 2- moderate leaf rolling, and 3- excessive leaf rolling. During the 2014 season, Dr. Adam Mahan recorded replicate leaf rolling notes on both the early and late observation trials, twice in the morning and twice in the evening on separate days in order to account for subjective measurement error and time of day, as it took several hours to complete notes on one trial. In 2015, leaf rolling notes were taken once per trial, in which each trial's note were begun in the morning at the same time but on separate days.

2.3.4 Statistical Analysis

The phenotypic data was highly unbalanced with large amounts of field spatial variation present. Each trait was accessed within individual environments for incorrect data entry as well as correct spatial variables to include within the final combined environment analysis model. All traits were analyzed on an individual environment basis by fitting the check as fixed, and the genotype, block, range and row as random effects. Additionally, residuals were check for normality following the Shapiro-Wilks test of normality (Shapiro and Wilk, 1965) and hats leverage points (Hoaglin and Welsch, 1978) were calculated to access the data for outliers. Random model effects were tested for significance through chi square (df=1) testing of two times the difference in log likelihoods between the full model and the model without the effect of interest removed (Pinheiro and Bates, 2000).

To partition variation into genetic, environmental and spatial components, we performed a linear mixed model using ASReml v4.1 (Gilmour, et al., 2009). Within this model, entry (X)

$$Y_{ijklm} = \mu + E_m + B_{l(m)} + i_{j(m)} + j_{l(m)} + C_i + X_i + XE_{i*m} + \varepsilon_{ijklm}$$

and check (C) genotypes were placed into respective dummy variables, and special variation was account for through nesting of block (B), range(i) and row(j) effects within environments. This model, deviates from the initially proposed model by including the genotype by environment interaction (XE), as well as, a non-nested entry effect. Previous authors (Scott and Milliken, 1993) have suggested that the entry effect must be nested. However, when the BLUP estimates for nested entry model were compared to the non-nested model, a constant increase to all entry BLUPs occurred. Fitting the model to include the entry by environment interaction was less computationally demanding when the entry effect is not nested within another effect. For these reasons, the non-nested model was used to estimate BLUPs (Summary can be found in Table 5).

2.3.5 Association Mapping using GAPIT

An association mapping approach was performed with compressed mixed linear model (Zhang, et al., 2010) implemented in the GAPIT R package (Lipka, et al., 2012). Genotype data (G) was converted to double bit HapMap (Gibbs, et al., 2003) format which GAPIT internally converts to a numeric format. Phenotypic data (Y) was imported read in using the formatting recommended in the GAPIT user manual. Kinship variables (KI) were calculated automatically by GAPIT and no covariate variables (CV) were added to the GWA study. The total number of principle components used within the study was set to three (PCA.total=3) as it is require to execute the GAPIT function, although GAPIT was commanded to automatically select the optimal number of principle components to include in the GWAS models (Model.selection=TRUE) using the Bayesian information criterion (BIC)-based model selection. Markers with minor allele frequencies (maf), default in GAPIT, less than five percent (SNP.MAF=0.05) were excluded from the analysis as they tend to significantly increase false positives (Tabangin, et al., 2009) due to their variability; because this population was a linkage population, markers with less than 25% frequency had already been removed. To reduce the rate of false discoveries a conservative significance threshold was calculated for the large number of markers using the Bonferroni correction in which a significant LOD score equals the negative log of alpha (0.05) over the number of markers.

Analysis of the entire set of full population or the dihybrid subpopulations used 118,509 markers with a Bonferroni corrected significance threshold of 6.37 LOD. Analysis of the independent biparental populations required separate significance thresholds based on the number of markers segregating within each respective population. The B73*olc1* by Tx903 population contained 39,461 segregating markers with a significant LOD of 5.90 and the Tx772 by Tx906 population contained 62,750 segregating markers with a significant LOD of 6.10. When analyzing both biparental populations jointly, 12,740 markers were segregating in both populations with a significant LOD of 5.41.

Peak markers were analyzed to determine the positive allele and parent line that contributed the allele, which was more challenging in the multi-parent crosses than bi-parental crosses, where there are four parental but only two marker states. This was determined by comparing the allelic effects associated to the markers, as indicated by GAPIT, and analyzing the trend in the flanking markers (haplotypes) for each parent (Appendix A1). Trends in the segregating markers of the entire 4-way subpopulation were then compared to the B73*olc1* x Tx903 and Tx772 x Tx906 biparental populations individually. Analyzing the distribution of the allele calls at the flanking SNPs, it was possible to assign the singular allelic effect estimate from GAPIT to the base call that comes second in alphabetical order for that marker (i.e. if the effect is -0.5 and the SNPs are A and C, C decreases the trait by 0.5). Analysis of the effect trends allowed assignment of positive and negative effects to specific parental lines.

2.4 Results and Discussion

2.4.1 Individual Environment Phenotypes and Analysis

2.4.1.1 Raw Phenotype Data

The years 2013, 2014 and 2015 were significantly different (Fisher LSD; $\alpha=0.05$) in their range of phenotypic values (Appendix B1). College Station, 2014 (CS14) had the highest mean plant height, while College Station, 2013 (CS13) had the greatest mean for ear height, DTA, DTS and leaf rolling. College Station, 2014 (CS14) had the shortest mean flowering times and the least severe leaf rolling, while College Station, 2015 (CS15) had the shortest mean plant and ear heights.

Plant height was significantly less in the CS15T trial, followed by the CS15TP, CS14N and CS14I in an increasing manner (Figure 2[a]; Table 4). This effect was visibly noticeable in field and was likely caused by excessive rainfall and high standing water in the back ranges of the field where these trials were located. Plants near the back of the trial were severely stunted in their growth. The CS14D trial had the highest plant height mean of all the environments which was noticeable in the field. The CS14D trial was located in areas with increased drainage efficiency explaining the increase in plant height. Additionally, the CS15 trials had the shortest ear heights of all the trials (Figure 2[b]; Table 4), which is expected as the trials experienced significantly stunted growth.

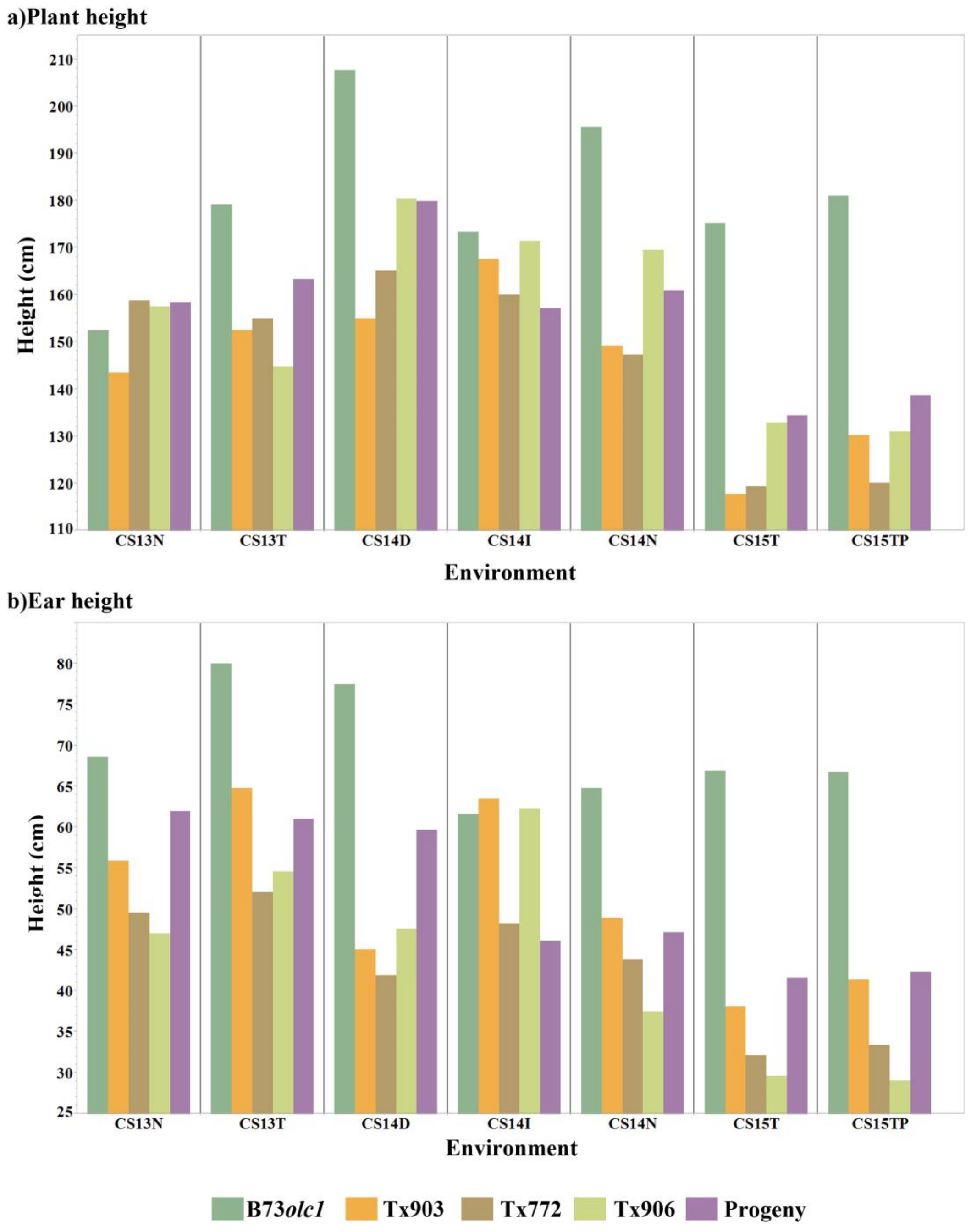


Figure 2. Mean of raw phenotype data among environments for [a] plant height and [b] ear height of parent lines and progney

Table 4. Summary statistics of parental lines and progeny for plant height (PH), ear height (EH), days to anthesis (DTA), days to silking (DTS) and leaf rolling (LR) by environment.

Trait	Env	ID	N	Mean	Std. Dev.	Min	Max
PH	CS13N	B73*olc1*	2	152.4 ± 0.0	0.0	152.4	152.4
PH	CS13N	Tx903	2	143.5 ± 16.1	1.8	142.2	144.8
PH	CS13N	Tx772	2	158.8 ± 16.1	1.8	157.5	160.0
PH	CS13N	Tx906	2	157.5 ± 161.4	18.0	144.8	170.2
PH	CS13N	Progeny	1278	158.4 ± 1.3	22.8	83.8	233.7
PH	CS13T	B73*olc1*	2	179.1 ± 48.4	5.4	175.3	182.9
PH	CS13T	Tx903	2	152.4 ± 0.0	0.0	152.4	152.4
PH	CS13T	Tx772	2	154.9 ± 32.3	3.6	152.4	157.5
PH	CS13T	Tx906	2	144.8 ± 32.3	3.6	142.2	147.3
PH	CS13T	Progeny	1212	163.3 ± 1.1	18.9	91.4	238.8
PH	CS14I	B73*olc1*	4	173.4 ± 6.9	4.3	167.6	177.8
PH	CS14I	Tx903	4	167.6 ± 11.9	7.5	160.0	177.8
PH	CS14I	Tx772	2	160.0 ± 193.6	21.6	144.8	175.3
PH	CS14I	Tx906	4	171.5 ± 7.0	4.4	167.6	177.8
PH	CS14I	Progeny	1105	157.1 ± 1.3	21.2	76.2	228.6
PH	CS14D	B73*olc1*	4	207.7 ± 16.0	10.0	195.6	215.9
PH	CS14D	Tx903	4	154.9 ± 27.8	17.5	129.5	167.6
PH	CS14D	Tx772	4	165.1 ± 11.9	7.5	157.5	175.3
PH	CS14D	Tx906	4	154.9 ± 27.8	17.5	129.5	167.6
PH	CS14D	Progeny	1126	179.9 ± 1.3	22.4	96.5	243.8
PH	CS14N	B73*olc1*	4	195.6 ± 17.5	11.0	185.4	210.8
PH	CS14N	Tx903	4	149.2 ± 13.8	8.6	142.2	160.0
PH	CS14N	Tx772	4	147.3 ± 8.7	5.5	142.2	154.9
PH	CS14N	Tx906	4	169.6 ± 5.1	3.2	165.1	172.7
PH	CS14N	Progeny	641	161.0 ± 1.8	23.6	78.7	238.8
PH	CS15T	B73*olc1*	3	175.3 ± 33.4	13.4	165.1	190.5
PH	CS15T	Tx903	3	117.7 ± 42.0	16.9	99.1	132.1
PH	CS15T	Tx772	3	119.4 ± 27.5	11.1	106.7	127.0
PH	CS15T	Tx906	3	132.9 ± 23.9	9.6	121.9	139.7
PH	CS15T	Progeny	1202	134.4 ± 5.2	20.5	58.4	198.1
PH	CS15TP	B73*olc1*	7	181.1 ± 10.8	11.7	162.6	193.0
PH	CS15TP	Tx903	7	130.3 ± 7.6	8.3	114.3	139.7
PH	CS15TP	Tx772	7	120.1 ± 6.8	7.3	111.8	132.1
PH	CS15TP	Tx906	7	131.0 ± 8.9	9.6	119.4	144.8
PH	CS15TP	Progeny	381	138.7 ± 2.6	25.6	71.1	195.6
EH	CS13N	B73*olc1*	2	68.6 ± 0.0	0.0	68.6	68.6
EH	CS13N	Tx903	2	55.9 ± 161.4	18.0	43.2	65.6
EH	CS13N	Tx772	2	49.5 ± 112.4	12.6	40.6	58.4
EH	CS13N	Tx906	2	47.0 ± 113.0	12.6	38.1	55.9
EH	CS13N	Progeny	1277	62.0 ± 0.9	15.4	17.8	106.7
EH	CS13T	B73*olc1*	2	80.0 ± 16.1	1.8	78.7	81.3
EH	CS13T	Tx903	2	64.8 ± 16.1	1.8	63.5	66.0
EH	CS13T	Tx772	2	52.1 ± 145.2	16.2	40.6	63.5

Table 4. Continued

Trait	Env	ID	N	Mean	Std. Dev.	Min	Max
EH	CS13T	Progeny	1211	61.1 ± 0.8	14.2	22.9	101.6
EH	CS14I	B73olc1	4	61.6 ± 10.6	6.7	55.9	71.1
EH	CS14I	Tx903	4	63.5 ± 8.7	5.5	55.9	68.6
EH	CS14I	Tx772	2	48.3 ± 258.2	28.7	27.9	68.6
EH	CS14I	Tx906	4	62.2 ± 7.0	4.4	55.9	66.0
EH	CS14I	Progeny	1105	46.1 ± 0.8	13.7	7.6	101.6
EH	CS14D	B73olc1	4	77.5 ± 20.5	12.9	66.0	94.0
EH	CS14D	Tx903	4	45.1 ± 23.4	14.7	25.4	61.0
EH	CS14D	Tx772	4	41.9 ± 5.2	3.3	38.1	45.7
EH	CS14D	Tx906	4	45.1 ± 23.4	14.7	25.4	61.0
EH	CS14D	Progeny	1126	59.7 ± 1.0	17.4	2.5	109.2
EH	CS14N	B73olc1	4	64.8 ± 17.0	10.7	53.3	76.2
EH	CS14N	Tx903	4	48.9 ± 20.2	12.7	35.6	61.0
EH	CS14N	Tx772	4	43.8 ± 19.4	12.2	30.5	58.4
EH	CS14N	Tx906	4	37.5 ± 9.0	5.6	33.0	45.7
EH	CS14N	Progeny	642	47.2 ± 1.1	14.7	5.1	94.0
EH	CS15T	B73olc1	3	66.9 ± 14.6	5.9	63.5	73.7
EH	CS15T	Tx903	3	38.1 ± 16.7	6.7	30.5	43.2
EH	CS15T	Tx772	3	32.2 ± 14.6	5.9	25.4	35.6
EH	CS15T	Tx906	3	29.6 ± 19.3	7.8	22.9	38.1
EH	CS15T	Progeny	1203	41.6 ± 0.7	12.9	2.5	111.8
EH	CS15TP	B73olc1	7	66.8 ± 9.3	10.0	53.3	81.3
EH	CS15TP	Tx903	7	41.4 ± 7.1	7.7	30.5	50.8
EH	CS15TP	Tx772	7	33.4 ± 4.4	4.7	27.9	38.1
EH	CS15TP	Tx906	7	29.0 ± 4.9	5.3	22.9	38.1
EH	CS15TP	Progeny	381	42.3 ± 1.7	16.5	2.5	86.4
DTA	CS13N	B73olc1	2	84.5 ± 6.4	0.7	84.0	85.0
DTA	CS13N	Tx903	2	80.0 ± 25.4	2.8	78.0	82.0
DTA	CS13N	Tx772	2	78.0 ± 25.4	2.8	76.0	80.0
DTA	CS13N	Tx906	2	84.0 ± 25.4	2.8	82.0	86.0
DTA	CS13N	Progeny	1271	82.2 ± 0.2	2.8	72.0	92.0
DTA	CS13T	B73olc1	2	90.5 ± 6.4	0.7	90.0	91.0
DTA	CS13T	Tx903	2	88.5 ± 6.4	0.7	88.0	89.0
DTA	CS13T	Tx772	2	77.0 ± 22.7	1.4	76.0	78.0
DTA	CS13T	Tx906	2	91.0 ± 25.4	2.8	89.0	93.0
DTA	CS13T	Progeny	1211	89.2 ± 0.2	2.8	81.0	99.0
DTA	CS14I	B73olc1	4	78.8 ± 0.8	0.5	78.0	79.0
DTA	CS14I	Tx903	4	80.0 ± 0.0	0.0	80.0	80.0
DTA	CS14I	Tx772	4	82.8 ± 5.7	3.6	78.0	86.0
DTA	CS14I	Tx906	4	79.0 ± 0.0	0.0	79.0	79.0
DTA	CS14I	Progeny	1106	81.2 ± 0.2	3.1	70.0	95.0
DTA	CS14D	B73olc1	4	73.0 ± 1.8	0.6	72.0	74.0
DTA	CS14D	Tx903	4	71.3 ± 3.0	1.9	70.0	74.0
DTA	CS14D	Tx772	4	69.8 ± 0.8	0.5	69.0	70.0
DTA	CS14D	Tx906	4	70.5 ± 7.2	4.5	65.0	76.0
DTA	CS14D	Progeny	1114	71.3 ± 0.2	3.4	64.0	84.0
DTA	CS15T	B73olc1	3	82.7 ± 7.6	3.1	80.0	86.0
DTA	CS15T	Tx903	3	78.0 ± 5.0	2.0	76.0	80.0

Table 4. Continued

Trait	Env	ID	N	Mean	Std. Dev.	Min	Max
DTA	CS15T	Tx906	3	78.7 ± 7.6	3.1	76.0	82.0
DTA	CS15T	Progeny	1188	78.0 ± 0.2	3.2	68.0	97.0
DTA	CS15TP	B73olc1	7	81.1 ± 3.2	2.4	77.0	84.0
DTA	CS15TP	Tx903	7	75.7 ± 0.9	1.0	74.0	77.0
DTA	CS15TP	Tx772	7	76.4 ± 1.1	1.1	75.0	78.0
DTA	CS15TP	Tx906	7	77.7 ± 0.7	0.8	76.0	78.0
DTA	CS15TP	Progeny	380	78.3 ± 0.4	4.0	68.0	94.0
DTS	CS13N	B73olc1	2	84.5 ± 6.4	0.7	84.0	85.0
DTS	CS13N	Tx903	2	83.0 ± 38.1	4.2	80.0	86.0
DTS	CS13N	Tx772	2	82.0 ± 0.0	0.0	82.0	82.0
DTS	CS13N	Tx906	2	85.0 ± 12.7	1.4	84.0	86.0
DTS	CS13N	Progeny	1252	83.8 ± 0.2	2.8	74.0	92.0
DTS	CS13T	B73olc1	2	92.0 ± 12.7	1.4	91.0	93.0
DTS	CS13T	Tx903	2	92.0 ± 0.0	0.0	92.0	92.0
DTS	CS13T	Tx772	2	83.0 ± 22.7	14.1	82.0	84.0
DTS	CS13T	Tx906	2	95.5 ± 6.4	0.7	95.0	96.0
DTS	CS13T	Progeny	1209	91.7 ± 0.2	3.3	82.0	101.0
DTS	CS14I	B73olc1	4	87.8 ± 2.0	1.3	86.0	89.0
DTS	CS14I	Tx903	4	85.8 ± 0.8	0.5	85.0	86.0
DTS	CS14I	Tx772	4	85.0 ± 1.3	0.8	84.0	86.0
DTS	CS14I	Tx906	4	87.8 ± 2.7	1.7	86.0	90.0
DTS	CS14I	Progeny	1102	85.3 ± 0.2	3.8	73.0	101.0
DTS	CS14D	B73olc1	4	73.8 ± 3.2	2.1	72.0	76.0
DTS	CS14D	Tx903	4	75.3 ± 3.6	2.2	73.0	78.0
DTS	CS14D	Tx772	4	74.5 ± 3.0	1.9	72.0	76.0
DTS	CS14D	Tx906	4	75.5 ± 3.8	2.4	73.0	78.0
DTS	CS14D	Progeny	1106	74.7 ± 0.2	3.5	66.0	87.0
DTS	CS15T	B73olc1	3	86.3 ± 16.2	6.5	80.0	93.0
DTS	CS15T	Tx903	3	82.7 ± 7.4	3.1	80.0	86.0
DTS	CS15T	Tx772	3	82.7 ± 2.9	1.2	82.0	84.0
DTS	CS15T	Tx906	3	84.0 ± 14.9	3.5	78.0	90.0
DTS	CS15T	Progeny	1198	81.9 ± 0.2	4.2	70.0	100.0
DTS	CS15TP	B73olc1	7	81.7 ± 1.7	1.8	80.0	84.0
DTS	CS15TP	Tx903	7	79.9 ± 1.6	1.7	78.0	82.0
DTS	CS15TP	Tx772	7	82.3 ± 1.7	1.8	80.0	86.0
DTS	CS15TP	Tx906	7	83.9 ± 2.2	2.4	81.0	88.0
DTS	CS15TP	Progeny	377	82.0 ± 0.5	5.1	70.0	100.0
LR	CS13N	B73olc1	4	0.8 ± 0.8	0.5	0.0	1.0
LR	CS13N	Tx903	4	0.8 ± 0.8	0.5	0.0	1.0
LR	CS13N	Tx772	4	1.0 ± 1.3	0.8	0.0	2.0
LR	CS13N	Tx906	4	1.8 ± 1.5	1.0	1.0	3.0
LR	CS13N	Progeny	2548	1.1 ± 0.0	0.6	0.0	3.0
LR	CS14D	B73olc1	8	0.0 ± 0.0	0.0	0.0	0.0
LR	CS14D	Tx903	8	0.0 ± 0.0	0.0	0.0	0.0
LR	CS14D	Tx772	8	0.3 ± 0.4	0.5	0.0	1.0
LR	CS14D	Tx906	8	0.3 ± 0.4	0.5	0.0	1.0
LR	CS14D	Progeny	2254	0.4 ± 0.0	0.5	0.0	1.0
LR	CS14I	B73olc1	8	0.8 ± 0.9	1.0	0.0	2.0

Table 4. Continued

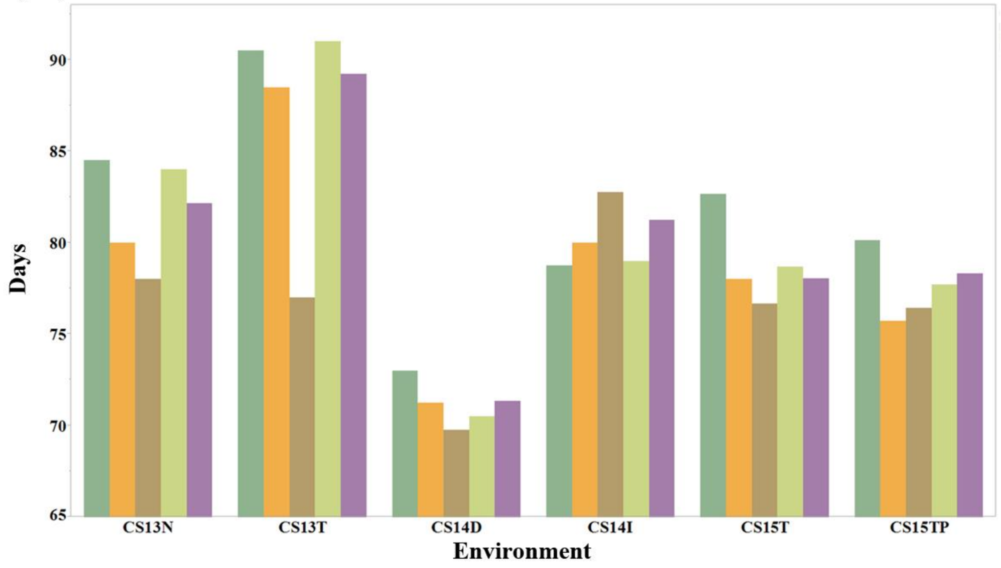
Trait	Env	ID	N	Mean	Std. Dev.	Min	Max
LR	CS14I	Tx772	8	0.3 ± 0.4	0.5	0.0	1.0
LR	CS14I	Tx906	8	0.3 ± 0.4	0.5	0.0	1.0
LR	CS14I	Progeny	2212	0.8 ± 0.0	0.8	0.0	3.0
LR	CS15T	B73olc1	1	2.0 ± NA	NA	2.0	2.0
LR	CS15T	Tx903	1	2.0 ± NA	NA	2.0	2.0
LR	CS15T	Tx772	1	0.0 ± NA	NA	0.0	0.0
LR	CS15T	Tx906	2	1.0 ± 0.0	0.0	1.0	1.0
LR	CS15T	Progeny	1202	0.7 ± 0.1	0.9	0.0	3.0
LR	CS15TP	B73olc1	7	0.6 ± 0.9	1.0	0.0	2.0
LR	CS15TP	Tx903	7	0.0 ± 0.0	0.0	0.0	0.0
LR	CS15TP	Tx772	7	0.0 ± 0.0	0.0	0.0	0.0
LR	CS15TP	Tx906	7	0.1 ± 0.4	0.4	0.0	1.0
LR	CS15TP	Progeny	381	0.6 ± 0.1	0.9	0.0	3.0

Of the parental lines, B73*olc1* was the highest or not significantly different from the highest parent in all environments (Figure 2[a]; Table 4; Appendix A3 [a]). Tx903 was consistently one of the shortest parental lines, while Tx906 was among the shortest ear heights except in CS13T and CS14I (Figure 2; Table 4; Appendix A3). Larger variation was observed for individual parental lines, commonly Tx772 (CS13N, PH; CS14I, PH; CS13N, EH; CS13T, EH; CS14I, EH), in certain environments due to the low replication of parent within the test accompanied with a large range in the measured height phenotypes. Larger range in measurement values is likely due to one of the two plots being located within an area of the field effected to a greater extent by standing water causing larger variation.

There were significant differences (Fisher's LSD, α=0.05) between the subpopulations within each environment for plant and ear height. The biparental Tx772 x Tx906 subpopulation was the shortest population across all environments for both plant and ear height (Appendix A2; Appendix B2). The 4way3sib subpopulation had the largest mean height phenotype in all environments except CS15TP, in which the 4way3sib was not significantly different from the highest subpopulation ($p<0.05$). Additionally, the 4way3sib population had the highest ear heights in all of the environments except CS13T, CS15T and CS15TP; where the B73*olc1* x Tx903 subpopulation was higher but not significantly different from 4way3sib (Appendix A3; Appendix B2).

Flowering time trends were consistent across DTA and DTS with CS13T trial having the longest mean flowering time interval and the CS14D trial having the shortest mean interval (Figure 3). This is likely due to the date in which the trials were planted, with later plantings exposing the trial to faster accumulation of heat units resulting in shorter vegetative to reproductive transitioning periods. CS14D was planted the latest of all seven trials (March 28; Table 3) and was expected to have the shortest flowering intervals; in contrast CS13T was not the earliest planting date (March 20) yet had the longest flowering time intervals beyond the CS15 trials which were planted the earliest (March 9). This is likely due to a more rapid accumulation of heat units during the year of 2015 than in other years of the experiment.

Parent *B73olc1* had the latest DTA (Figure 3[a]; Table 4; Appendix A3) among the parental lines and Tx906 had the latest DTS within environments (Figure 3; Table 4; Appendix A3). Significant differences were found between the subpopulations within each environment for DTA and DTS. The 4way1sib subpopulation was the earliest, or one of the earliest, flowering across all environments for DTA and DTS (Appendix A3; Appendix B3), but was not significantly different from the subpopulation with the a)Days to anthesis



b)Days to silk

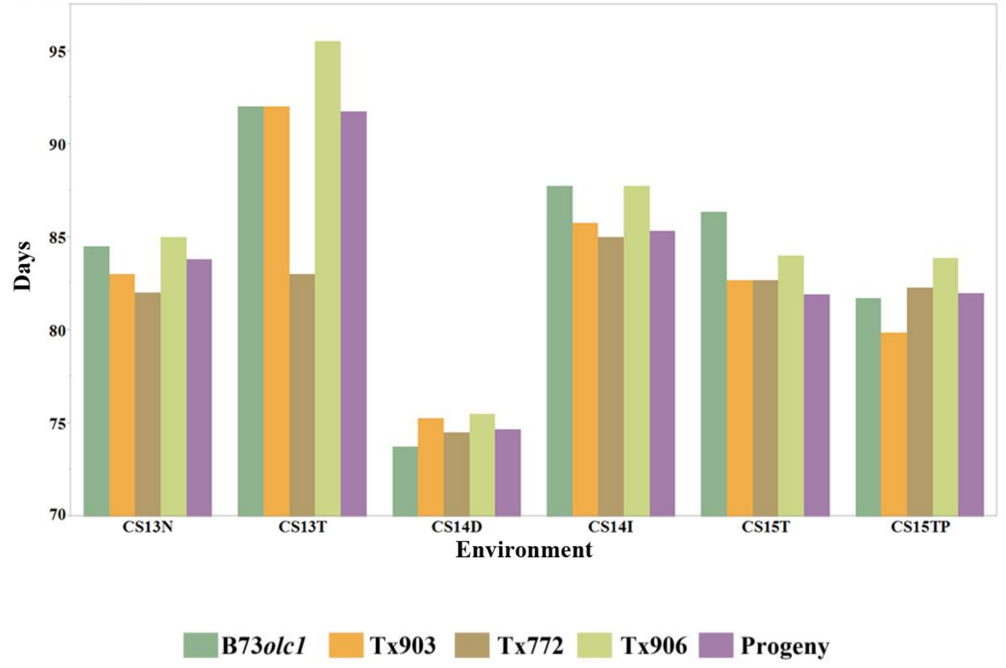


Figure 3. Mean of raw phenotype data among environments for [a] days to anthesis and [b] days to silk of parent lines and progney.

smallest mean; with the exception of DTA in CS15T. The 4way2sib subpopulation consistently had the latest flowering time (Appendix A3; Appendix B2) or was not significantly different from the subpopulation with the largest interval.

At the time taken, leaf rolling was the most severe in the CS13N trial and least severe in the CS14D trial (Figure 4).

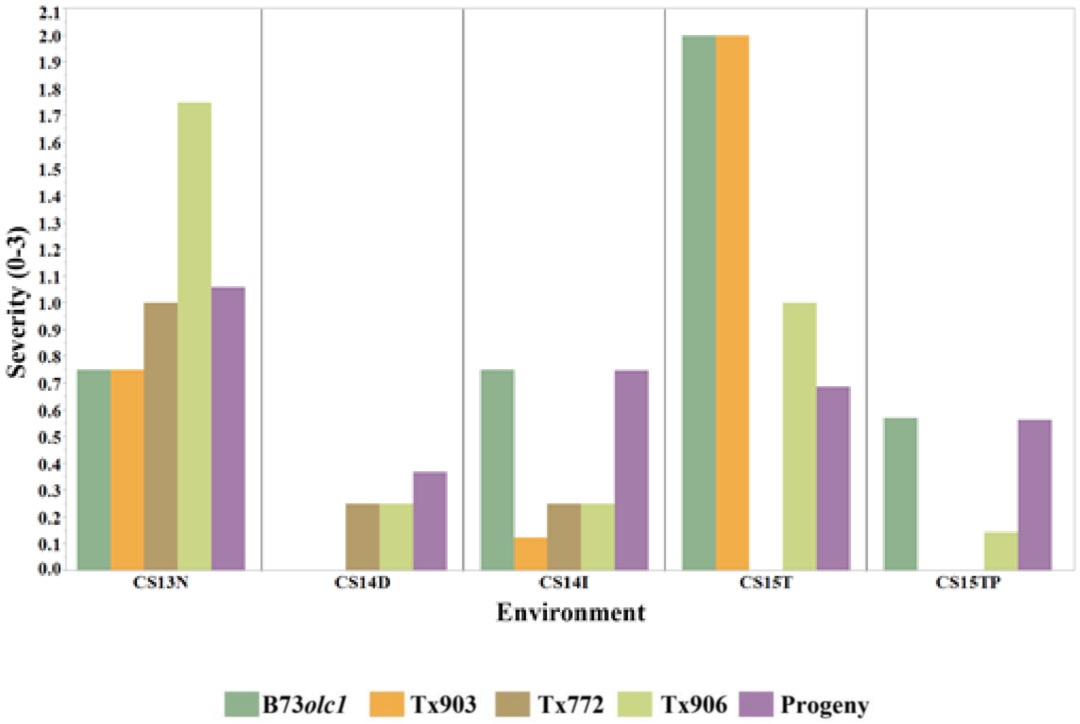


Figure 4. Mean of raw phenotype data among environments for leaf rolling severity. Environments lacking bar representations of parental lines was due to the parental line having a mean leaf roll scoring of zero within the environment.

Interestingly, the CS15 trials were significantly different from one another although they were planted on the same date as well as directly next to one another in the field. This could be explained by the standing water in the back ranges of CS15T limiting the root growth, causing a more severe leaf roll due to plants inability to access moisture deeper within the soil late in the season after the trials dried.

Intermating prior to selection is used to breakdown linkage blocks, increasing genetic variation leading to increased frequencies of extreme phenotypes which should cause increased phenotypic distributions. Unequal variance test were completed using Brown-Forsythe (Brown and Forsythe, 1974), Levene (Levene, 1960) and Bartlett's (Bartlett, 1937) methods to test for significant differences in the phenotypic distribution of all five traits in the dihybrid subpopulations due to intermating prior to inbreeding. We failed to reject (α=0.05) the null hypothesis of equal variance (H_0: $\sigma_{4w0s}= \sigma_{4w1s}= \sigma_{4w2s}= \sigma_{4w3s}$) between levels of intermating, which indicates that the phenotypic distribution within our subpopulations is not influenced by intermating (Table 5). Furthermore, the insignificance among variances suggests that the advanced generations of intermating does not decrease phenotypic variation due to the disassociation of favorably linked loci. Our results are consistent with that of previous studies which concluded that advance generations of intermating have little influence on the distribution of phenotypes (Lamkey, et al., 1995; Lima Neto and Souza Júnior, 2009).

Table 5. Comparison of generation of intermating effect on phenotypic distribution of plant height (PH), ear height (EH), days to anthesis (DTA), days to silk (DTS) and leaf rolling (LR) using unequal variance tests.

Trait	**Population**	**σ**	**Brown-Forsythe prob >F**	**Levene prob >F**	**Bartlett prob >F**
PH (cm)	4way 0sib	10.0	0.5938	0.6314	0.3669
	4way 1sib	10.0			
	4way2sib	10.0			
	4way3sib	10.4			
EH (cm)	4way 0sib	6.7	0.2874	0.2863	0.5132
	4way 1sib	6.7			
	4way2sib	6.4			
	4way3sib	6.7			
DTA (days)	4way 0sib	6.3	0.2686	0.2899	0.2474
	4way 1sib	6.4			
	4way2sib	6.8			
	4way3sib	6.4			
DTS (days)	4way 0sib	6.2	0.1777	0.1574	0.2243
	4way 1sib	6.4			
	4way2sib	6.8			
	4way3sib	6.5			
LR (0:3)	4way 0sib	0.7	0.3975	0.3843	0.224
	4way 1sib	0.8			
	4way2sib	0.8			
	4way3sib	0.8			

2.4.1.2 Individual Environment Analysis

The residuals all traits with all environments were tested for normality and only plant height within CS15TP was found to be significantly non-normal. Visual inspection of the residual histograms indicated normally distributed data and Q-Q plots were analyzed to verify normality. Parental lines Tx772, Tx903 and Tx906 were consistently the high leverage individuals for all traits within CS13N and CS13T (h>0.5). Upon inspection, the data was consistent with measurements taken within other environments, and were kept within the data sheet.

There was no single trait in which significance was found for all effects in the full model across all of the environments, although, all traits were significant for each full model effect in at least one environment (Table 6). This indicated that all spatial parameters of the model needed to be included within the combined analysis nested within the environments. Although certain effects may not have been significant within an environment, these effects still had an effect useful to produce a more accurate estimate of the BLUPs over all environments.

Further investigation of individual environments gave confidence in the analysis, specifically that the plant height showed a significant range effect in CS14I and CS15T as previously mentioned. Additionally, CS15TP was planted directly next to CS15T, but had seven fewer ranges in the rear of the field, since this trial was not subjected to the standing water, less plant height variation was noticed in the rear ranges and no significant effect was found for range in CS15TP. Ear height showed very little significance in row and range effect, likely due to the block variables ability to accurately explain the variation in ear height, supporting that the trials were blocked out in an efficient way to account for field variation. High block significance was found in all but four individual environmental analyses (PH, CS14I; EH, CS13T; LR, CS13N and CS15TP).

Most traits and environments had highly significant genotype effects. These ranged from 6% of the variation for DTA/CS14D to 92% of total variation for PH/CS13T. Across all traits PH and EH had higher proportion of variance from genotype than the other traits within each environment, suggesting that the variation was wide, the field variation was low, and/ or the phenotyping was very accurate for these traits.

Table 6. Individual environment analysis of agronomic traits and leaf rolling. Fixed effect (check, technical replicate [TRM]) are presented as significance levels while random effects are presented as their variance component estimates and their significance.

Trait	Env	Check	TRM†	Geno	Block	Range	Row	Residual
PH	CS13N	**	-	44.90**	10.25**	6.38*	6.10*	50.21
	CS13T	**	-	49.75**	0.51*	0.30	0.42*	4.12
	CS14D	**	-	57.50**	4.32**	2.09**	1.59*	11.47
	CS14I	*	-	31.73**	0.00	4.78**	0.60	31.74
	CS14N	**	-	69.76**	3.70*	1.74*	1.26	8.27
	CS15T	**	-	42.41**	14.17**	0.94*	0.80**	6.49
	CS15TP	**	-	77.56**	13.77**	0.24	0.48	5.81
EH	CS13N	**	-	19.08**	7.65**	0.25	0.74**	7.12
	CS13T	**	-	25.07**	0.29	0.23	.01	5.75
	CS14D	**	-	34.26**	1.16**	0.64*	0.77	9.72
	CS14I	**	-	10.27**	0.38**	0.29	0.11	17.96
	CS14N	**	-	22.90**	2.23**	0.13	0.33	8.62
	CS15T	**	-	18.75**	3.34**	0.13	0.00	3.83
	CS15TP	**	-	32.21**	4.87**	0.00	0.41	4.24
DTA	CS13N	**	-	4.16**	0.12*	0.15*	0.96**	2.78
	CS13T	**	-	6.43**	0.53**	.04	0.12**	0.55
	CS14D	ns	-	0.70	1.00**	0.45**	0.24*	8.44
	CS14I	**	-	1.91	0.14*	0.14*	0.15	7.02
	CS15T	**	-	5.12**	0.92**	0.00	0.18**	4.27
	CS15TP	**	-	13.57**	0.90**	0.27	0.00	2.05
DTS	CS13N	**	-	3.13**	0.18**	0.15*	1.55**	2.93
	CS13T	**	-	8.97**	0.75**	0.06	0.13*	0.63
	CS14D	**	-	5.43**	2.38**	0.57**	0.38**	3.05
	CS14I	**	-	10.52**	0.55**	0.00	0.37**	3.22
	CS15T	ns	-	1.50	3.03**	0.00	0.48**	13.28
	CS15TP	ns	-	16.90**	4.34**	0.00	0.34	6.11
LR	CS13N	**	**	0.03**	0.01**	0.00	0.00	0.31
	CS14D	**	**	0.16**	0.00	0.00	0.00	0.13
	CS14I	**	**	0.35**	0.06**	0.02**	0.02**	0.23
	CS15T	**	-	0.32*	0.23**	0.00	0.00	0.29
	CS15TP	ns	-	0.45**	0.01	0.00	0.02	0.23

* Significance at $\alpha=0.05$
** Significance at $\alpha=0.01$
ns Not significant at 0.05
† Technical Replicate Measurement (TRM)

Most traits and environments had highly significant genotype effects. These ranged from 6% of the variation for DTA/CS14D to 92% of total variation for PH/CS13T. Across all traits PH and EH had higher proportion of variance from genotype than the other traits within each environment, suggesting that the variation was wide, the field variation was low, and/ or the phenotyping was very accurate for these traits.

Non-significant genotype effects were found for DTA in CS14D and CS14I, as well as DTS in CS15T. It is likely that within these environments, climate factors constricted the flowering period to a small window of time, reducing the range of flowering and the variation that could be phenotyped (Appendix A2). It was interesting that the variation was not noted in the same environment for both flowering traits, but there is no clear reason why that is. Additionally, it is expected that DTA in CS15TP would also have insignificant genotype variation due to adjacent plant locations and the same planting date as CS15T, but this was not the case.

The technical replicate measurement (TRM) variable accounting for the person (AM, SA, SS) and time of note collection in leaf rolling ratings was significant in all three environments (Table 6). Significance indicated that there was a difference in both the note-takers perception of leaf rolling and that the plants likely showed different phenotypes at different times of the day. This variable was therefore included in the combined analysis of leaf rolling as a nested effect within its respected environment.

2.4.2 Multi Environment Trait Analysis

Based on the results of individual analysis we decided to combine environments and perform a multiple environment trial analysis (META). The spatial effects (Table 6) were significant across all seven environments and were included in the model. Spatial variation explained a higher proportion of the variation seen in plant height than that of flowering time. Many spatial factors such as varying irrigation coverage, adjacent plot competition and standing water due to excessive rainfall could be attributed to the higher proportion of spatial variation seen in plant height growth. This indicated that plant/ear height was affected to a greater extent by spatial variation than that of flowering time. Environmental effects accounted for ~30% of the variation in plant height and ~75% of the variation in flowering time. This is likely due to the variation in heat units accumulated within each environment, either compacting the flowering period into a short period of time (CS14D) or extending it over several weeks (CS13T). The genotypic effect of flowering time (~15%) was substantially less than that of plant/ear

Table 7. Summary statistics of BLUP estimates of progeny genotypes for plant height (PH), ear height (EH), days to anthesis (DTA), days to silking (DTS) and leaf rolling (LR).

	PH (cm)	**EH (cm)**	**DTA (days)**	**DTS (days)**	**LR**
Mean	152.53±0.86	48.84±0.56	80.77±0.12	83.54±0.13	0.45±0.01
Std Dev	15.62	10.13	2.20	2.43	0.22
Min	103.94	19.74	73.90	75.02	0
Max	205.69	82.19	87.71	93.97	1.42

Table 8. Combined analysis of agronomic traits: plant height (PH), ear height (EH), days to anthesis (DTA) and days to silking (DTS); presented as the variation component, significance level, and percent variation (%).

	PH		**EH**	
	Var Comp	% †	Var Comp	% †
Environment	37.57**	35.03	12.71**	27.97
Block[Env]	6.85**	6.39	1.97**	4.34
Range[Env]	1.33**	1.24	0.30**	0.66
Row[Env]	0.65**	0.60	0.40**	0.88
Entry	41.63**	38.82	18.12**	39.86
Entry*Env	3.06**	2.85	0.82*	1.81
Residual	16.16	15.07	11.13	24.48
Heritability	0.94		0.91	
	DTA		**DTS**	
	Var Comp	% †	Var Comp	% †
Environment	34.90**	77.60	31.40**	69.30
Block[Env]	0.78**	1.74	2.02**	4.46
Range[Env]	0.10**	0.23	0.12**	0.27
Row[Env]	0.26**	0.59	0.41**	0.90
Entry	5.53**	12.30	6.82**	15.07
Entry*Env	0.50**	1.12	1.04**	2.29
Residual	2.88	6.41	3.50	7.72
Heritability	0.91		0.90	

* Significance at α=0.05
** Significance at α=0.01
† Percentage of variation explained by effect

height (~40%), which was likely largely due to much larger variation in height that flowering time in the population (Table 8), despite a larger residual.

Though plant/ear height had a greater genetic effect, they also had a residual effect that was three to four times that of the residuals for flowering time. This was likely due to phenotyping error introduced through inconsistencies of multiple personnel assisting in collecting height notes. This was especially seen in ear height, ~25% residual variation, in which height measurements were supposed to be taken at the ear node, but with the node being hidden under the leaf sheath, consistency was more difficult to achieve between personnel. Genotype by environment interactions were small (1% to 3%) for flowering time and plant height, supporting a combined analysis was appropriate.

The combined analysis of leaf rolling over four environments, had a greater genotype by environment interaction of ~19% (Table 9) resulting in a lower heritability (H^2=0.5) than that of the quantitative agronomic traits (H^2 = 0.92 ± 0.02; Table 8). Leaf rolling had the least environmental variation (9%) and the greatest spatial variation of all the traits. This was likely due to two factors. First, the dynamic nature of the leaves rolling throughout the day influencing the order that notes were taken on each plot. Second, the standing water throughout the vegetative growth phase in 2014 and 2015, restricted deep root growth reducing the plants ability to access moisture deeper in the soil during the dryer summer months when leaf roll ratings were taken. Though, inconsistencies in ratings were accounted for with the TRM effect (~3%), leaf rolling showed a large residual effect (~40%). This indicated that some additional factors were not accounted for within the model to accurately explain the variation in leaf rolling and/ or that it is a difficult measurement to make. The smaller number of environments in which leaf rolling was measured compared to the agronomic traits, could also have increased the residual error. Continued evaluation of leaf rolling within more environments accompanied with more detailed rating methods, such as imaging by aerial vehicles, may help to partition the residual into its confounding effects.

Table 9. Combined analysis of leaf rolling presented as the variation component, significance level, and percent variation (%).

	LR	
	Var Comp	% †
Environment	0.0556**	9.30
Block[Env]	0.0683**	11.42
Range[Env]	0.0052**	0.87
Row[Env]	0.0069**	1.16
TRM[env]	0.0158**	2.64
Entry	0.0904**	15.12
Entry*Env	0.1123**	18.77
Residual	0.2435	40.72
Heritability	0.50	

** Significance at α=0.01

† Percentage of variation explained by effect

2.4.3 QTL Mapping Across the Full Population

BLUPS of entry effect from multi-environment trial (MET) analysis were used as phenotype data in mapping QTL for the agronomic traits. Analysis of full population (2way&4way) using the full marker set associated a single significant locus peak with all four agronomic traits upon the same region of chromosome 3 across a 1,314,463 base pair region (Figure 5, Table 10). This was both the largest peak and the only significant peak at the stringent multiple-testing LOD threshold.

With the FPM population being a linkage mapping population we assume that adjacent markers are likely linked, which contradicts the assumption of complete linkage equilibrium (D=O) among the markers used in Bonferroni multiple test adjustment implemented in GAPIT. Appendix B5 includes a list of all SNP with LOD≥3.00, as this is commonly considered a marker of interest in linkage mapping analyses (Broman, 2001). Additionally, we have identified loci based on a SNP being less than 1 Mbp from its' adjacent SNP. From this selection criteria we have identified 1,521 SNPs of interest: 231 for plant height, 328 for ear height, 522 for days to anthesis, and 490 for days to silking; which identify 38 loci for plant height, 28 for ear height, 39 for days to anthesis and 38 for days to silking.

2.4.3.1 Plant Height and Ear Height

The major QTL associated with plant height was located on chromosome 3 at 157,576,421 bp with a LOD of 7.00 (Figure 5,PH; Table 10). Analysis of the markers flanking either side of chr3_157576421 indicated that the negative allele (A) was donated by founder line Tx903 with an allelic effect of 4.16 cm decrease in overall plant height across the full population explaining one percent of the variation. It was not surprising that Tx903 contained the allele that decreases height as it was one of the shorter founders (Appendix B3 and Mahan (2015)). A significant QTL with a LOD of 13.07 was also found upon chromosome 3 for ear height at 158,780,918 bp, within 1.4 million base pairs of the plant height locus. Chr3_158780918 decreased ear height by 3.73 cm when a "G" allele was donated by Tx903 and explained three percent of the genetic variation (Figure 5,EH ; Table 10) across the full population.

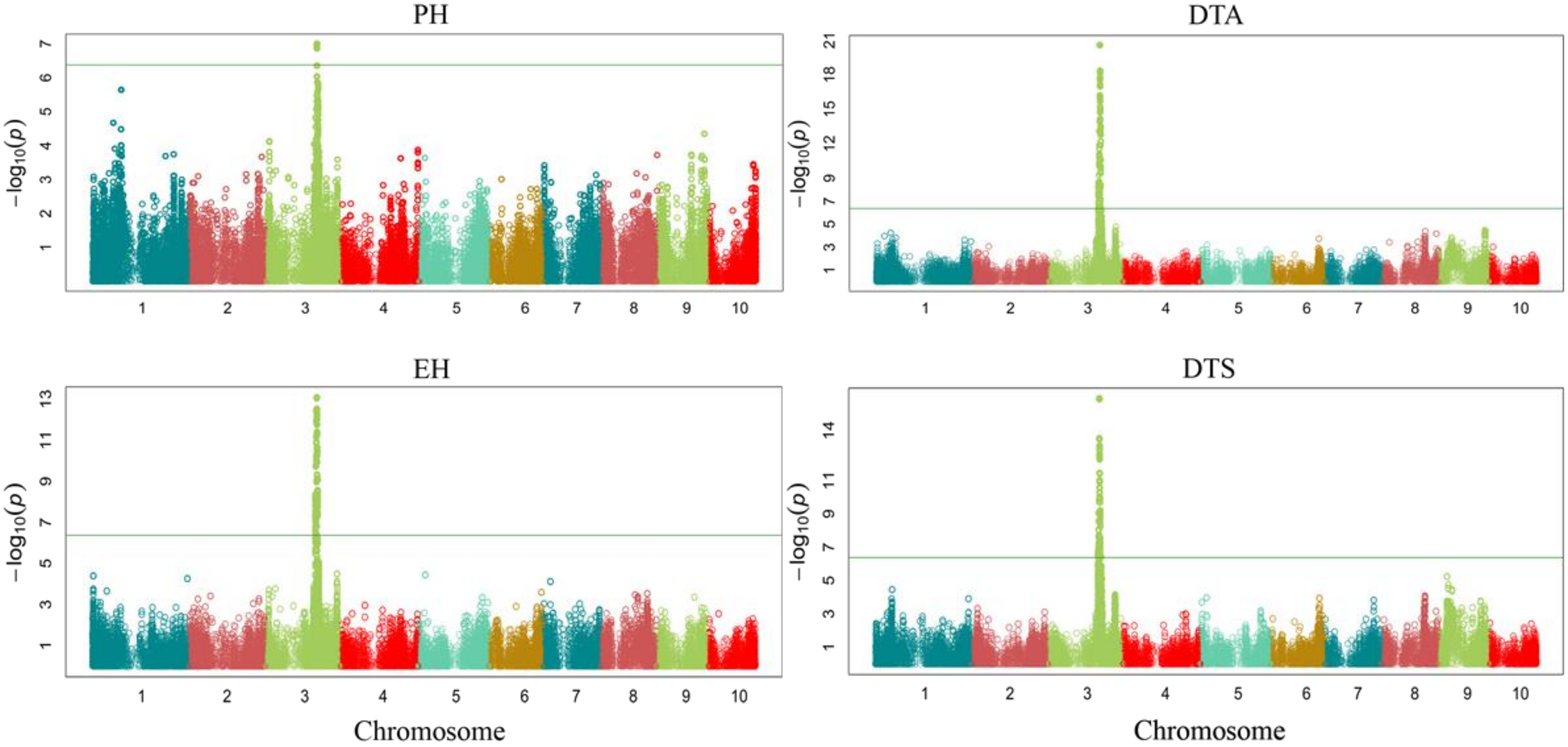


Figure 5. Manhattan plot summaries of association peaks for plant height (PH), ear height (EH), days to anthesis (DTA) and days to silking (DTS) within the entire population. Horizontal green line indicates significance threshold (α=0.05) set using Bonferroni multiple test adjustment. See appendix B4 for complete list of SNP above 3.0 LOD.

Table 10. Summary of peak markers for the four agronomic traits including LOD support intervals, minor allele frequency (maf), allelic effect estimate and allele donated by parent causing the effect.

Trait	Chr	Pos	maf	Peak LOD	1-LOD SI	2-LOD SI	3-LOD SI	Allelic Effect	Allele Call	Parent
PH	3	157,576,421	0.30	7.00*	157,417,448 - 157,576,733	155,803,532 - 161,650,243	148,877,069 - 161,650,452	-4.16 cm	A	Tx903
EH	3	158,780,918	0.30	13.07*	157,417,448 - 159,801,043	157,417,448 - 159,807,447	157,417,448 -160,665,463	-3.73 cm	G	Tx903
DTA	3	158,890,884	0.48	20.58*	-	-	158,890,884 - 159,807,447	-0.88 days	T	Tx903 Tx772
DTS	3	158,890,884	0.48	15.91*	-	-	158,890,884 - 159,385,192	-0.87 days	T	Tx903 Tx772

*Significant at α=0.05 using Bonferroni adjustment

The variation in the most significant SNPs for plant height (chr3_157,576,421) and ear height (chr3_158,780,918) may be explained by an adjacent gene semi-dwarf 2 (sdw2) locus (Neuffer, 1992) (chr3:158,841,148..161,311,068; RefGenV2 and IBM2 2008 Neighbors map). Although, sdw2 exact location is unknown, it is a probable candidate gene due to its close proximity to the height QTLs. Previous analysis of maize diversity panels have identified significant associations within this region of the genome for all agronomic traits (Wallace, et al., 2014) increasing our confidence in the peak associations of this study, allowing for identification of parent allele donation and its effect.

2.4.3.2 Flowering Time

Significant QTL associated with flowering time were located within 120 kb of the ear height loci, on chromosome 3 at 158,890,884 bp with a LOD score for 20.58 for DTA and 15.91 for DTS. The allelic effect at this locus was roughly a one day change in flowering time within the entire population explaining four percent of the variation (Figure 5,DTA and DTS; Table 10). The peak SNP (chr3_158,890,884) flanks a MADS-transcription factor 69 (mads69) locus (GRMZM2G171650 [zmm22]) (chr3:158,979,321..159,007,265; RefGenV2 and IBM2 2008 Neighbors map). MADS-box genes such as zmm22 encode transcription factors important in regulating plant development, specifically zmm22 has been shown to be important in improved selection in maize (Zhao, et al., 2011). Additionally, modulating the expression of GRMZM2G171650 can alter timing of vegetative to reproductive phase (Kaeppler, et al., 2014), making it a likely candidate gene of flowering time in our study. It is also possible that this gene could be responsible for the semi-dwarf 2 (sdw2) locus.

Parental lines, Tx903 and Tx772 carried the negative effect allele in their respective bi-parental subpopulations, making it difficult to conclude which of the two founder lines had the greater allelic impact on the entire population (Appendix A1[c:d]). For this reason, introgression of the “T” allele from either line could reduce flowering time by one day. Although Tx903 showed a consistent negative effect across the flanking markers within the di-hybrid population, further investigation is need to determine which parent, if not both, is causing the effect.

Comparison of the Manhattan plots of the two biparental populations using only the markers that segregate within both populations (Figure 6) allowed a better understanding of which parental lines contributed the phenotypic association seen in the dihybrid population. It is evident that the variation associated with chromosome 3 originated within the B73*olc1* x Tx903 population (Figure 6[a]), in which significant peaks are located within the same region of chromosome 3 as that of the GWAS results conducted on the dihybrid population. When compared to the Tx772 x Tx906 population (Figure 6[b]), we can see distinguishable peaks upon chromosome 3 for plant height,

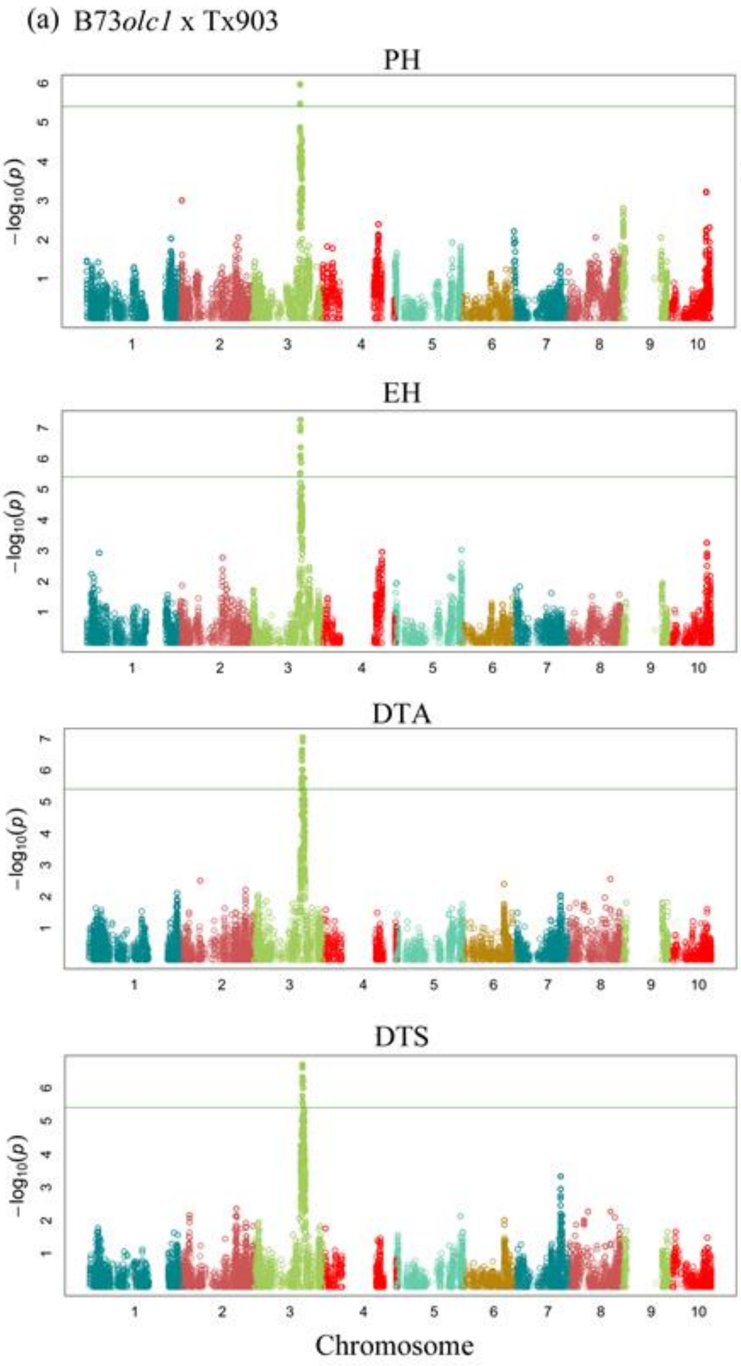


Figure 6. Comparison of Manhattan plots from [a] B73*olc1* x Tx903 and [b] Tx772 x Tx906 bi -parental populations using a restricted ~12,000 marker set segregating between the populations. Horizontal green line indicates significance threshold (α=0.05) set using Bonferroni multiple test adjustment. See appendix B5 and B6 for complete list of SNP above 3.0 LOD.

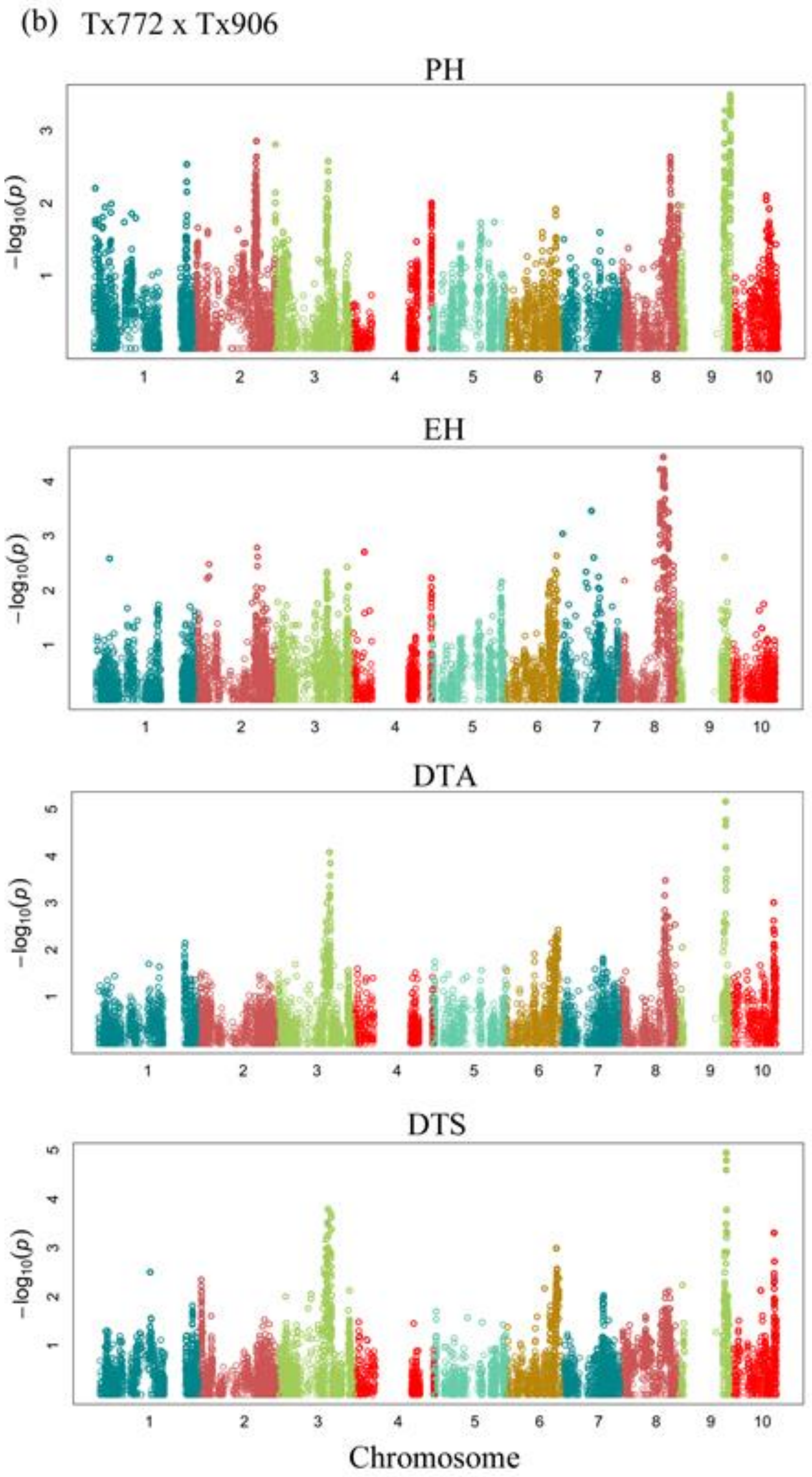


Figure 6 Continued.

DTA and DTS, although greater association are found upon chromosome 9 for these traits. Additionally, EH variation was highly associated with a region upon chromosome 9 within the Tx772 x Tx906 population. These comparisons, further strengthen our conclusion that variation for all the traits is being explained to a higher degree an allele segregating in the B73*olc1* x Tx903 population with the negative effect allele being contributed by Tx903 for the agronomic traits, though it cannot be ruled out that the Tx772 allele could be contributing a comparable negative effect allele for flowering time. The allelic effects of the QTLs must be validated through analysis of near isogenic lines at these loci.

2.4.4 Genome Wide Association Study of Leaf Rolling

Significant variation has been captured within the FPM population for the trait of leaf rolling. Following evaluation across five environments, BLUPs were estimated and used in mapping to decipherer underlying genetic factors that explain the leaf rolling phenotype. Mapping using the high stringency of GAPIT resulted in no significant peaks, however the highest peak was located on chromosome 3 at 217,213,085 bp with a 5.06 LOD score (Figure 7, combined environment). The 1-LOD support interval covers 5,388,148 bp (chr3:212,548,086. 217,936,234) where the peak lies directly upon wrky64 (chr3:217,212,882..217,215,223; RefGenV2 and IBM2 2008 Neighbors map), a member of a group of transcription factors that have shown to cause leaf senescence when up regulated within Arabidopsis (Eulgem, et al., 2000). Furthermore, this region of the genome is flanked by two cytochromes cyp10 (chr3:216,986,019..216,989,235; RefGenV2 and IBM2 2008 Neighbors map) and cyp11 (chr3:217,137,202..217,140,695;

RefGenV2 and IBM2 2008 Neighbors map), which are important oxidative-reductase proteins within the electron transport chain of ATP synthesis. These results may be an indication that our evaluation of leaf rolling may be related to leaf senescence, though additional experiments will be necessary beyond the scope of this study to validate such hypotheses. Additionally, the high genotype by environment variation cannot be dismissed, as it may be causing the genetic association to be dispersed across the genome effectively reducing marker association when the combined analysis entry BLUPs are used in the GWA study and single environment phenotypes could be useful.

To access the degree at which the association was dispersed across the genome due to the GEI leaf rolling, GEI BLUP estimates of each entry and the corresponding environment were used as phenotypic data. Resulting Manhattan plots depicted noticeable variation in marker association between environments (Figure 7).

Additional smaller focused trials as well as improved scoring systems will reduce the residual error within leading to more accurate BLUPs. Followed by implementing a variance-covariance (VCOV) model (Malosetti, et al., 2013), with the additional data, to better understand differential expression of leaf rolling QTL across environments.

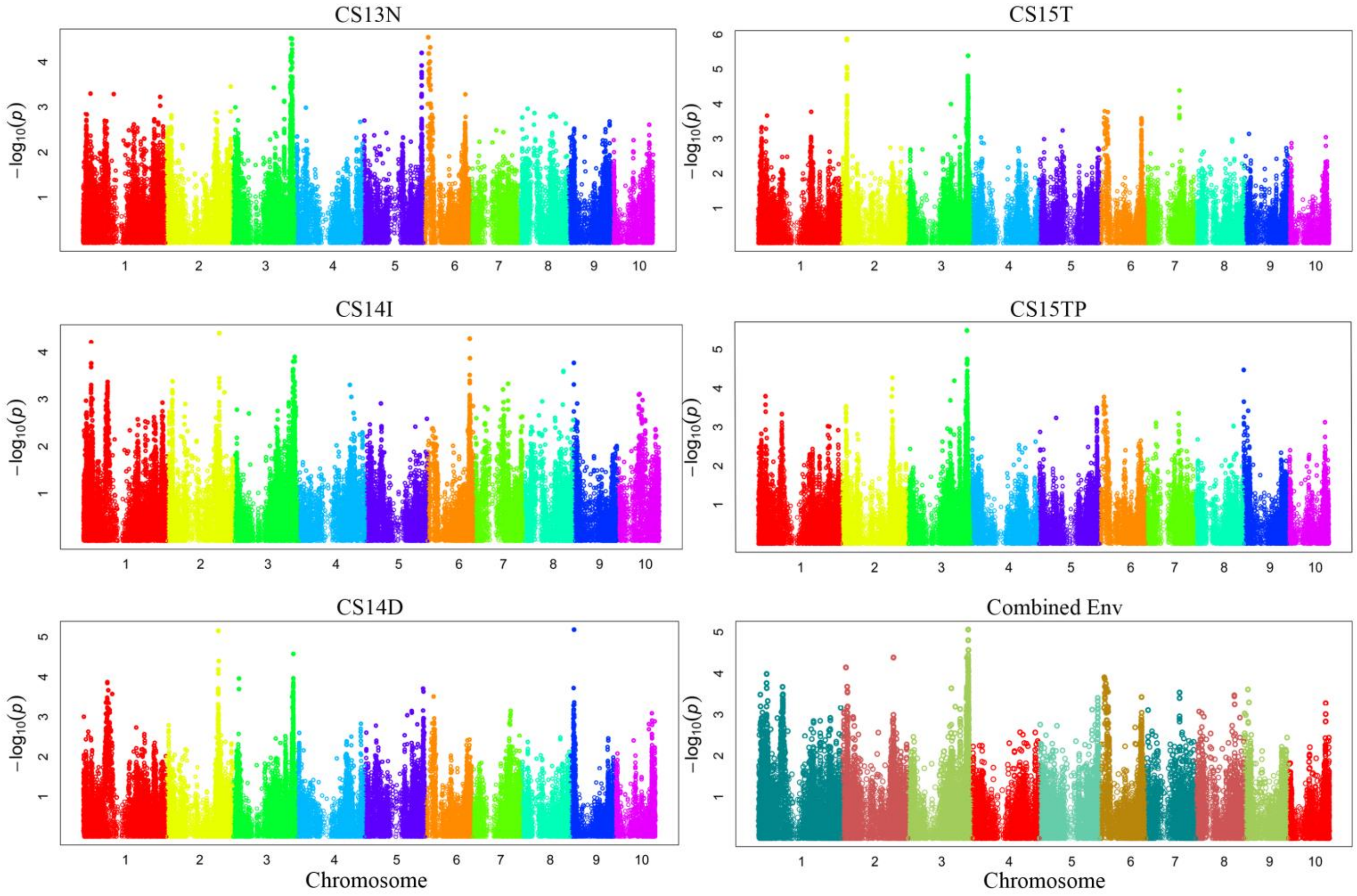


Figure 7. GWAS Manhattan plots of leaf rolling using GxE BLUPS by environment to analyze the effect of the large GxE variation. Additionally, the combined environment analysis of leaf rolling using entry BLUP estimates. See appendix B7 for complete list of SNP above 3.0 LOD.

2.4.5 Comparison of Mapping Resolution

2.4.5.1 Mapping Resolution Across Subpopulations

One of the major objectives of this study was to determine the effect of mating design on QTL locus detection power and resolution. Significant peaks for the major QTLs on Chromosome 3 were identified within the entire population, all of the four-way crosses, the combined two-way crosses and the B73*olc1* by Tx903 subpopulation alone for plant height (Table 11). Additionally, the 4way3sib and 4way1sib populations were capable of detecting significant associations in the three other agronomic traits (EH, DTA and DTS) (Tables 11; Table 12). It was not surprising that the entire population and all four-way crosses had significant associations because they had the two largest population sizes of all the groupings, and a reduction in LOD score correlated with a reduction in population size could be seen across the all dihybrid crosses. Significance within the two way crosses and the B73*olc1* x Tx903 subpopulation, could also be explained by the reduction in polymorphic markers within these populations, reducing the significance threshold for multiple testing correction. It was expected that the 4way3sib population would have the highest mapping resolution, due to increased effective recombination events compared to other the subpopulations. Mapping resolution was determined through comparison of 1-LOD support interval of peak SNPs. Support intervals were calculated as the furthest SNP on either side of the peak within 1-LOD of the peak. When comparisons were made among the dihybrid subpopulations this assumptions of increased mapping resolution appeared to hold true as the support intervals reduced as intermating increased. The 4way2sib population’s support interval was greater than the 4way1sib in all cases, though this may have been due to the small population size incapability of capturing the phenotypic variation to accurately estimate the association and in the case of PH and DTS it places the largest peak upon a different chromosome (Table 11; Table 12). If the 4way2sib subpopulation is overlooked, the assumption of increased resolution as the generations of intermating increase holds true for ear height, DTA and DTS.

Similarly, the mapping resolution of the bi-parental population was expected to be less than that of the intermated four-way subpopulations populations. The B73*olc1* x Tx903 population exhibited SI that were of higher resolution than all of the dihybrid subpopulations, with the exception of the 4way3sib for flowering time which could be to stochastic chance. However, as LOD SI should be adjusted according to the number of individuals, marker density and QTL effect size (Manichaikul, et al., 2006), it is rational to conclude that using 1-LOD support intervals as an estimation of mapping resolution when using GWA methods is an inaccurate technique for comparison of mating designs mapping resolution in regions of the genome where causative genes are unknown. Construction of linkage maps and estimation of recombination fractions will shed insight on the true resolution potential of mapping QTL within the FPM subpopulations.

A number of studies have found that unrealistic LOD significance thresholds result from using an association mapping approach for genome wide markers (Dudbridge and Gusnanto, 2008; Gao, et al., 2010; Johnson, et al., 2010). In a true association population, most markers will be relatively independent (Bush and Moore, 2012), however in this linkage-based population, adjacent markers are highly

Table 11. Summary of peak positions within subpopulations for height traits on the region of chromosome 3 where the whole entire population peak is estimated including 1-LOD support interval (SI), maf and location of largest peak off chromosome 3.

Trait	Pop	N	Peak LOD Chr3	Position on Chr3 (bp)	maf	1-LOD SI (bp)	SI distance (bp)	Captures true peak	Largest peak location
PH	Entire Pop	1149	7.00*	157,576,421	0.30	157,417,448 -157,576,733	159,285	TRUE	-
	All 4way	912	6.76*	157,576,226	0.28	154,075,824 -157,576,421	3,500,597	TRUE	-
	4way3sib	491	5.20	161,573,010	0.25	154,075,824 -161,650,452	7,574,628	TRUE	-
	4way2sib	93	3.52	154,124,966	0.46	146,252,852 -157,576,432	11,323,580	TRUE	Chr8
	4way1sib	212	5.78	156,071,244	0.42	154,124,966 -157,576,733	3,451,767	TRUE	-
	4way0sib	107	4.92	154,077,729	0.19	154,077,726 -159,810,023	5,732,297	TRUE	-
	All 2way	238	5.57*	159,820,547	0.38	159,385,192 -159,820,547	435,355	FALSE	-
	B73*olc1* x Tx903	126	5.88*	159,381,162	0.30	159,381,121 -161,573,250	2,192,129	FALSE	-
	Tx772 x Tx906	112	-	-	-	-	-	FALSE	Chr9

*Significant at α=0.05 using Bonferroni adjustment

Table 11. Continued

Trait	Pop	N	Peak LOD Chr3	Position on Chr3 (bp)	maf	1-LOD SI (bp)	SI distance (bp)	Captures true peak	Largest peak location
EH	Entire Pop	1149	13.07*	158,780,918	0.30	157,417,448 -159,801,043	2,383,595	TRUE	-
	All 4way	912	11.74*	158,780,918	0.28	155,803,532 -159,801,043	3,997,511	TRUE	-
	4way3sib	491	8.99*	158,780,918	0.27	157,576,226 -158,780,918	1,204,692	TRUE	-
	4way2sib	93	4.45	161,369,818	0.27	153,764,074 -162,034,831	8,270,757	TRUE	-
	4way1sib	212	9.74*	157,576,421	0.33	155,803,532 -159,868,843	4,065,311	TRUE	-
	4way0sib	107	5.99	154,625,415	0.22	141,982,972 -157,576,725	15,593,753	FALSE	-
	All 2way	238	5.11	158,890,884	0.39	158,890,884 -159,820,547	929,663	FALSE	Chr10
	B73*olc1* x Tx903	126	7.85*	159,381,162	0.30	159,381,121 -159,810,124	429,003	FALSE	-
	Tx772 x Tx906	112	-	-	-	-	-	FALSE	Chr8

*Significant at α=0.05 using Bonferroni adjustment

Table 12. Summary of peak positions within subpopulations for flowering time traits on the region of chromosome 3 where the whole entire population peak is estimated; including 1-LOD support interval (SI) , maf and location of largest peak off chromosome 3.

Trait	Pop	N	Peak LOD Chr3	maf	Position on Chr3 (bp)	1-LOD SI (bp)	SI distance (bp)	Captures true peak	Largest peak location
DTA	Entire Pop	1149	20.59*	0.49	158,890,884	-	0	TRUE	-
	All 4way	912	18.17*	0.26	159,868,843	159,678,426 -159,868,843	190,417	FALSE	-
	4way3sib	491	14.27*	0.26	159,868,843	159,868,843 -161,732,785	1,863,942	FALSE	-
	4way2sib	93	4.80	0.27	159,678,426	154,592,422 -162,096,206	7,503,784	TRUE	-
	4way1sib	212	8.99*	0.31	159,807,447	154,739,847 -159,810,023	5,070,176	TRUE	-
	4way0sib	107	5.13	0.23	149,398,810	141,982,972 -161,575,140	19,592,168	TRUE	-
	All 2way	238	8.48*	0.39	158,890,884	-	0	TRUE	-
	B73*olc1* x Tx903	126	7.17*	0.29	161,563,404	157,576,643 -161,732,785	4,156,142	TRUE	-
	Tx772 x Tx906	112	3.86	0.49	156,287,758	146,607,404 -159,385,356	12,777,952	TRUE	Chr9

*Significant at α=0.05 using Bonferroni adjustment

Table 12. Continued

Trait	Pop	N	Peak LOD Chr3	maf	Position on Chr3 (bp)	1-LOD SI (bp)	SI distance (bp)	Captures true peak	Largest peak location
DTS	Entire Pop	1149	15.91*	0.48	158,890,884	-	0	TRUE	-
	All 4way	912	11.93*	0.49	158,890,884	-	0	TRUE	-
	4way3sib	491	10.48*	0.26	161,732,785	159,868,843 -161,732,785	1,863,942	TRUE	-
	4way2sib	93	3.39	0.48	150,873,575	146,250,349 -162,096,206	15,845,857	TRUE	Chr9
	4way1sib	212	6.49*	0.31	156,486,164	152,208,905 -159,807,447	7,598,542	TRUE	-
	4way0sib	107	4.91	0.23	149,398,810	147,677,287 -159,801,043	12,123,756	TRUE	-
	All 2way	238	7.33*	0.39	158,890,884	156,287,758 -159,385,192	3,097,434	TRUE	-
	B73olc1 x Tx903	126	6.86*	0.30	159,381,162	159,380,134 -161,732,785	2,352,651	FALSE	-
	Tx772 x Tx906	112	4.12	0.49	148,974,648	141,493,046 -158,890,884	17,397,838	TRUE	Chr9

*Significant at α=0.05 using Bonferroni adjustment

correlated. Therefore the stringent significance threshold is certainly too stringent.

The original intent of the project was to construct linkage maps for the varying subpopulations and compare mapping abilities using linkage mapping techniques. Currently there are several programs available for analysis of multi-parental mapping populations including: R/mpMap (Huang and George, 2011), R/ricalc (Broman, 2005), R/mpwgainm (Verbyla, et al., 2014), R/qtl (Broman, et al., 2003), R/spclust (Huang, et al., 2013) and HAPPY (Mott, et al., 2000). Though these software packages are capable of simulations and QTL analysis, only R/mpMap has the capabilities of *de novo* linkage map construction for a MAGIC population. Unfortunately, R/mpMap is not currently capable of handling heterozygous alleles and those calls must be treated as missing or the marker must be removed. Additionally, R/mpMap is not capable of analyzing markers in which a parental call is a heterozygous; in this case that marker must be removed from the data set. R/mpMap inefficiently uses computing memory (RAM) and requires extreme amounts of hard drive space to construct the pairwise marker comparisons, necessitating supercomputing facilities equipped with parallel GPU and CPU processing to accomplish linkage map construction with the large marker set the FPM population possesses. Due to time constraints and lack of knowledge in parallel processing, a preliminary mapping analysis was conducted using R/GAPIT to access the population's ability to detect QTL.

2.4.5.2 Effect of Intermating on Mapping Resolution of Quantitative Traits

The FPM population was designed to compare mapping results across a diverse set of population designs to analyze the difference in bi-parental and MAGIC populations and their effects on the mapping resolution, excluding founders as a factor. To analyze the effect of intermating on mapping resolution without confounding population size, subsets of the equivalent population size were randomly selected from each dihybrid subpopulation and tested. The 4way2sib sub-population, comprised of 93 individuals, was the lower bounds for sampling the other populations to make comparisons independent of population size; from the remaining dihybrid sub-populations, three independent random samples of 93 individuals were taken. The 4way3sib sub-population was expected to have the highest recombination frequency due to a greater number of generations of intermating prior to inbreeding; resulting in more accurate, higher resolution mapping of each trait. The peak positions using the entire population (n=1400, Tables 10 and 11) were expected to be the most accurate location of the QTL due to the large population size, dense marker set, allelic diversity and high recombination frequencies. For this reason they were referred to as the true peak.

At chromosome 3 for plant height (Figure 8[a]) the mapping resolution, indicated by a 1-LOD support interval from the peak, would encompass the entire chromosome (4w3s_1; Data not shown) or the peak position is 50 Mb from the true peak (4ws3_2; 4ws3_3; Data not shown). Additionally, the 4way3sib samplings show a consistent trend in which at least one of the subsamples had equivalent or poorer mapping resolution than that of the 4way0sib population for ear height (4w3s_1) and DTS (4w3s_1;Figure 8[b:d]), or were in the wrong positions DTA (4w3s_1;4w3s_3). While the 4way1sib population had greater precision in the placement of the peak on chromosome 3 for plant height, ear height, and DTA, with respect to the other sub-populations.

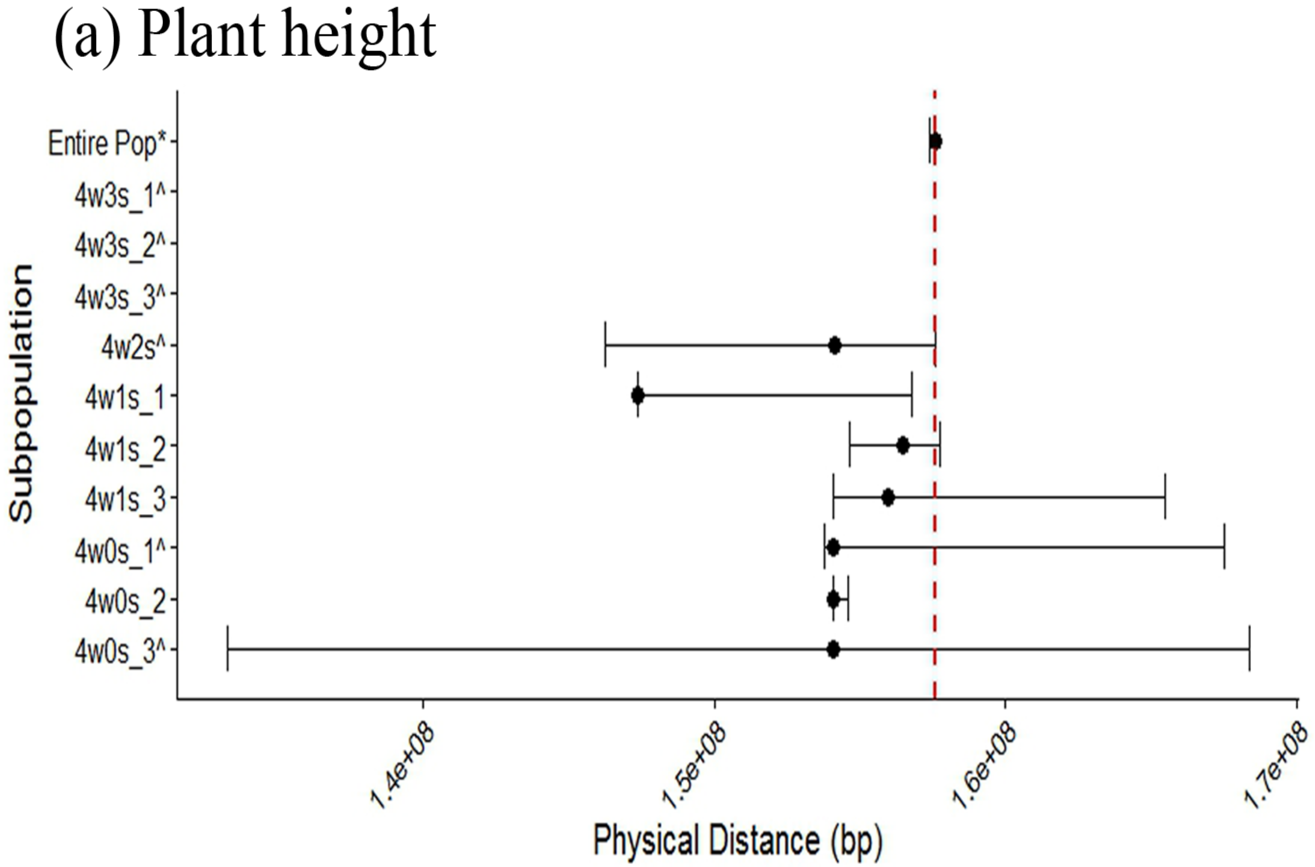


Figure 8. Peak QTL and 1-LOD support interval comparison of entire population, 4way2sib (4w2s) and randomly sampled 4way3sib (4w3s), 4way1sib (4w1s) and 4way0sib (4w0s) subpopulations for [a] plant height, [b] ear height, [c] days to anthesis and [d] days to silking on chromosome 3. Red dashed line indicates position on peak association within entire population. Significant samplings are indicated with an asterisk (*). Samples which the QTL SI encompassed the majority of the chromosome or the peak SNP was greater than 50Mbs from the true peak are indicated by circumflex accent (^).

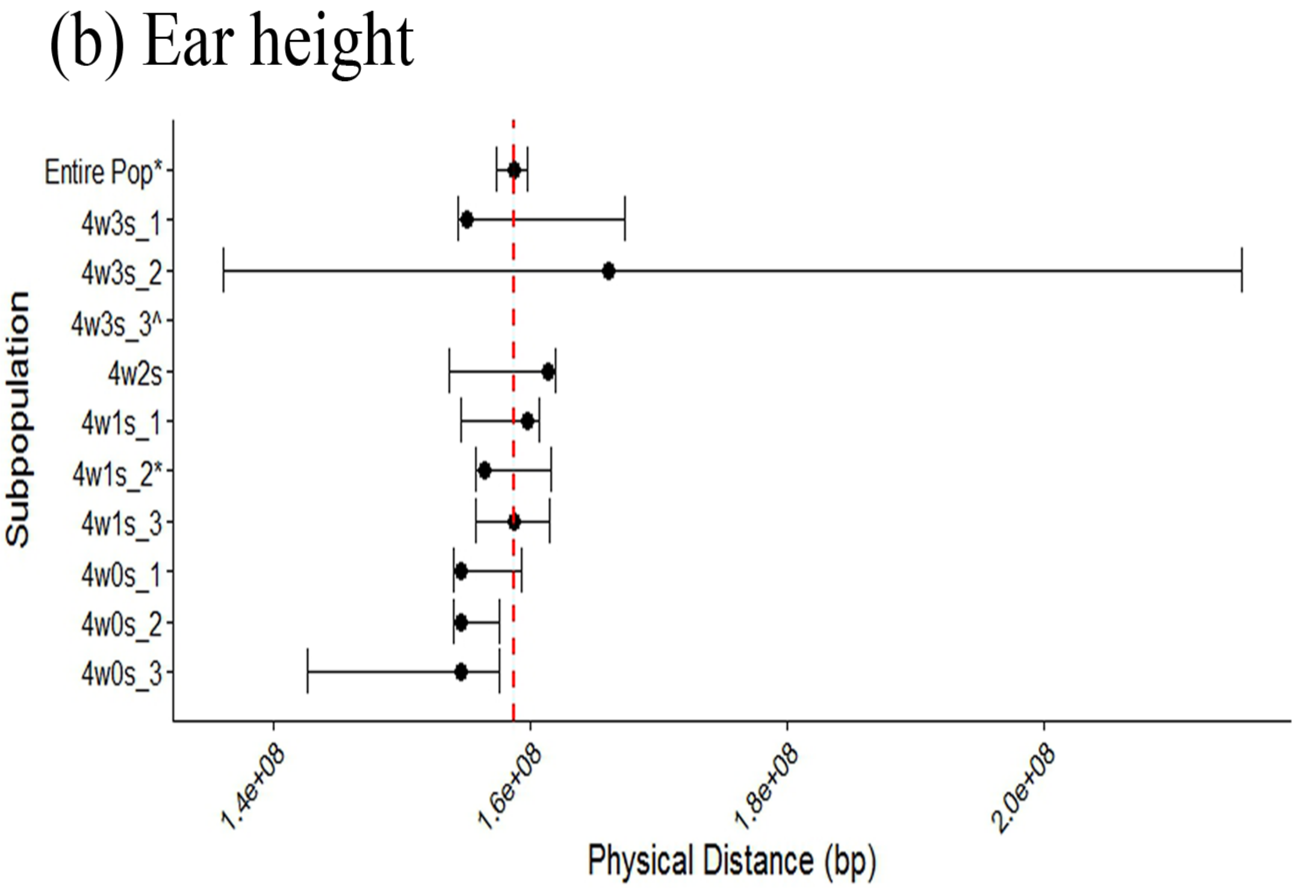

(b) Ear height

Figure 8 Continued.

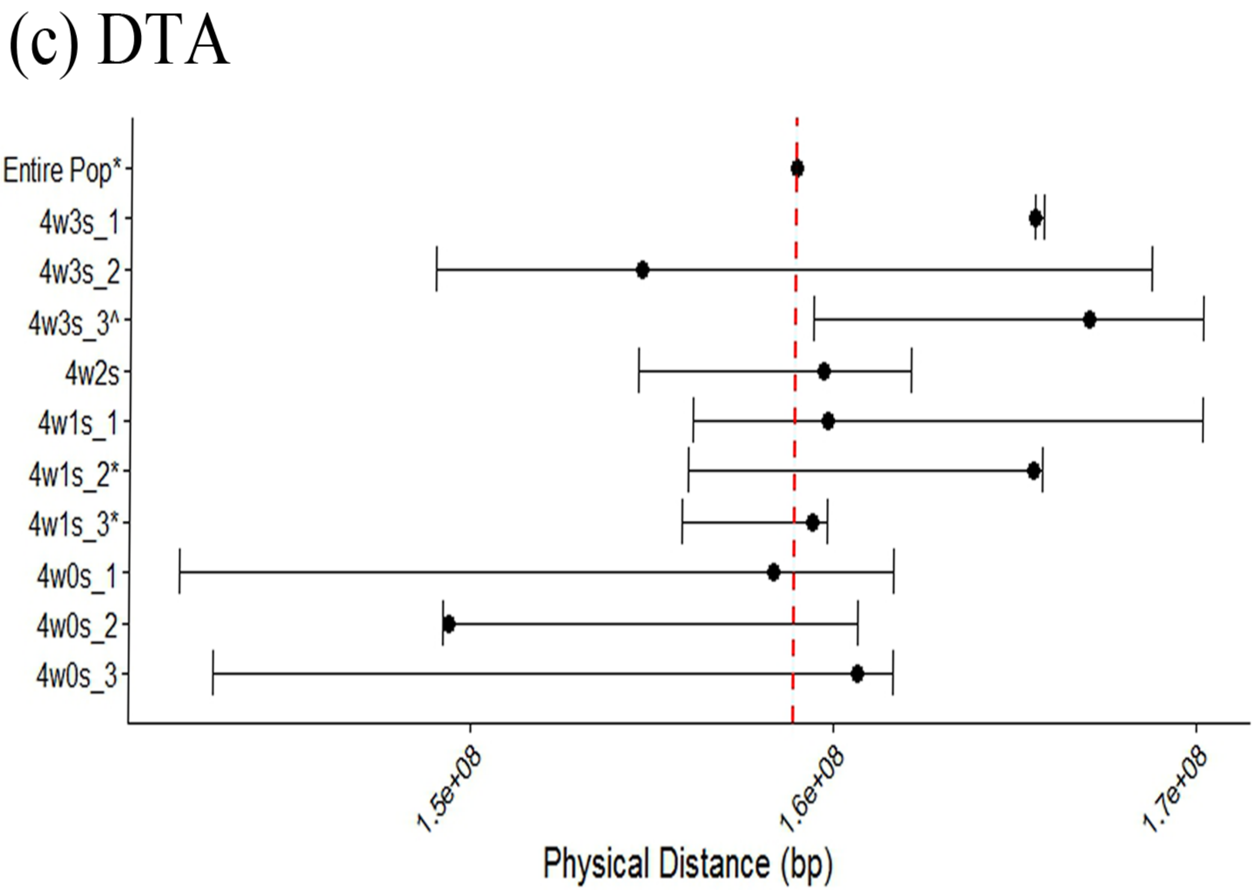
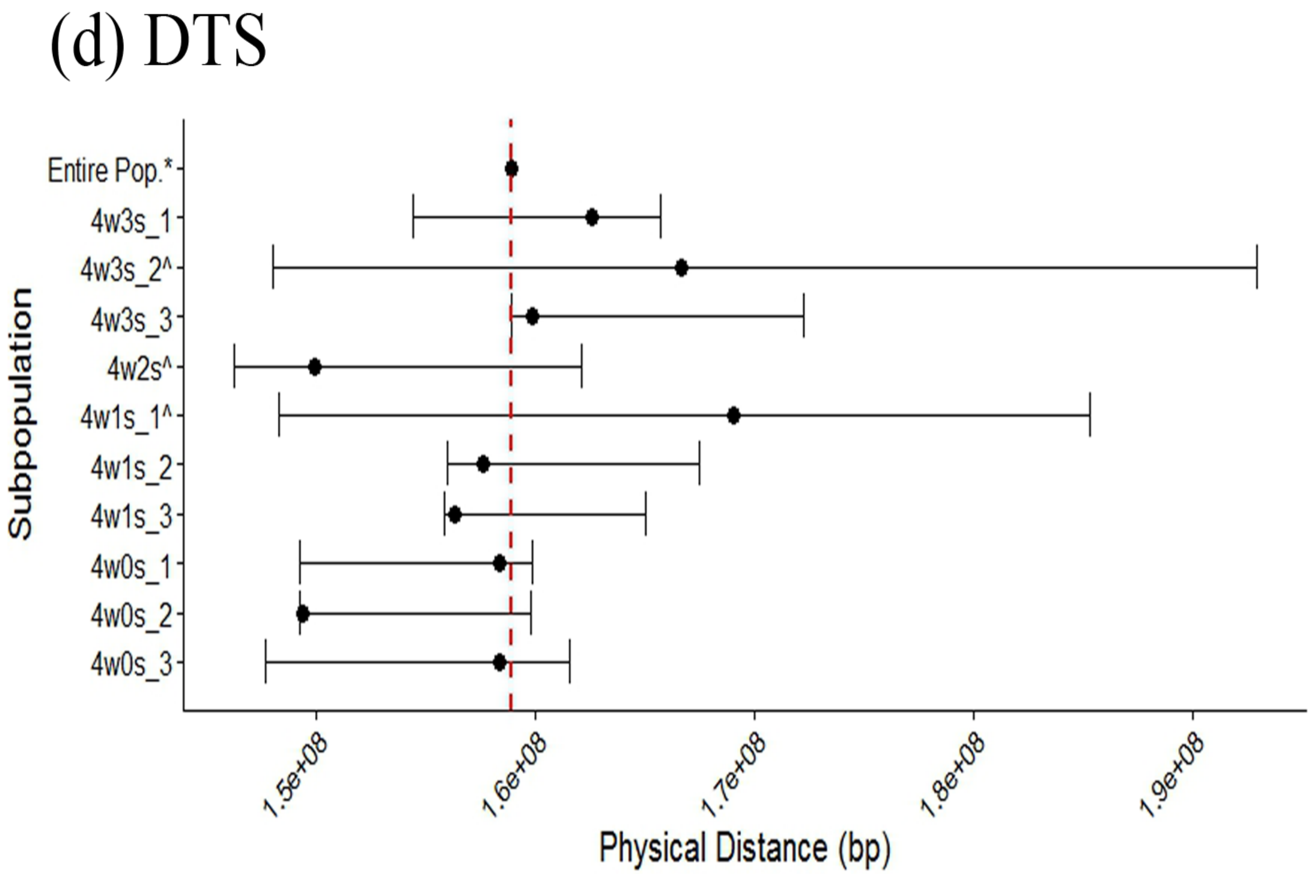


Figure 8 Continued.



(d) DTS

Figure 8 Continued

In general, this approach did not show any conclusive patterns as to the independent effect of intermating upon QTL mapping resolution. This may be due to small sampling size relative to the 4way3sib sub-population (N=~500), in which, subsampling of the 4way3sib population may not have accurately captured the phenotypic variation associated with chromosome 3, causing the phenotypic variation to be associated with different regions of the genome. The 4way3sib 93-subsamples with major peaks upon chromosome 3 had relatively poor mapping resolution as indicated by the large support intervals, further suggesting that the subsampling diluted the phenotypic/marker variation associated with the traits at chromosome 3. From this, it appears that 93 individuals have results that are too stochastic to compare mapping resolution. This stochasticity could come from differences in the variation in phenotypes, phenotype measurement error, or variation in genotypes. A major outcome was to lend empirical support to the idea that 93 individuals are not sufficient for QTL mapping and that peak locations are not at all trustworthy in this small of a population.

3. DEVELOPMENT OF *IN VITRO* CELL CYCLING PROTOCOL FOR RAPID GENERATION ADVANCEMENTS

3.1 Introduction

A major limiting factor in the plant or animal breeding process is time. The time required for the development of new varieties, specifically, the interval required for a single round of generation advancement from seed to sexual maturity to seed can be onerous to a breeding program. Current variety development consists of numerous generations of line development followed by several years of performance trials; resulting in cultivar releases requiring from seven years to several decades, depending on the species. Because of such time sinks, breeders have continually developed new techniques for rapidly advancing through generations such as: off season nurseries, gene introgression, chemical treatment of immature seed, doubled haploids, and grafting (Lee and Tracy, 2009). However, minimal research has been conducted in the area of cell culture based variety development other than genetic modification via transformation.

Culturing plant cells *in vitro*, allows the unique opportunity of manipulating cell differentiation through controlled exposure to phytohormones. For a complete review of the scientific progression of plant cell culturing, refer to Thorpe (2013). *In vitro* cell culturing has led to the monumental discovery of a singular plant cell's ability to divide, produce somatic embryos and regenerate into a fully functioning plant (i.e. totipotency). In many species, by providing a particular ratio of auxins to cytokinins, cells can be made to grow as undiffentiated callus cells and by altering this ratio and environmental conditions, these cultured cells can be induced to form organized tissues, such as somatic embryos, shoots or roots. Calli, composed of clusters of cells, can be broken into single-cell units (protoplasts), through enzymatic degradation of the cell wall. Through proper calibration of fluorescence activated cell sorters (FACs), protoplasts can be rapidly processed and individually isolated by detection of fluorescent tags (Galbraith, 2012). These isolated cells can be cultured by incubation in nurse cell conditioned media, that provided the required factors/nutrients to induce the singular cells to divide into monoclonal colonies (Schäffler and Koop, 1990).

Nurse cells are a collection of cells, usually grown as suspension cultures from which the protoplasts are isolated, that are embedded/suspended within the media. These nurse cells serve to overcome the minimum cell density threshold required within a volume of media to induce cell wall synthesis in the protoplasts, mitotic division and cell colony formation. The nurse cells release sufficient nutrients and growth factors into the media necessary to stimulate singular protoplasts to divide (Davey, et al., 2005). Adjustment of phytohormone levels, will stimulate the colonies to produce somatic embryos that will develop into plantlets. Extensive research has gone into accelerating the process of cell totipotency, mainly for the purposes of transgene integration, through optimization of media supplements and culture conditions. While each of these steps has been demonstrated individually, a cell line has not been taken through repeated cycles of *in vitro* cycling. Integration these different mature components will likely create new unanticipated barriers.

Recently in mice, stem cells have been induced to differentiate into gametes through mimicry of testicular/ovarian fluids, followed by fusion to form zygotes that were capable of developing into living offsprings (Hayashi, et al., 2012). Development of similar *in vitro* gamete cycling provides a possible option to bypass the vegetative plant growth stage through *de novo* gametogenesis in culture, drastically reducing the generation time requirements. Cycling of gametes *in vitro* (CoGiV), would provide the opportunity to implement a radically new technology to improve plants and animals, through rapid cell cycling accompanied by marker assisted selection. However, several challenges must be overcome to make this technology possible: (i) the concept of cell cycling must be demonstrated efficiently; (ii) unintended selection of favorable cell culturing traits must be avoided; and (iii) unwanted somaclonal variation due to rapid cellular division must be minimized to avoid *de novo* mutations (De La Fuente, et al., 2013; Murray, et al., 2013).

As a result, the primary objectives of this research include: (i) assessing current protocols involved in the cellular totipotency dogma for areas that include improving cell growth rates and protoplast isolation efficiency; (ii) evaluating the process of FAC sorting of singular cells across species in order to develop a comprehensive FACs protocol; (iii) assessing the true potential of CoGiV in rapid cultivar development; and (iv) investigation of methods/conditions that further accelerate of the process of cell cycling.

3.2 Literature Review

3.2.1 Accelerating Generation Times

With the world population projected to grow above 9 billion by the year 2050, there is a perpetual need to produce a sufficient supply of food and fiber to sustain the growing population requirements (FAO, 2013). Being at the forefront of solving this endemic problem, breeders are continually working to develop varieties that encompass higher yields, nutritional benefits and tolerance to continually shifting environmental conditions of the world. The production of improved/novel traits is dependent on subsequent meiotic events allowing for new allelic combinations to occur by means of genetic recombination. Annual species, making up the majority of the world's crops, complete one meiotic event during a life cycle requiring multiple generations, if ever, to produce the desired recombination events, if known. To combat the issue of time, breeders are continually searching for methods of rapid generation advancement.

A major driver of the gains that came from the green revolution was the reduction of time to a finished cultivar. During the Mid-20th century, introgression of new traits into wheat required 10-12 years of breeding. With the development of off season nurseries and the serendipitous selection of photoperiod insensitivity, new cultivars could now be developed in four to six years (Borlaug, 2007). An additional improvement made in wheat was the low temperature hydrogen peroxide treatment of immature seed harvests, 15-20 day post anthesis (DPA), that has been shown to produce viable germination, allowing 4-6 generations of wheat per year (De Pauw and Clarke, 1976; Mukade, et al., 1973). In other species, additional approaches have been undertaken. Wang, et al. (2011) developed procedures for in vitro culturing of cotton plantlets from 10-20 DPA embryos followed by grafting to a rootstock. This allows for three generations of advancement per year through reduction in generation time by 43 days.

More recently, specific genetic modifications have been developed to decrease generation times. Constitutive over expression of *FLOWERING LOCUS T* (FT) gene (35S::FT) induces early flowering in late day plants (Kardailsky, et al., 1999). Average generation time has been reduced by 90 days in tobacco varieties trough transgenic incorporation of 35S::FT into backcrossing schemes (Lewis and Kernodle, 2009).

Perhaps the most extreme example for the necessity for rapid breeding generation advancement comes in the form of forest tree domestication. With conventional breeding averaging several decades for introgression and release of a new variety, such as in loblolly pine (*Pinus taeda*), there is a great need for new genomic technologies (Harfouche, et al., 2012). Due to these necessities, tree breeders were among the first adopters to use genomic selection (GS) methods. With the use of genome-wide dense marker maps, it is now possible to estimate breeding values of species which lack phenotypic data or progeny. GS of breeding values in combination with modern reproductive techniques will enable substantial increases in genetic gain accompanied with reduced generation intervals (Hayes and Goddard, 2001). Additionally, incorporation of relevant quantitative trait polymorphism discoveries and their effects on phenotypes in relevant conditions will further improve the accuracy of GS training models (Resende, et al., 2012). Through the use of top grafting, genomic selection and clonal propagation, single cycle of genetic improvement in Southeastern United States pine species has been reduced from twenty six to five years, with the breeding period accounting for four of those years (Harfouche, et al., 2012). CoGiV could potentially provide a solution by reducing the breeding period of these species.

3.2.2 Doubled Haploids Can Improve Pure Line Generation Speed

Doubled Haploids (DH) have been a major component in the reduction of generations necessary to produce homozygous inbred lines (IBL), particularly in maize (Geiger and Gordillo, 2009). Current methods of haploid isolation include *in vivo* haploid induction (Forster, et al., 2007; Rober, et al., 2005) *in vitro* anther culture (Jain, et al., 1998; Luckett and Smithard, 1992; Pink, et al., 2008) and *in vitro* microspore cultures (Möllers, et al., 1994). Artificial chromosome doubling, such as through the use of colchicine, is necessary to produce reliable double haploids (Gayen, et al., 1994; Wan, et al., 1989). Advantages of DH lines in hybrid breeding can include: maximized genetic variation, complete homozygosity, simplified logistics, reduced costs, high reproducibility of early selection results. These pure lines are also ideal for marker applications (Geiger and Gordillo, 2009; Rober, et al., 2005). When combined with marker-assisted selections (MAS), doubled haploids have the ability to greatly increase the efficiency of breeding programs incorporating DH technology.

3.2.3 Plant Tissue Culture

Thorpe (2007) defines plant tissue culture as the sterile cultivation of cells, tissue or organs along with their components within defined physical and chemical conditions *in vitro.* The development of cellular theory arose through the extensive microscopic research of plants and animals by Schleiden and Schwann. Schleiden (1838) theorized that all components of plants are compose of cells. Concurrently, Schwann (1839) concluded that the basis for development of all tissues and organisms is the formation of cells. Accredited with establishing the concept of totipotency, Gottlieb Haberlandt, the ‘father of plant tissue culture’, predicted the ability of all vegetative cells to proliferate, divide and produce artificial embryos (Hussain, et al., 2012; Krikorian and Berquam, 1969). Pioneering developments of in vitro cell culture included: Isolated root tip cultures (Robbins, 1922; White, 1934), excised stem tips cultures (Ball, 1946; Loo, 1945) and culturing of isolated embryos (Laibach, 1929; LaRue, 1936; Tukey, 1934). It is important to note that initial culture explants were derived from meristematic tissue, but this nevertheless paved the way for future studies.

Great advances in plant cell culturing commenced with the development of media supplements, new techniques and improvements upon those already available. Continuous plant tissue cultures with the ability for sub culturing was achieved through the incorporation of Went (1926) growth substance indole-3-acetic acid (IAA), extracted from brewer’s yeast, within agar media (Gautheret, 1939; Gautheret, 1985; Nobécourt, 1939; White, 1939). Miller, et al. (1955) demonstrated that IAA, as the sole phytohormone, was incapable of initiating cell division. Upon addition of kinetin, found in high concentration in yeast and herring sperm, an increase in fresh and dry callus weight, along with a 31:1 (treated to non-treated) ratio of cell numbers was observed within six days. Auxin-cytokinin interactions have an effect on DNA production, mitosis and cytokinesis; demonstrating the counteractive nature of the phytohormones in manipulating cellular development *in vitro* (Skoog and Miller, 1957). Cytokinin supplements are capable of supporting bud growth, which is suppressed upon addition of auxins and callus growth is favored. Additionally, cytokinin levels as low as 0.2 ppm are sufficient for suppression of root development.

Murashige and Skoog (1962) obtained a four to five fold increase in callus yield when aqueous tobacco leaf extract was added to White's modified media (White, 1939) supplemented with kinetin and IAA. Upon further experimentation it was discovered that this increase in yield was due to a fourfold increase in the inorganic elements. With success in callus initiation, cell suspension and morphological studies, MS media success is due to its ability to fulfill the physiological requirements of plant cells due to the correct quantities of inorganic elements it provides (Gamborg, et al., 1976). This is not to say that MS media is the optimal recipe - each species has its own optimal media requirements that must be empirically evaluated for ideal *in vitro* cell growth.

3.2.4 Single Cell Totipotency

A critical necessity of CoGiV is that single cells must be isolated and remain totipotent (capable of regenerating into a fully functioning plant). Initially in the history of tissue culture, single cell isolates originally had little success at being cultured. The first successful single cell isolation to divide and produce a culture was placed upon filter paper on top of 'host' tissue (Muir, et al., 1954). This ability of the single cells to successfully divide was attributed to improved gas exchange as well as transmission of nutrients, growth factors and metabolites between the cell and the 'host' callus (termed nurse tissue) below (Muir, et al., 1958). Division of isolated single cells has been achieved using an agar hanging drop techniques (Torrey, 1957) as well as isolation from liquid suspensions using 0.1 mm gauze needle? (Bergmann, 1959). Unfortunately, cells either succumbed to dehydration or only divided a finite set of times. With the development of microculturing techniques, in which single cells isolated from liquid suspension cultures were placed within a droplet of "conditioned" media (liquid media conditioned by growing cell suspensions), single cells were capable of dividing to form daughter populations containing greater than 100 cells within 35 days (Jones, et al., 1960). The capability of a singular cell to produce a monoclonal colony of adequate cell density, that it can stimulate its own cellular division, was a vital step in demonstrating Haberlandt's dogma of plant cell totipotency.

The final barrier in achieving Haberlandt (1902) prediction of cellular totipotency overcame through the experimental production of somatic embryos. Isolated single cells must undergo a series of mitotic divisions forming a complex of embryogenic and parenchymatic cells, in which the embryonic cells are capable of embryogenesis within four weeks (Backs-Hüsemann and Reinert, 1970). Halperin (1966) concluded that external gradients, within embryo sac or culture media, do not influence initiation of polarized growth, which in fact originates from factors within the proembryonic cell mass. Transition of the embryo from radial to bilateral symmetric growth is also due to endogenous factors. Jakob Reinert (1958) was the first to stimulate somatic embryogenesis in carrot callus cultures, while concurrently Frederick C. Steward (1958) successfully produced somatic embryos in suspension cultures of carrot cells (Vasil, 2008). Induced division of isolated single cells is possible through conditioned media, followed by differentiation of the single cell derived masses into organ tissues by means of varying phytohormones supplements (Vasil and Hildebrandt, 1967). Furthermore, cultures have been known to lose their capacity to initiate somatic embryogenesis following multiple subcultures (Halperin, 1966), indicating that embryogenic initiation should be conducted as timely as possible.

3.2.5 Protoplast

Cells with cell walls removed (protoplast) were generally an unknown and unused biotechnology tool until the work of Cocking (1960). Following successful isolation of bacterial/fungal protoplast through cellulase enzymatic degradation, Cocking was interested in seeing if these techniques effectively transitioned to *planta*. Upon treatment of root tip with cellulase, two types of protoplasts were isolated: vacuolated (vacuolated root cap cells) and unvacuolated (meristematic region cells). There is importance in creating a hypertonic buffer (0.3 M sucrose) using the proper osmotic stabilizer in maintaining stable vacuolated protoplast for six hours; this is significant for the reason that the absence of or reduction in sucrose concentration results in rapid cell lysing (Cocking, 1960). Through these preliminary experiments, interest in protoplast based research increased but was hindered by the difficulties to acquire cell wall degrading enzymes.

Due to their totipotent nature, as well as representing the sole singular-cell organization obtainable in higher plants, protoplasts were propelled to a state high interest in the field of plant biology. Commercially available cellulase and other cell wall degrading enzymes led to rapid advances in protoplast biotechnology (Thorpe, 2007).

Great interest was focused on studying cell wall formation, isolation of cellular components, membrane transport, cell division, cell fusion, genetic transformation, somaclonal variation and mutant isolation (Fehér and Dudits, 1994; Galun, 1981).

Though protoplast isolation techniques have been optimized, successful protoplast regeneration occurs at low frequency. In order for isolated protoplasts to divide and form multicellular colonies an optimal cell plating density is required, ranging from 500 to 1,000,000 cells/mL depending upon cultivar of interest (Gibbs and Dougall, 1963). The cause of this phenomenon is unknown but it has been hypothesized that the dividing cells release growth factors and amino acids into the media which stimulates neighboring cells to divide (Davey, et al., 2005; Nagata and Takebe, 1971). Through micro-droplet culturing, a single cell is placed within a droplet of media, mimicking equivalent cell density of a population, in which the cell is capable of self-conditioning the media to induce its own (Schweiger, et al., 1987). Although promising, such techniques require upwards of five to six months to generate a three millimeter diameter callus, demanding techniques to expedite cell colony growth.

The discoveries of protoplasts and their need for sufficient signals from nurse cells offered an alternative method to produce plant cell clones using the protoplasts, which was previously only possible using cultured callus cells (Nagata and Takebe, 1971). It is now generally believed that empirical fine tuning of experimental parameters may be required to successfully achieve a protoplast-to-plant system for cultivar/species of interest (Davey, et al., 2005). Specifically, the external supplementation of phytohormones, in optimized amounts, will be critical in achieving cell division from protoplast derived cells

(Pasternak, et al., 2000). Auxin and cytokinin in particular have been shown to play a critical role in the regulation of cell division of *in vitro* cultures through reactivation of the cell cycle; auxin to stimulate DNA synthesis and cytokinin in relationship to peaks just before initiation of S-phase of the cell cycle (Carle, et al., 1998; Cooke and Meyer, 1981; Pasternak, et al., 2000; Schell, et al., 1999). While these are two widely known hormones there may be other "factors" that are yet unknown.

The discovery and commonality of protoplasts led to the discovery of the ability to cross sexually incompatible species through somatic hybridization accomplished by means of protoplast fusion. The immediate fusion of isolated protoplast was first accomplished upon treatment with sodium nitrate (Power, et al., 1970). Today's commonly used procedures for protoplast fusion include polyethylene glycol treatment and/or electroporation (Davey, et al., 2005; Thorpe, 2007). Interspecific plant hybridization of tobacco; indicated that the chromosome number of the newly fused somatic hybrids are in fact a summation of the two diploid protoplast donor species. Such hybrids exhibit herterosis (vigorous culture growth without hormone supplements) in culture stage prior to plant regeneration, which can be used to select out successful parasexual hybrids (Carlson, et al., 1972). Additionally, chromosome numbers from regenerated fusion of tomato by potato represented summation of donor species chromosome number (Melchers, et al., 1978). Somatic hybridization has opened doors to produce original nuclear/cytoplasmic combinations, resulting in greater genetic diversity while avoiding the apprehension accompanying transgenic biotechnology.

3.2.6 Somaclonal Variation

Somaclonal variation is defined as tissue culture-derived heritable variation (Bairu, et al., 2011). Culture-derived variation is correlated to positive and negative effects; producing new variation and genetic diversity in crops (Bouharmont, 1994; Larkin and Scowcroft, 1981), while also causing unwelcome, uncontrollable, arbitrary variation in cultured tissue (Karp, 1994). Somaclonal variation, ranging from a single trait to the entire genome, has a possibility of being a permanent change or a non-heritable, reversible change caused by a physiological or epigenetic effect (Bairu, et al., 2011). Additionally, this *in vitro* variation could be a result of pre-existing variation or it could be culture induced (George, 1993). Though not fully understood, somaclonal variation has been linked to: use of chimeric plants, differences in ploidy level, chromosome rearrangement, DNA methylation, histone modifications, RNA interference (RNAi), interruption of cell cycle, transposons, source material, growth factor applications, culture proliferation rate, culture conditions, culture age and number/duration of subcultures (Bairu, et al., 2011; Jain, et al., 1998; Larkin and Scowcroft, 1981; Miguel and Marum, 2011; Skirvin, et al., 1994).

Like many important discoveries in plants and animals, the issue of somaclonal variation is likely best minimized by avoiding undue and unnecessary stress to the cells. Avoiding procedures that may disrupt the normal process of the cell cycle can reduce somaclonal variation (Bairu, et al., 2011), as well as direct formation of plant structures from culture tissue may reduce variation by avoiding the callus phase typical of tissue culture protocols (Karp, 1994). Furthermore, isolation of undifferentiated tissue as source material can reduce the frequency of variation (Sahijram, et al., 2003).

Nevertheless, estimated rates of somaclonal variation range from 1% to 3% of the regenerated plants (Skirvin, et al., 1994). In an attempt to statistically calculate variant percentages, Côte, et al. (2001) concluded: (1) expected variant rates are an exponential function of the number of multiplication cycles and (2) expected variable off-type frequencies can be determined based on the number of multiplication cycles. Due to undesirable status of somaclonal variants, different techniques have been developed to detect said variants consisting of: morphological detection, biochemical detection, molecular marker detection, flow cytometry, proteins and isozymes, high performance capillary electrophoresis (HPCE), high performance liquid chromatography (HPLC), chromatin immunoprecipitation (ChIP)-chip, restriction fragment length polymorphism (RFLP), polymerase chain reaction (PCR) based techniques, (Reviewed by: Bairu et al., 2011; Miguel and Marum, 2011). Development and optimization of detection protocols on an individual species basis, may enable scientist to control and direct somaclonal variation to achieve desirable outcomes.

3.2.7 Florescence Activated Cell Sorting

Florescence activated cell sorting (FACS) instruments have become a crucial biotechnology tool capable of non-destructive, selective purification of heterogeneous cell mixtures resulting in viable, functioning cells (Ibrahim and van den Engh, 2007). Samples are injected into an isotonic (usually phosphate based) flow stream, where hydrodynamic focusing centers samples within the stream exiting the flow tip to avoid clogging and optical discrepancy (Bonner, et al., 1972). Particles/cells within the flow stream are illuminated by a combination of laser beams, producing light-scatter and/or fluorescent emission signals which are received by photodetectors and processed by a computer system (Galbraith, 2007). Additionally, selection thresholds, known as gates, can be modeled to specific sub-populations of cells within the mixture, increasing the purity of desired cells while avoiding sorting of unwanted debris and apoptotic cells (Weaver Jr, et al., 2000). A piezoelectric transducer is coupled to the fluid stream, harmonically disrupting the surface tension through excitation of the piezoelectric crystal, resulting in precise, synchronous droplet formation (Galbraith and Lucretti, 2000). Given its fluid dynamic nature, droplet formation can be calculated as a fixed, constant time interval between object detection and the last attached droplet below the flow tip (Galbraith, 2010). If the desired particle is detected, an electrical charge is applied to the droplet containing this particle preceding its detachment from the fluid stream (Ibrahim and van den Engh, 2003). Droplets proceed through an electrostatic field, wherein charged droplets are deflected from the droplet stream and collected into separate containers based on their trajectory (Bonner, et al., 1972). Additionally, charges of different magnitudes can be applied to droplets enabling multiple subpopulations of cells to be differentiated concurrently (Ibrahim and van den Engh, 2007).

3.2.8 Sorting Plant Cells

Unlike most animal cells, higher plant cells form complex structures connected by shared cell walls and subcellular plasmodesmata networks causing incompatibilities with homogeneous single cell requirement of FACS (Shapiro, 2005). To achieve single cell suspensions for sorting, protoplasts isolation is the commonly used method of achieving viable, totipotent single cells from clusters of higher plant cells. Due to protoplast's (15-150 µm) comparably larger diameter to that of commonly analyzed mammalian cells (10-20 µm), several adaptations may need to be applied to the flow cytometer before analyzing protoplast (Davey, et al., 2005; Galbraith, 2007; Harkins and Galbraith, 1987; Shapiro, 2005). The most crucial aspect for efficient analysis and sorting being the application of a wider diameter flow tip (100 - 200 µm). Consequently, greater diameter flow stream requires lower system pressure which reduces flow rate, higher transducer wavelength application for droplet formation and lower sorting rate (Galbraith, 2007).

One of the major challenges in live plant cell FACS sorting is the optical trigger to identify a cell. In order for flow cytometers to detect and analyze light scatter and fluorescence signals the cell must contain some form of fluorochrome to produce said signals, be it endogenous (chlorophyll, fluorescence protein (GFP), ect.) or added exogenously (antibodies, fluorescence diacetate (FDA), ect) (Galbraith, 2010). Light scatter data can be separated into two axes in respect to the laser plane: parallel forward scatter (FS) and orthogonal side scatter (SS) (Figure 9). Scatter or fluorescence intensity versus count univariate histogram analysis peaks indicate subpopulations and their relative count within the solution at specific frequencies (Ibrahim and van den Engh, 2007). Furthermore, fluorescence and scatter signals are generally compared in biparametric scatter plot analysis to reveal subpopulations within a cell suspension mixture, in which gates can be modeled to define and separate individual subpopulations from the cell solution using FACs (Galbraith, 2007).

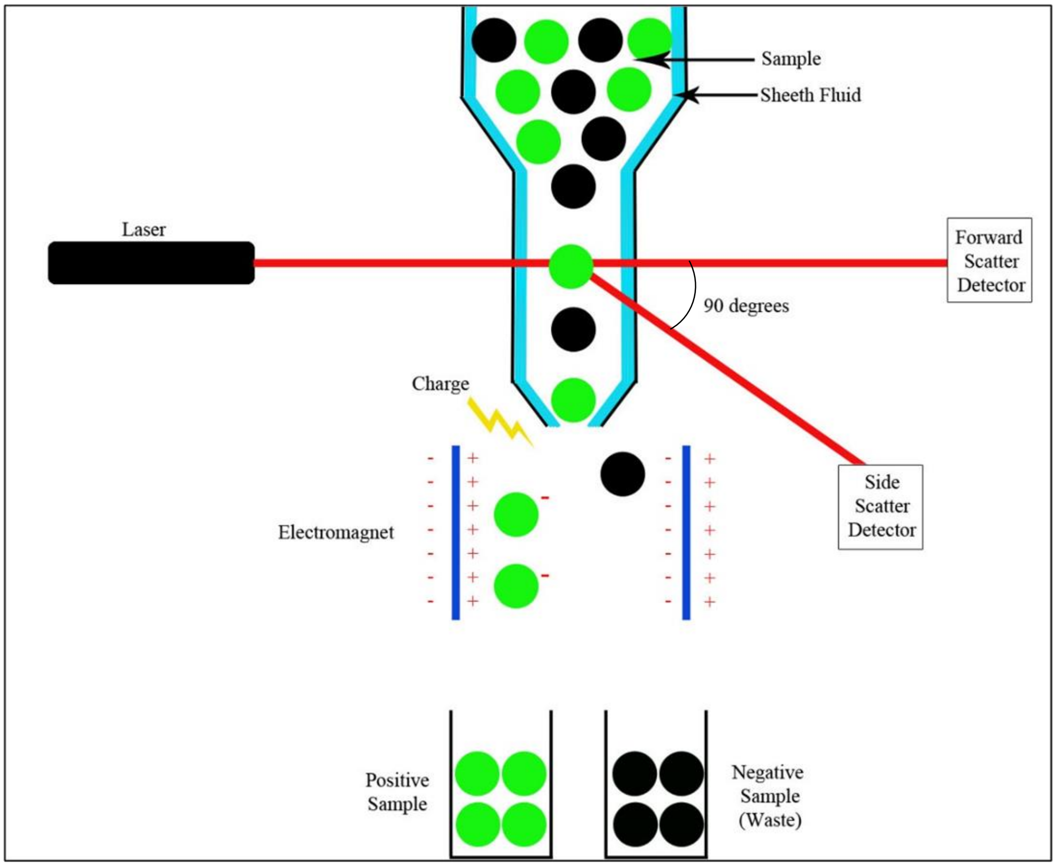


Figure 9. Fluorescence activated cell sorting (based off Sabban (2011))

One endogenous trigger of potential use in sorting is chlorophyll. Chlorophyll is a green pigment which absorbs blue and red light found in chloroplasts of algae and plants. Furthermore, chlorophyll is known to be an endogenous fluorochrome capable of producing fluorescence emissions when excited by the proper frequency beam. When using the proper laser and emission filter, FACs is capable of detecting the endogenous chlorophyll, which emanates red autoflourescence when an excitation wavelength of 447 nm and emission wavelength of 667 nm is applied (Galbraith, et al., 1988). Flow cytometric analysis of leaf protoplasts result in one dimensional histograms of red autoflourescence, indicating two subpopulations: freely suspended chlorophyll/chloroplast and intact protoplasts (Galbraith, 2007). Modeling of gates defining intact protoplasts emitting red autofluorescence produced 100% pure sorts at an 82% sorting efficiency (Galbraith, et al., 1988).

3.3 Materials and Methods

Callus induction was performed on several varieties of carrot and tobacco. These species were chosen because the methods and protocols for cell cultures are mature (Clemente, 2006). Four carrot varieties were provided by the USDA Carrot and Garlic Genetics program at the University of Wisconsin-Madison by Dr. Philip Simon. Three tobacco varieties were provided by the Nicotiana Breeding Program at North Carolina State University by Dr. Ramsey Lewis, as well as two varieties from the IPGB Laboratory for Crop Transformation at Texas A&M University by Dr. Keerti Rathore. Varieties were chosen by the donors to represent a wide genetic background within their respective crop and be tolerant to *in vitro* manipulation (Table 13**)**.

Culture media, glassware and all other autoclavable materials were autoclaved before use for cell cultures. All protocols, with the exceptions of suspension culture agitation and cell sorting, were conducted within a laminar flow hood to avoid contamination of cell cultures. Upon plating on various media (protocol in Appendix C1

Table 13. Crop varieties and sources used to demonstrate *in vitro* cell cycling proof of concept.

Variety	Crop	Source
B493B	Carrot	USDA Wisconsin-Madison
B2566B	Carrot	USDA Wisconsin-Madison
B7262B	Carrot	USDA Wisconsin-Madison
B9547B	Carrot	USDA Wisconsin-Madison
LCT B	Tobacco	Texas A&M
LCT X	Tobacco	Texas A&M
TC 551	Tobacco	North Carolina State
TI 1562	Tobacco	North Carolina State
TI 1741	Tobacco	North Carolina State

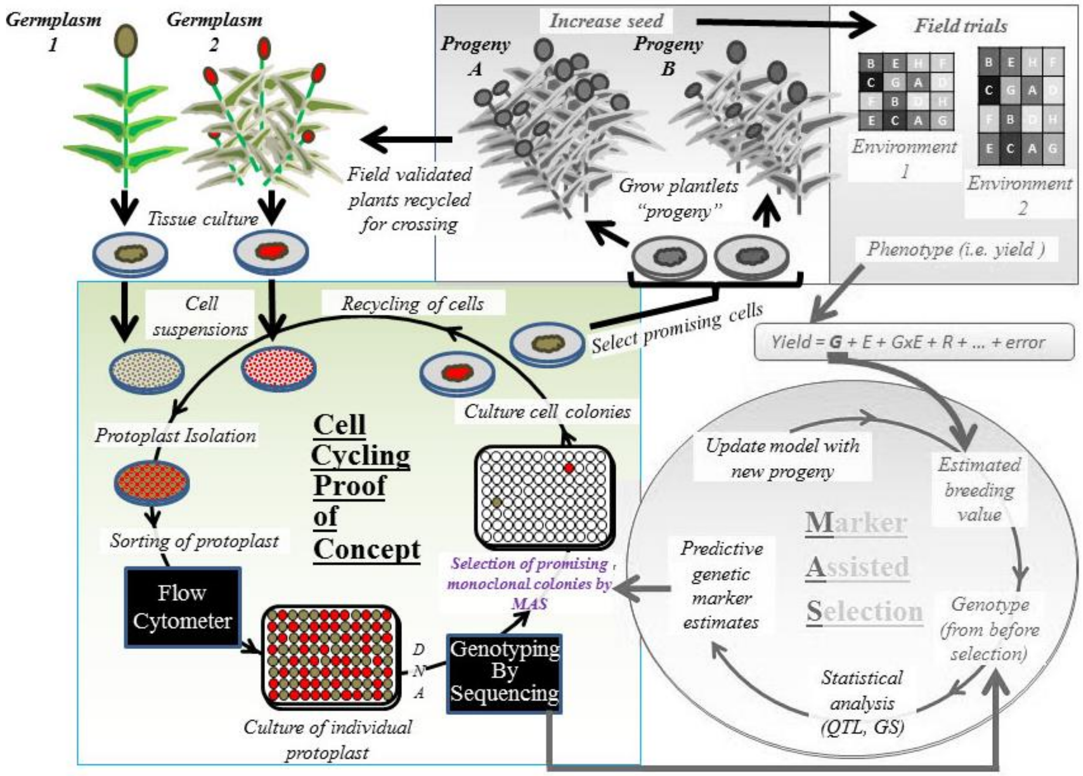


Figure 10. Schematic of *in vitro* cell cycling proof of concept (color) and future steps including training populations, model development and implantation of marker assisted selection when *de novo* gametogenesis is achieved (grey). Altered from Murray, et al. (2013).

and C2), germination and callus induction were conducted in an incubator at 25º C. Following successful callus formation, calli sub samples were suspended in liquid media and agitated at 150 rpm in an orbital shaker (New Brunswick Innova 42) set to 29º C. Refer to Figure 10 for schematic of in vitro cell cycling.

3.3.1 Seed Sterilization and Germination

Surface sterilization of seed is the crucial step in reducing contamination in culture. Surface sterilization techniques were provided by Dr. Keerti Rathore (unpublished – protocol in Appendix C1 and C2). In brief, tobacco varieties were soaked in 70% ethanol for 20 seconds and rinsed with sterilized water; followed by 15 minutes of continuous shaking in a solution of 5% bleach with Tween 20 (one drop per 50 mL). Seeds were rinsed six times with sterile water and plated (20 seeds per Petri dish) onto tobacco growth medium (Appendix D1). Sealed plates were placed in a 25º C incubator to germinate under light. Two-week-old tobacco seedlings were transferred to 100 mL glass jars (two seedlings per jar) containing the modified MS medium above to allow for sufficient leaf tissue growth needed for callus induction.

Carrot varieties followed the same sterilization procedure with 20% bleach, carrot growth medium (Appendix D2) and germination without light. Intial concentrations of bleach (5%) were largely ineffecient at sanitizing the rough carrot seed coats that carry high levels of fungal contamination. To resolve such issues, *Daucus* seeds were subjected to 20% bleach under vacuum, resulting in noticeable reduction in contamination following plating on the germination media. Seeds were germinated in darkness to induce longer hypocotyl to obtain enough tissue for callus generation. Seven days after plating of seeds, and for every seven days afterwards, plates were examined for contamination. Plates showing contamination were discarded or uncontaminated seedlings were transferred to new MS medium, depending on the severity of the contamination.

3.3.2 Callus Induction

Tobacco leaf tissue was cut into one centimeter by one centimeter squares and plated (nine squares per plate) abaxial side up (Clemente, 2006) on tobacco callus induction (TCI) medium (Appendix D3). Plates were sealed and placed back into the 25º C incubator to allow formation of callus (Appendix C3).

Carrot cultures were initiated (Appendix C4) using the seedlings one-week post-germination. The hypocotyls were cut into one centimeter sections and plated (nine sections per plate) on carrot callus induction medium (Appendix D4). Plates were sealed and placed into the 25º C incubator to allow callus formation.

Synthetic phytohormones have a half-life of roughly 30 days, therefore tissue was transferred to new callus medium every three weeks to avoid embryogenesis and shoot formation. Additionally, routine subculturing was necessary to replenish available medium nutrients and to reduce inhibitory compounds that leach out of cultures. During transfer, any tissue sections that showed poor callus growth were discarded. Subculturing of calli were necessary in subsequent medium transfers to ensure healthy callus growth.

3.3.3 Cell Suspension

Friable callus was sub-cultured into 75 mL of species-specific suspension medium without phytagar, within a 250 mL Erlenmeyer flask sealed with sterilized aluminum foil. Liquid cultures were incubated at 29° C in an Innova 42 orbital shaker (Thermo Fisher Scientific, Waltham, MA) and agitated at 150 rpm. Once logarithmic growth stage was reached in suspension cultures, subculturing was conducted every five days to avoid overpopulation of the suspension. Protoplast isolations were made from cultures that had reached logarithmic growth rate as the higher rate of cell division within the suspension cultures resulted in thinner cell walls and provided enough cellular material for protoplast isolation.

3.3.4 Protoplast Isolation

3.3.4.1 Tobacco

Procedures for isolation of tobacco protoplast followed those of Lee, et al. (1989) and Kirchhoff, et al. (2012); a protocol is found in Appendix C5. Suspension cells 3-5 days after subculturing were centrifuged, supernatant was removed and the pellet was suspended in tobacco protoplast isolation medium containing cell wall degrading enzymes (Appendix D5). After 16 hours of incubation at 26° C with gentle agitation, the cell suspension in the enzyme solution was filtered through a 100 µm and 40 µm cell strainer (PluriSelect, Leipzig, Germany) and the filtrate was centrifuged. The pellet was gently suspended in two milliliters of modified KAO medium (Appendix D6) and carefully layered above a sucrose solution (Appendix E1) using a Pasteur pipette and centrifuged (Lee, et al., 1989; Menczel, et al., 1981). Viable protoplasts localized at the interphase between the two solutions and were carefully extracted with a Pasteur pipette. Isolated protoplasts were washed twice with modified KOA medium followed by one wash with W5 (Appendix E2) salt solution (Menczel, et al., 1981). Each wash was followed by centrifugation. Supernatant was discarded and protoplasts were suspended in KAO 8p medium (Kao and Michayluk, 1975) (Appendix D7). Suspended protoplasts were cultured for 72 hours to allow partial regeneration of their cell walls, followed by final passage through the 100 µm cell strainer. Strained protoplasts were placed into a sterile tube for flow cytometry sorting (Kirchhoff, et al., 2012).

3.3.4.2 Carrot

Procedures for the isolation of carrot protoplasts followed those of Lee, et al. (1989) and Grzebelus, et al. (2012); a protocol is found in Appendix C6. Suspension cells 3-5 days after subculturing were centrifuged, supernatant was removed and the pellet was suspended in carrot protoplast isolation medium (Appendix D8) with enzymes (Appendix D5). After 16 hours of incubation at 26° C with gentle agitations, protoplasts were passed through cell strainers (40 and 100 µm) and centrifuged. The pellet was suspended within W5 salt wash and carefully layered above a sucrose solution using a Pasteur pipette and centrifuged. Viable protoplasts localized at the interphase between the two solutions and were carefully extracted with a Pasteur pipette. Isolated protoplasts were washed twice: first with W5 wash, then with carrot protoplast regeneration medium (Appendix D9). Subsequent centrifugation followed each wash and the final pellet was suspended in carrot protoplast regeneration medium.

3.3.5 Optimize Cell Sorting

Isolated protoplasts were left for 72 hours to allow for partial regeneration of the cell walls to give cells enough rigidity to survive the sorting process. Isolated protoplasts were sorted by means of a FACs flow cytometer (Beckman Coulter MoFlo Astrios Cell Sorter) to isolate individual protoplasts into a respective well of a clear, flat bottom, 96-well microtiter plate. Each well was filled with 50 µL of protoplast culture medium, dependent on the species, to receive the sorted cells. Initial attempts to sort singular cells utilized endogenous chlorophyll fluorescence as the selection parameter. If chlorophyll fluorescence was found insufficient, exogenous cellular staining with fluorescein diacetate (Appendix E3) was then used as a fluorescent tag indicating the viability of the cells (Widholm, 1972). Single protoplast sorts were confirmed with an inverted microscope (Olympus IX71 system) equipped to analyze microtiter plates. The FAC sorter and inverted microscope were located within the Flow Cytometry and Digital Imaging Core Facilities at the Texas A&M University Veterinary Medical Research building.

3.3.6 Single Cell Derived Colonies

The following steps of the research are outlined but were not performed due to complications in reliable protoplast isolation protocols. Single well micro plates will be filled with species-respective protoplast regeneration medium supplemented with 20% (v/v) nurse cells. The nurse cells will be collected from the same suspension culture that the protoplasts were isolated from and embedded within the low-melting temperature-agarose solidified regeneration medium. Grade 40 ash-less filter paper will be cut to fit within the well of the microplate, followed by autoclave sterilization. This filter paper will be placed upon the agarose solidifies medium to act as a contamination barrier between the protoplast derived colonies and the nurse cell culture. Plates will then be placed within the FACs and singular protoplasts will be sorted upon the filter paper following a 96-well pattern. Plates will then be sealed and placed into a 25° C dark incubator to allow protoplasts to divide and grow into monoclonal colonies. Once colonies have reached visible size, they will be transferred to callus culture medium to continue growth until they reach the appropriate size for successful genotyping and continued cell cycling.

3.4 Results and Discussion

3.4.1 Seed Sterilization, Germination and Calli Induction

Sterilization of seeds prior to germination is a crutial step in reducing foreign DNA within cell cultures. Tobacco seed sterilization procedures (Appendix C2) were effective resulting in little to no visible contaminations. Although intial concentrations of bleach (5%) were largely ineffecient at sterilizing the rough carrot seed coats, resulting in greater than 90% contamination, specifically fungal, rate upon germination media. It is thought that either the varring contour of the seed coat provides results in air pockets which the bleach solution can not from sterilization or the field production of the germplasm seed increase the degree of foriegn organisms present. To resolve such issues, *Daucus* seeds were subjected to 20% bleach treatment under vacuum, resulting in noticeable reduction in contaminant colony growth upon germination media. These methods allowed for consistent, healthy tissue samples for callus induction free of foreign DNA.

Following seed sterilization, seedlings must grow to a size in which tissue samples can be obtained to induce callus formation. Carrot samples were easily obtained within two weeks of germination plating, in which hypocotyl segments were induced to form callus. Plated hypocotyls, then required four to eight weeks, depending on the line, to form sizable callus capable of initiating suspension cultures without exausting the availible calli cultures. Additionally, tobacco requires a longer time scale of six to eight weeks to produce leaves capable of providing tissue samples, with an additional four to eight week required to form sizable callus. Though the intial time investment of germinating and growing the lines was long, it is an intial investment as vegetative plants are maintained in cultured conditons eliminating the need to repeat the initial germination and growth period prior to callus indution. Callus formation may be the largest time limitation within the cell cyling process and methods of accelerating callus formation may be necessary to reduce such time requirements; this reduction could also help to minimize somaclonal variation.

Upon induction of calli, large phenotypic variation was observed within both species. Tobacco calli, ranged in color for white TI 1741 (Figure 12[a]) to vibrant green of LCT B (Figure 12[d]). Additionally, callus struture/friability was quite variable. TI 1741 resembeling the consitency of cotton fibers with little to no detectible hard callus. TI 1526 was a spongy, fiiable callus capable of transitioning to the cotton like state of TI 1741. While the remaining tobacco germplasm (Figure 12) were the three most similar, TC 551 and LCT X were more friable than LCT B, which was the least friable of all the tobacco entries but the most prone to organogenesis.

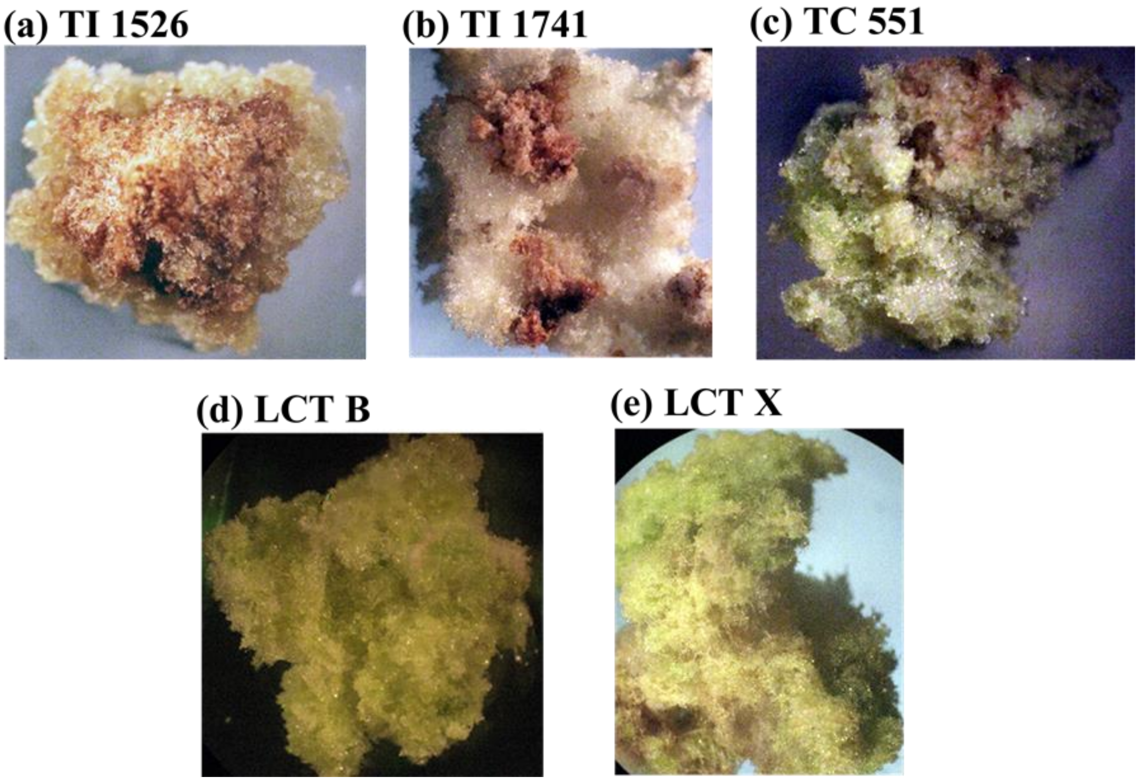


Figure 11. Tobacco lines as non-differentiating callus tissue.

Carrot samples showed similar trends as that of tobacco in regards to visible *in vitro* phenotypic variation. B9547B was a green callus that expressed purple pigmentation as the culture ages (Figure 13[c]), this was not suprising as B9547B is a purple carrot varriety. The production of the purple pigment inhibits the

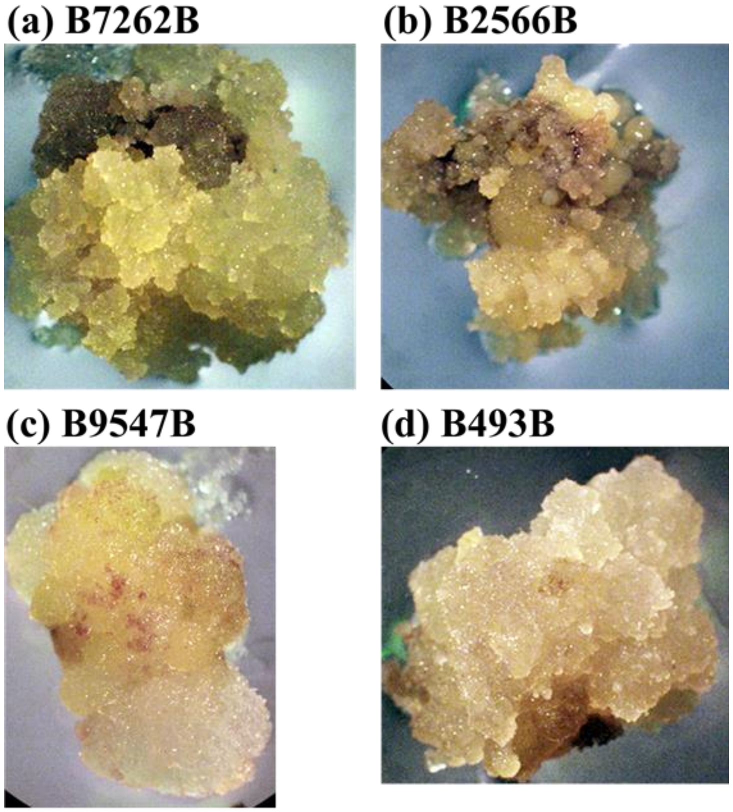

(a) B7262B
(b) B2566B
(c) B9547B
(d) B493B

Figure 12. Carrot lines as non-differentiating callus tissue.

cell division due to increase anthocyanin levels as well as somatic embroyos were commonly noticed once the callus transitioned to the purple state, which is an indication that auxin supplements are too low in the medium (Ozeki and Komamine, 1986). Additionally, B493B was an off white/grey color, B7262B was a light green callus that transitioned to off white/yellow as it aged and B2566B was an off yellow/orange callus (Figure 13). All carrot varieties were similar in terms of friable nature, while B439B had mucilaginous secretion that may have inhibited callus gowth. Furthermore, the carrot entries more readily transitioned to somatic embryogensis as compared to the tobacco lines. It is plausible that the carrot lines were more sensitive to phytohormone fluctuations of environmental fluctuations during callus growth. Though it seems that B9547B and B2566B were more susceptible to somatic embryogenesis formation; no noticeable trend was observered within the carrot lines as somatic embryogenesis was observed within all of the lines.

3.4.2 Suspension Cultures and Protoplast Isolations

Initiation of suspension cultures involved a simple process of placing callus tissue within liquid culture media, followed by constant agitation in an orbital shaker. This process enabled the production of abundant small callus clusters, which facilitated enzymatic degradation of the cell walls during subsequent protoplast isolation. Successful initiation of suspension cultures were established for all of the carrot and tobacco lines, although each variety required different time intervals to acclimate to the liquid conditions and reach the logarithmic growth stage. B7262B (carrot) and TI 1741 (tobacco) were the most stable lines with regards to suspension conditions; while all other lines were lost at one point due to contamination issues, somatic embryogenesis or failure to continue dividing. Due to these setbacks, it was more practical to focus on a limited number of varieties (B7262B and TI 1741) with additional replicate lines to reduce the odds of losing a particular line completely and having to reinitiate suspension cultures. B7262B was the first line to reach logarithmic growth after four weeks within suspension, resulting in protoplast isolation focused upon this line.

Initial protoplast isolations were not successful as a result of inadequate enzyme concentrations and incorrect execution of the isolation procedures; specifically during the sucrose pad layering. Enzyme concentrations were doubled, as initial enzyme concentrations of 1.5 % (m/v) cellulase and 0.5 % (m/v) macerozyme resulted in inconsistent protoplast yields. The increase in enzyme concentrations resulted in consistent production of protoplasts, which was evident upon the interphase layer of the sucrose pad after centrifugation. Such prolific protoplast production required multiple 10x dilutions to reach a final concentration that the FAC sorter could handle without obstructing the flow.

3.4.3 Florescence Activated Cell Sorting of Protoplast

Initial attempts to isolate individual protoplasts with FACs were focused on indigenous chlorophyll fluorescence. Though it was possible to model the gates to capture viable protoplasts during bulk collection, said protoplasts were accompanied with large quantities of lysed cells and debris, “waste” (Figure 14). Sorting of waste following the gate model indicated that the model was selected based on object size rather than chlorophyll fluorescence. Analysis of unsorted protoplast under a fluorescence microscope showed no indication of red chlorophyll fluorescence. This was not surprising as suspension cultures were maintained under dark conditions, in which chlorophyll synthesis was unnecessary and did not fully develop. Furthermore, due to the rapid cellular division occurring under suspension conditions, protoplasts were isolated from newly formed cells prior to full development of chlorophyll. In order to effectively isolate viable protoplasts from the waste material, an exogenous fluorochrome was implemented.

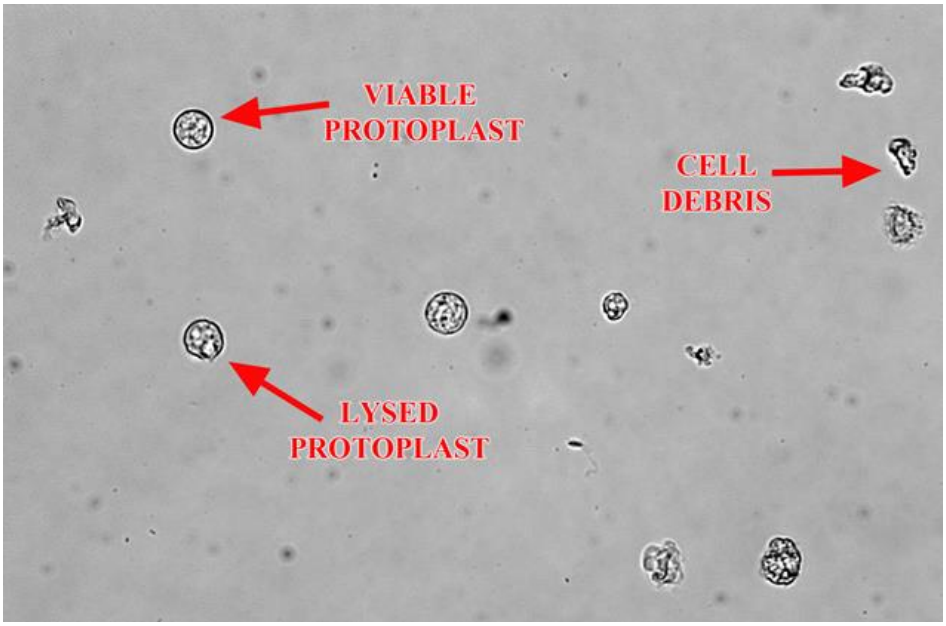


Figure 13. Solution of products following FAC sorting using chlorophyll as the endogenous flourochrome indicator (40x).

Fluorescein diacetate (FDA) is an exogenous fluorochrome that diffuses through the cell membrane, once within the protoplast, ester bonds are broken producing the fluorescent compound which is incapable of diffusing out of the cell (Haugland, et al., 1996). These characteristics make FDA a useful fluorescent indicator of viable, non-lysed protoplasts during FAC sorting. Protoplasts treated with 0.001 M FDA effectively stained viable protoplast, which exhibit green fluorescence when activated using fluorescent microscopy (Figure 15[f]). Using FDA as a selection marker of FACs, allowed for isolation of viable protoplasts (Figure 15[g]) whose viability was confirmed

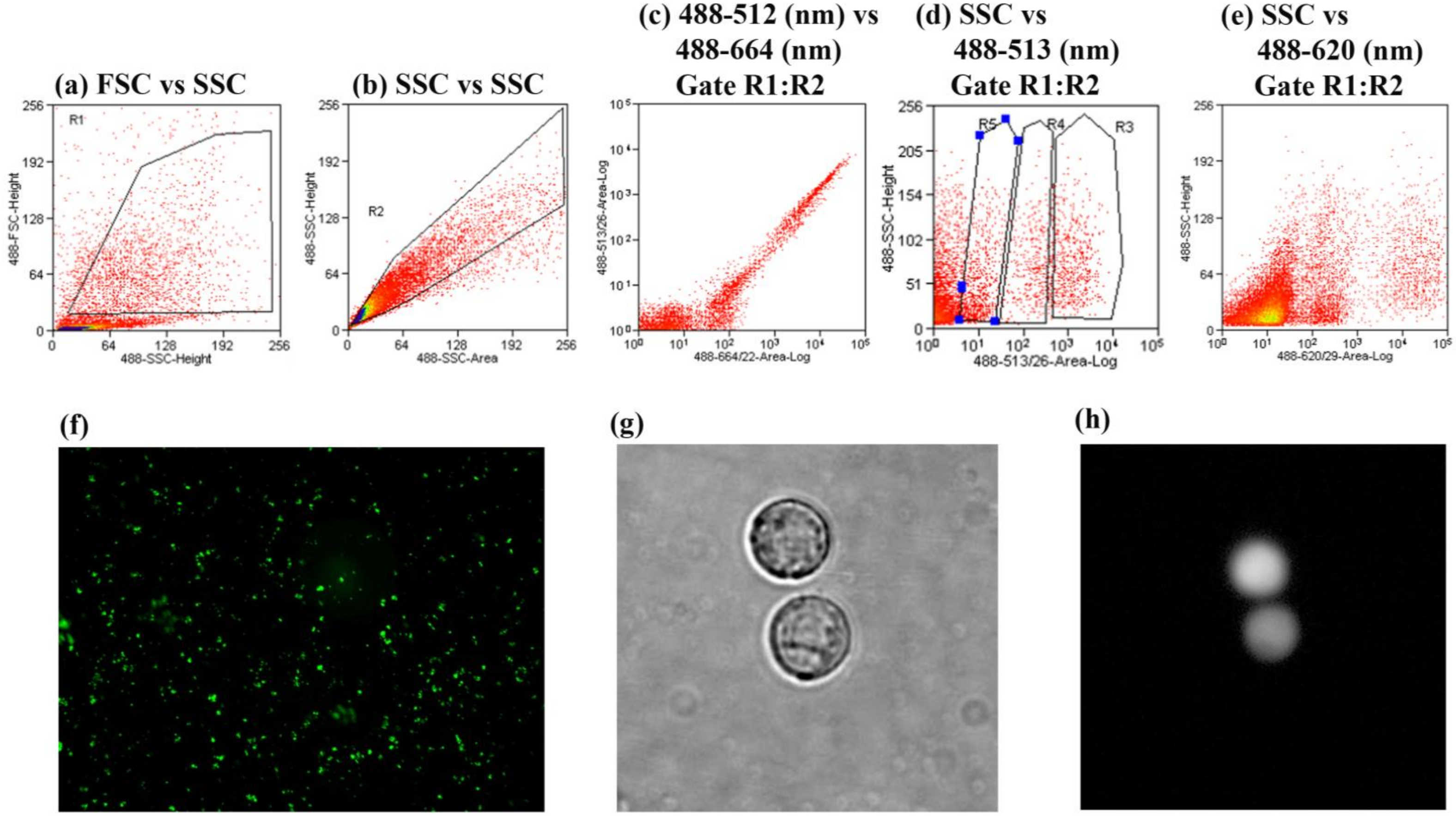


Figure 14. [a:e] Training of FAC sorter through analysis of side scatter (SSC), forward scatter (FSC) and varying levels of fluorescent activation wavelengths; setting selection gates to isolate viable protoplast. [f] FDA staining ability prior to sorting (10x), [g] viable sorted protoplasts (40x) and [h] viable sorted protoplast under fluorescent microscopy activating of FDA (40x).

based on their fluorescence after sorting (Figure 15[h]). Original scatterplot and gate calibration resulted in a mixture of viable protoplast and waste (Figure 14), using FDA the scatterplots (Figure 15[a:e]) indicated three identifiable populations: (R3) viable protoplast, (R4) lysed/irregular protoplast and (R5) cellular debris. These results demonstrated that FDA was an effective endogenous fluorochrome for use in viable protoplast selection using FAC sorters as previous publications have concluded, as well as, the ability of our lines to withstand the cell-sorting conditions.

3.4.4 Noteworthy Setbacks

Throughout the duration of the experiment many challenges arose. To begin with, it is suggested that greenhouse produced seed be used in the germination process as it resulted in noticeably lower contamination rates, after surface sterilization. Furthermore, consistencies in callus growth may have been negatively affected by a malfunctioning growth chamber resulting in temperature spike shocking the cultures. Additionally, difficulties arose in producing rapidly dividing suspensions cultures; which could be due to the growth chamber problems, inconsistent temperature within the shaker or culture age. Finally, prolific protoplast isolation suddenly ceased, likely due to loss of enzyme kinetics caused by condensation deactivating the enzymes. This likely resulted from degradation and reinforced that it was necessary to allow the enzyme to reach room temperature before removal from desiccation chamber; although protoplast isolation has not been attempted since due to loss of suspension cultures due to contamination, this was the most likely cause.

4. CONCLUSION

It is important to remember that the FPM population is a linkage population and a traditional analysis would construct a linkage map to compare the effect of founder number and generations of intermating on mapping resolution. Although a single QTL was found for each quantitative trait, it is expected that many addition QTL are present; but were undiscovered due to the stringent, conservative nature of the Bonferroni multiple test correction criteria. Looking forward, it would be interesting to see what the significance threshold would be set to if a FDR or M_{eff} procedure were used to set the significance level, as we know not all markers will be independent due to nature of the FPM population as assumed when using the Bonferroni correction. If these methods accurately lower the false discovery threshold to the correct level it is likely that more true QTL would be identified in an association.

Association mapping methods in this study were informative in demonstrating that QTL resolution does increase when addition generations of intermating are incorporated into the mating design; although precision is difficult to compare across mating design when analyzing QTL for quantitative traits in regions of the genome that a causative gene is unknown. It is apparent that mapping resolution cannot be effectively compared across population using the likelihood drop off support interval, as it must be adjusted for the population size, QTL effect size and marker density of each subpopulation. A more robust method such as Bayesian credible support intervals may be appropriate for such comparisons within association mapping studies (Manichaikul, et al., 2006). Bayesian methods may be the favorable method for QTL linkage mapping once the challenges of constructing the map have been overcome.

Furthermore, the rapid advancement of generations *in vitro* has been met with many challenges as expected, but with slower than anticipated progress. Still, much progress was made and the limitations in the use of CoGiV in plant breeding is now better understood. Studying the rate at which cell totipotency can be accomplished has indicated that the original hypothesized generation length under CoGiV methods was optimistic, but could become more realistic with improve protocols. Time requirements to achieve calli of practical size can take from four to eight weeks indicating that an equal amount of time would be required to stimulate a single protoplast to divide into a monoclonal colony for genotyping. FAC sorting has proven to be one key to accelerating the cell cycling process by sorting individual viable protoplasts rapidly at high efficiency. It is becoming evident that CoGiV will have a greater impact in the development of slow growth species (hard woods, citrus, fruiting trees) that require many years of growth to reach sexual maturity, and the potential for use in annual species pending improved medium supplements and protocols which rapidly increase cellular growth *in vitro*. Nevertheless, once consistent methods of protoplast isolation are achieved, chemical library screening may commence for compounds that induce *de novo* gametogenesis and rapid cellular division, as well as, continued refinement of *in vitro* cell cycling protocols.

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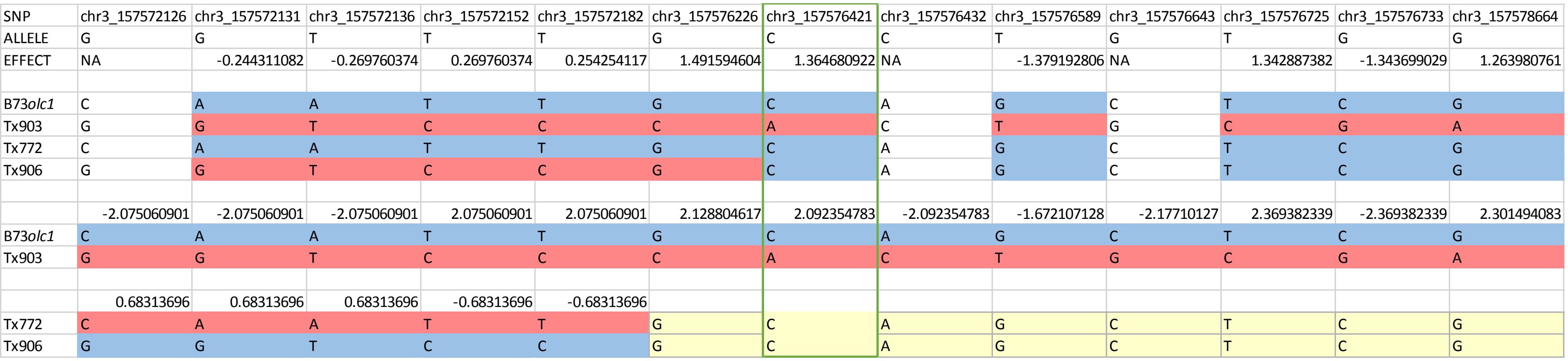
APPENDIX A. FIGURES

A1. Comparison of peak marker in entire population with flanking markers using parental allele calls to elucidate trend in parental donor of effect allele in the bi-parental and dihybrid populations for (a) plant height, (b) ear height, (c) days to anthesis and (d) days to silking. Negative effect (red), positive effect (blue), monomorphic marker (yellow)

(a)



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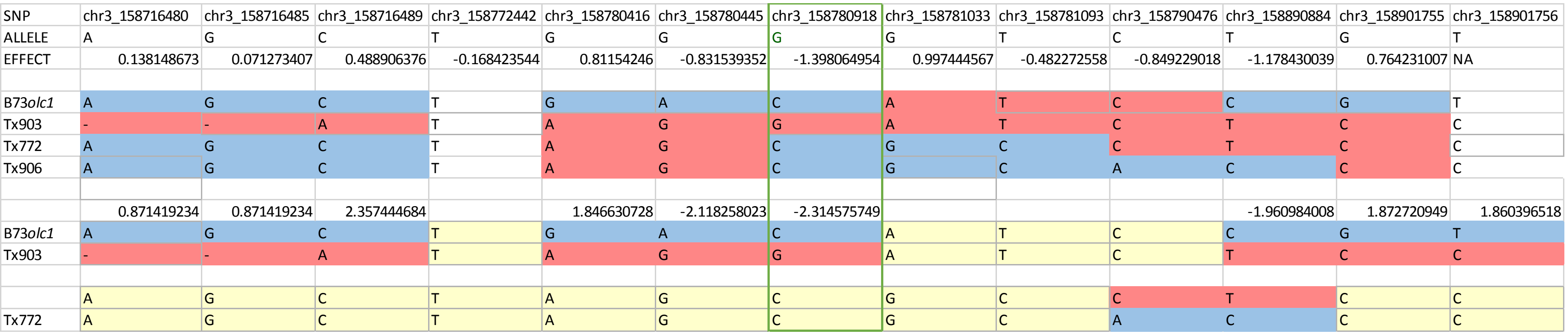
ALLELE	G	G	T	T	T	G	C	C	T	G	T	G	G
EFFECT	NA	-0.244311082	-0.269760374	0.269760374	0.254254117	1.491594604	1.364680922	NA	-1.379192806	NA	1.342887382	-1.343699029	1.263980761
B73*olc1*	C	A	A	T	T	G	C	A	G	C	T	C	G
Tx903	G	G	T	C	C	C	A	C	T	G	C	G	A
Tx772	C	A	A	T	T	G	C	A	G	C	T	C	G
Tx906	G	G	T	C	C	G	C	A	G	C	T	C	G
	-2.075060901	-2.075060901	-2.075060901	2.075060901	2.075060901	2.128804617	2.092354783	-2.092354783	-1.672107128	-2.17710127	2.369382339	-2.369382339	2.301494083
B73*olc1*	C	A	A	T	T	G	C	A	G	C	T	C	G
Tx903	G	G	T	C	C	C	A	C	T	G	C	G	A
	0.68313696	0.68313696	0.68313696	-0.68313696	-0.68313696								
Tx772	C	A	A	T	T	G	C	A	G	C	T	C	G
Tx906	G	G	T	C	C	G	C	A	G	C	T	C	G

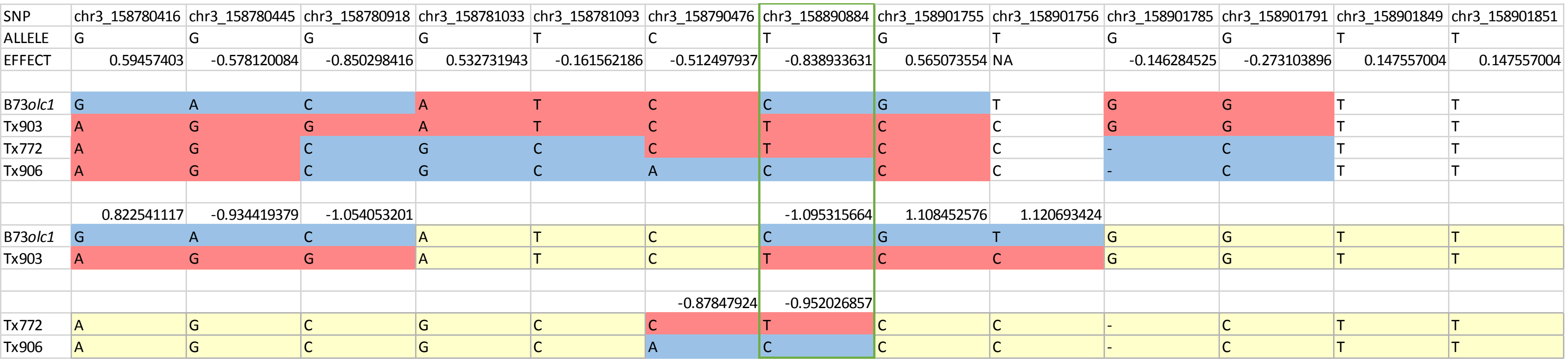
A1. Continued

(b)



SNP	chr3_158716480	chr3_158716485	chr3_158716489	chr3_158772442	chr3_158780416	chr3_158780445	chr3_158780918	chr3_158781033	chr3_158781093	chr3_158790476	chr3_158890884	chr3_158901755	chr3_158901756
ALLELE	A	G	C	T	G	G	G	G	T	C	T	G	T
EFFECT	0.138148673	0.071273407	0.488906376	-0.168423544	0.81154246	-0.831539352	-1.398064954	0.997444567	-0.482272558	-0.849229018	-1.178430039	0.764231007	NA
B73*olc1*	A	G	C	T	G	A	C	A	T	C	C	G	T
Tx903	-	-	A	T	A	G	G	A	T	C	T	C	C
Tx772	A	G	C	T	A	G	C	G	C	C	T	C	C
Tx906	A	G	C	T	A	G	C	G	C	A	C	C	C
	0.871419234	0.871419234	2.357444684		1.846630728	-2.118258023	-2.314575749				-1.960984008	1.872720949	1.860396518
B73*olc1*	A	G	C	T	G	A	C	A	T	C	C	G	T
Tx903	-	-	A	T	A	G	G	A	T	C	T	C	C
	A	G	C	T	A	G	C	G	C	C	T	C	C
Tx772	A	G	C	T	A	G	C	G	C	A	C	C	C

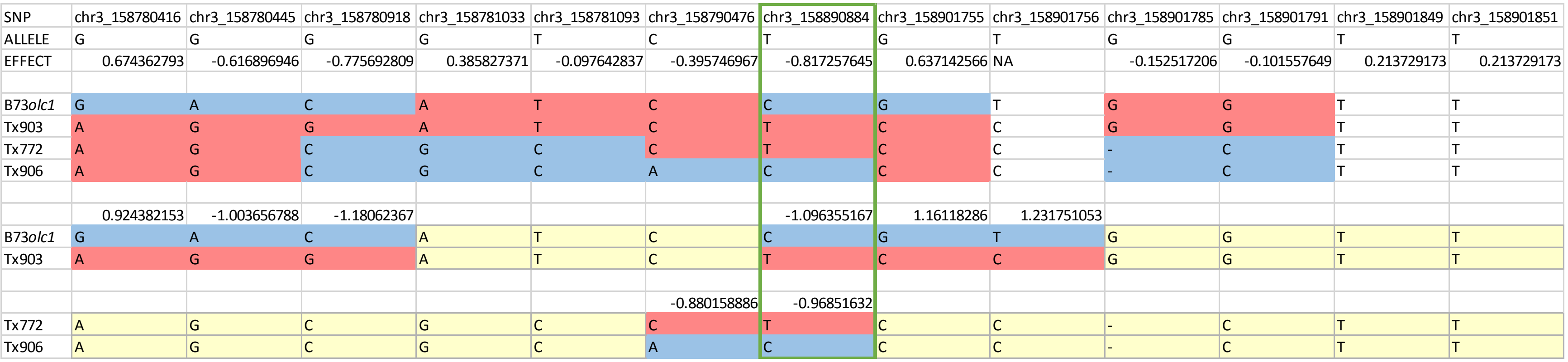
(c)



SNP	chr3_158780416	chr3_158780445	chr3_158780918	chr3_158781033	chr3_158781093	chr3_158790476	chr3_158890884	chr3_158901755	chr3_158901756	chr3_158901785	chr3_158901791	chr3_158901849	chr3_158901851
ALLELE	G	G	G	G	T	C	T	G	T	G	G	T	T
EFFECT	0.59457403	-0.578120084	-0.850298416	0.532731943	-0.161562186	-0.512497937	-0.838933631	0.565073554	NA	-0.146284525	-0.273103896	0.147557004	0.147557004
B73*olc1*	G	A	C	A	T	C	C	G	T	G	G	T	T
Tx903	A	G	G	A	T	C	T	C	C	G	G	T	T
Tx772	A	G	C	G	C	C	T	C	C	-	C	T	T
Tx906	A	G	C	G	C	A	C	C	C	-	C	T	T
	0.822541117	-0.934419379	-1.054053201				-1.095315664	1.108452576	1.120693424				
B73*olc1*	G	A	C	A	T	C	C	G	T	G	G	T	T
Tx903	A	G	G	A	T	C	T	C	C	G	G	T	T
						-0.87847924	-0.952026857						
Tx772	A	G	C	G	C	C	T	C	C	-	C	T	T
Tx906	A	G	C	G	C	A	C	C	C	-	C	T	T

A1. Continued

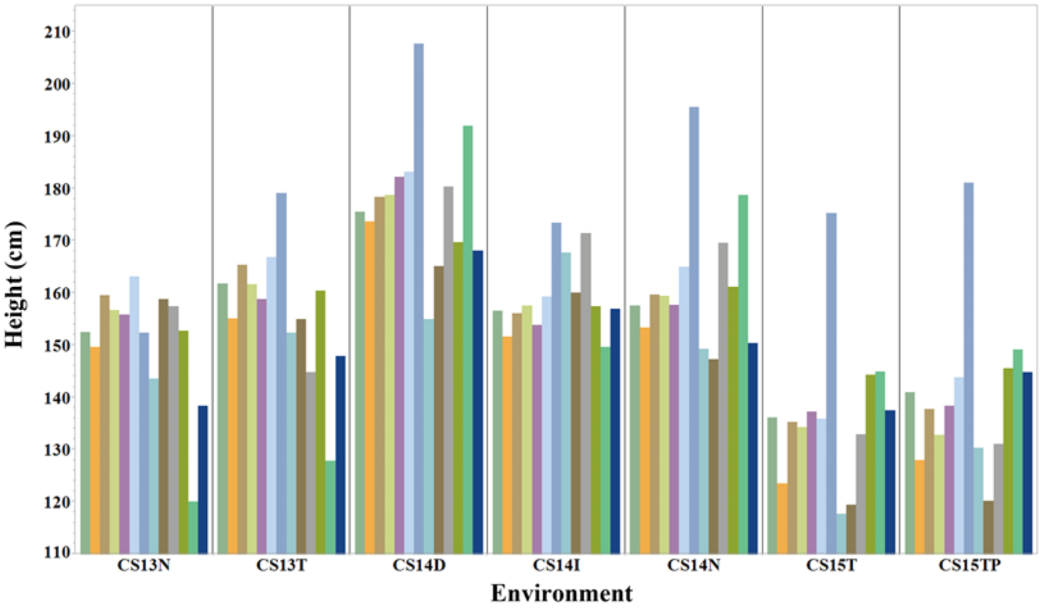
(d)



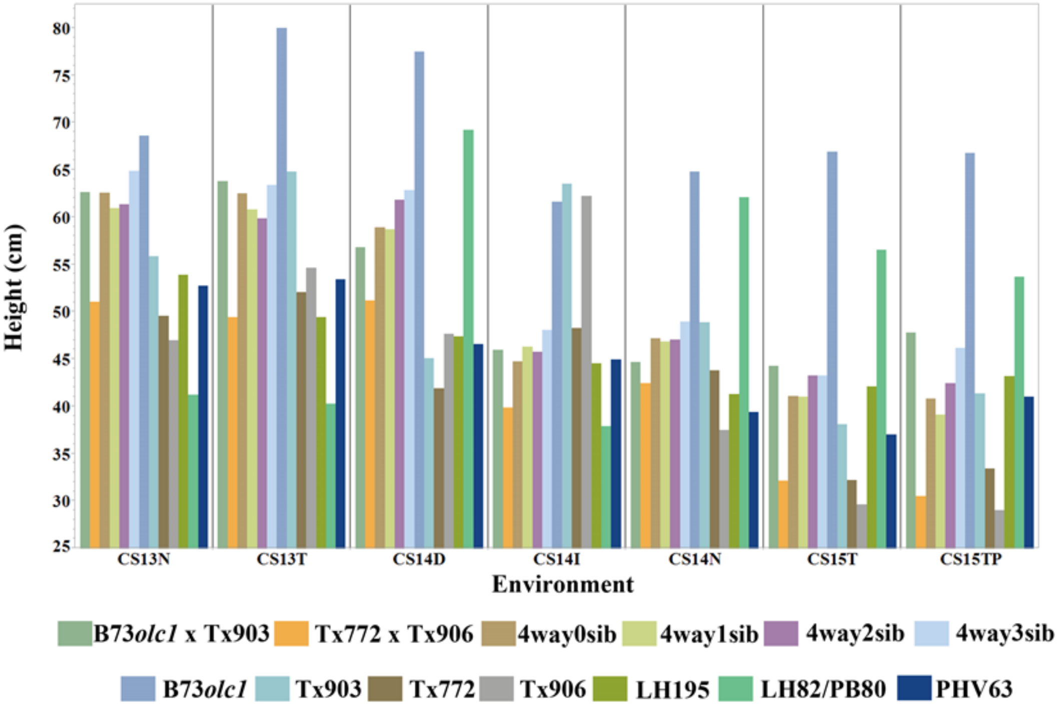
SNP	chr3_158780416	chr3_158780445	chr3_158780918	chr3_158781033	chr3_158781093	chr3_158790476	chr3_158890884	chr3_158901755	chr3_158901756	chr3_158901785	chr3_158901791	chr3_158901849	chr3_158901851
ALLELE	G	G	G	G	T	C	T	G	T	G	G	T	T
EFFECT	0.674362793	-0.616896946	-0.775692809	0.385827371	-0.097642837	-0.395746967	-0.817257645	0.637142566	NA	-0.152517206	-0.101557649	0.213729173	0.213729173
B73*olc1*	G	A	C	A	T	C	C	G	T	G	G	T	T
Tx903	A	G	G	A	T	C	T	C	C	G	G	T	T
Tx772	A	G	C	G	C	C	T	C	C	-	C	T	T
Tx906	A	G	C	G	C	A	C	C	C	-	C	T	T
	0.924382153	-1.003656788	-1.18062367				-1.096355167	1.16118286	1.231751053				
B73*olc1*	G	A	C	A	T	C	C	G	T	G	G	T	T
Tx903	A	G	G	A	T	C	T	C	C	G	G	T	T
						-0.880158886	-0.96851632						
Tx772	A	G	C	G	C	C	T	C	C	-	C	T	T
Tx906	A	G	C	G	C	A	C	C	C	-	C	T	T

A2. Mean of raw phenotype data among subpopulations, parents and ex-PVPs for [a] plant height and [b] ear height.

a)Plant height

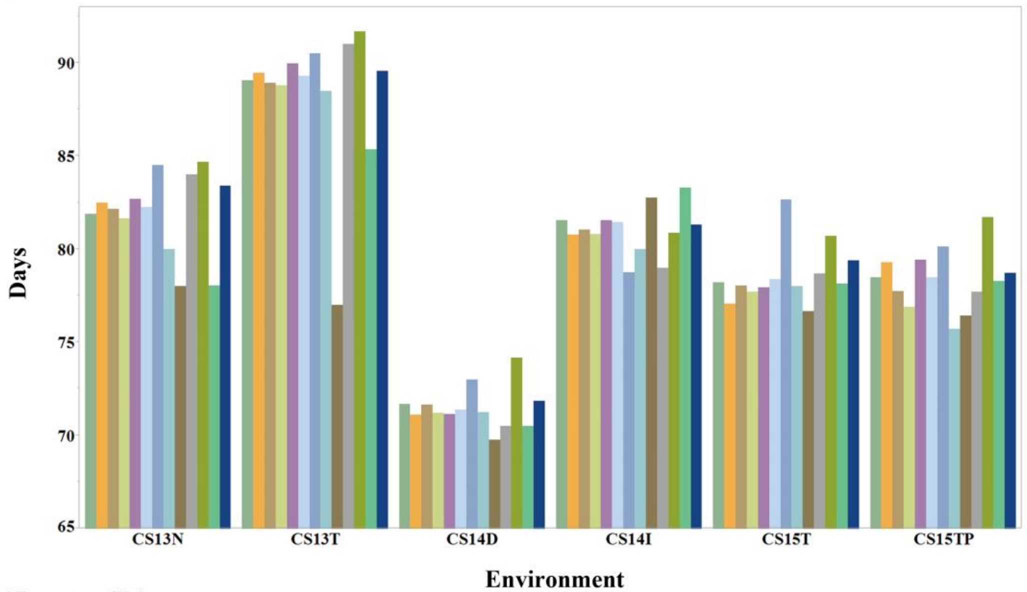


b)Ear height

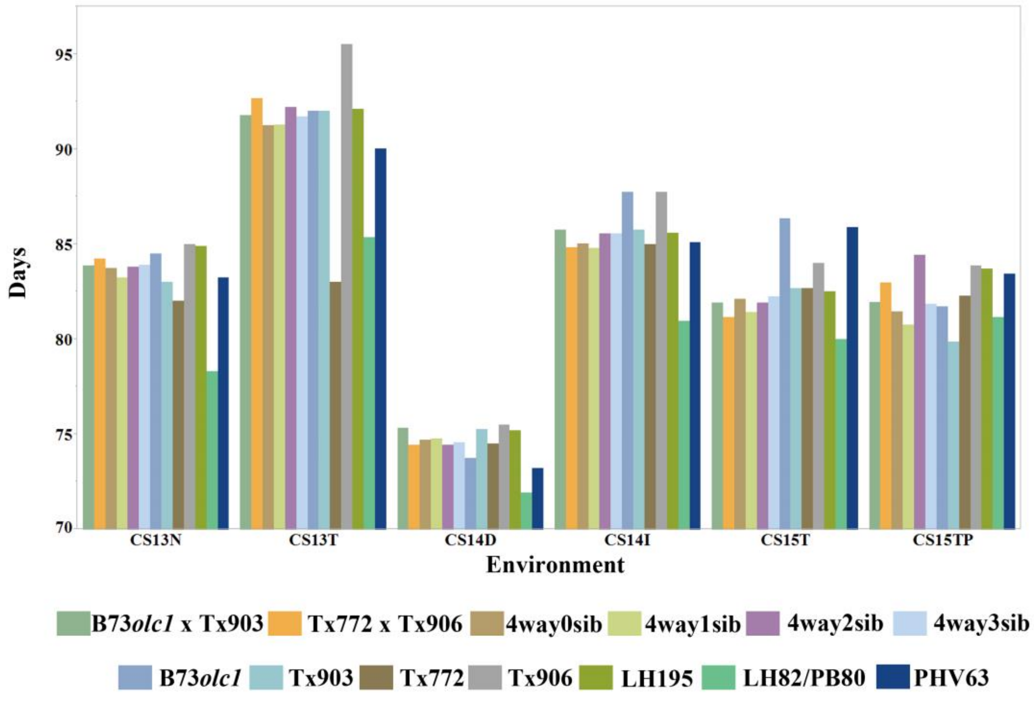


A3. Mean of raw phenotype data among subpopulations, parents and ex-PVPs for [a] days to anthesis and [b] days to silking.

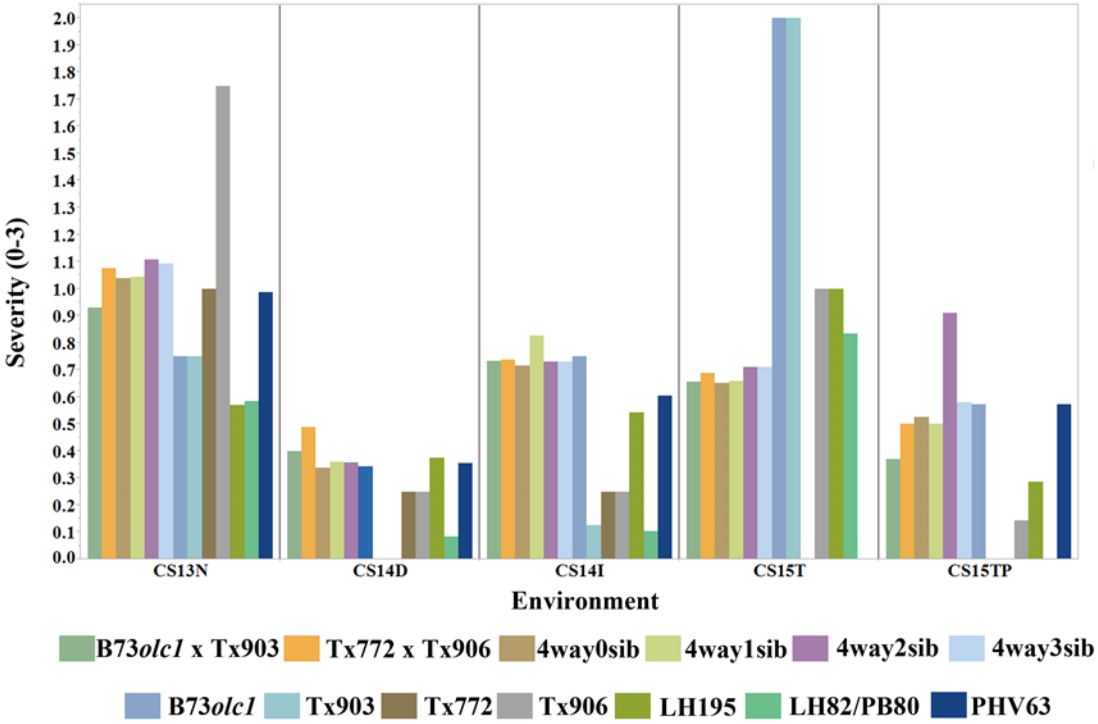
a)Days to anthesis



b)Days to silking



A4. Mean of raw phenotype data among subpopulations, parents and ex-PVPs for leaf rolling.



APPENDIX B. TABLES

B1. Connecting letter report comparing significant differences in years by phenotype using Fisher's least significant differences test (α=0.05 for plant height (PH), ear height (EH), days to anthesis (DTA), days to silking (DTS) and leaf rolling (LR).

Trait	Year	Least sq mean	Connecting letters		
PH (cm)	2013	156.9		B	
	2014	168.5	A		
	2015	135.9			C
EH (cm)	2013	61.0	A		
	2014	52.7		B	
	2015	41.9			C
DTA (days)	2013	85.6	A		
	2014	76.2			C
	2015	78.1		B	
DTS (days)	2013	87.5	A		
	2014	79.9			C
	2015	82.0		B	
LR (0:3)	2013	1.0	A		
	2014	0.5			C
	2015	0.6		B	

B2. Summary statistics of subpopulations, parental lines and ex-PVP lines for plant height (PH), ear height (EH), days to anthesis (DTA), days to silking (DTS) and leaf rolling (LR) by environment.

Trait	Env	Check/Pop	N	Mean	Std. Dev.	Min	Max
PH	CS13N	LH195	36	152.8 ± 2.9	8.6	134.6	172.7
PH	CS13N	LH82	35	120.0 ± 2.5	7.2	106.7	132.1
PH	CS13N	PHV63	35	138.4 ± 2.9	8.3	116.8	154.9
PH	CS13N	4way0Sib	117	159.5 ± 3.9	21.4	114.3	205.7
PH	CS13N	4way1Sib	233	156.6 ± 2.9	22.7	83.8	213.4
PH	CS13N	4way2sib	103	155.9 ± 4.2	21.4	104.1	208.3
PH	CS13N	4way3sib	542	163.1 ± 2.0	23.4	104.1	233.7
PH	CS13N	B73*olc1* x Tx703	149	152.5 ± 3.4	21.2	101.6	203.2
PH	CS13N	Tx772 x Tx906	134	149.6 ± 3.3	19.5	106.7	215.9
PH	CS13T	LH195	33	160.4 ± 1.5	4.1	152.4	167.6
PH	CS13T	LH82	31	127.8 ± 2.3	6.2	116.8	147.3
PH	CS13T	PHV63	36	147.9 ± 2.3	6.9	129.5	157.5
PH	CS13T	4way0Sib	115	165.3 ± 3.4	18.4	114.3	210.8
PH	CS13T	4way1Sib	215	161.7 ± 2.6	19.3	114.3	218.4
PH	CS13T	4way2sib	100	158.8 ± 3.8	19.1	116.8	203.2
PH	CS13T	4way3sib	513	166.9 ± 1.7	19.0	114.3	238.8
PH	CS13T	B73*olc1* x Tx703	136	161.8 ± 3.0	17.5	91.4	203.2
PH	CS13T	Tx772 x Tx906	133	155.1 ± 2.8	16.3	114.3	205.7
PH	CS14I	LH195	24	157.4 ± 5.1	12.1	137.2	182.9
PH	CS14I	PB80	24	149.7 ± 4.7	11.0	127.0	170.2
PH	CS14I	PHV63	22	156.9 ± 8.4	18.8	132.1	203.2
PH	CS14I	4way0Sib	104	156.1 ± 3.9	20.0	114.3	203.2
PH	CS14I	4way1Sib	209	157.6 ± 2.9	21.1	111.8	213.4
PH	CS14I	4way2sib	87	153.9 ± 4.7	22.1	76.2	208.3
PH	CS14I	4way3sib	469	159.3 ± 1.9	20.7	94.0	228.6
PH	CS14I	B73*olc1* x Tx703	118	156.5 ± 4.2	23.3	86.4	226.1
PH	CS14I	Tx772 x Tx906	118	151.6 ± 3.8	20.9	96.5	221.0
PH	CS14D	LH195	22	169.7 ± 4.9	10.9	129.5	180.3
PH	CS14D	PB80	23	191.9 ± 4.4	10.1	180.3	228.6
PH	CS14D	PHV63	24	168.1 ± 4.5	10.6	144.8	182.9
PH	CS14D	4way0Sib	105	178.4 ± 4.5	23.4	127.0	241.3
PH	CS14D	4way1Sib	209	178.7 ± 3.1	23.1	119.4	241.3
PH	CS14D	4way2sib	91	182.2 ± 4.6	22.3	127.0	241.3
PH	CS14D	4way3sib	473	183.1 ± 2.0	22.5	96.5	243.8
PH	CS14D	B73*olc1* x Tx703	126	175.5 ± 3.8	21.7	116.8	223.5
PH	CS14D	Tx772 x Tx906	122	173.6 ± 3.3	18.1	134.6	215.9
PH	CS14N	LH195	16	161.1 ± 3.4	6.4	152.4	170.2
PH	CS14N	PB80	16	178.8 ± 5.4	10.2	157.5	193.0
PH	CS14N	PHV63	16	150.3 ± 5.3	9.9	134.6	175.3
PH	CS14N	4way0Sib	63	159.7 ± 6.3	25.0	78.7	205.7
PH	CS14N	4way1Sib	129	159.5 ± 3.4	19.5	109.2	231.1
PH	CS14N	4way2sib	49	157.6 ± 6.1	21.3	119.4	198.1
PH	CS14N	4way3sib	274	164.9 ± 3.0	25.0	101.6	238.8
PH	CS14N	B73*olc1* x Tx703	74	157.6 ± 4.7	20.3	111.8	205.7
PH	CS14N	Tx772 x Tx906	52	153.4 ± 7.5	46.9	86.4	210.8
PH	CS15T	LH195	16	144.3 ± 4.5	8.5	129.5	157.5

Trait	Env	Check/Pop	N	Mean	Std. Dev.	Min	Max
PH	CS15T	PB80	16	144.9 ± 6.9	12.9	116.8	165.1
PH	CS15T	PHV63	16	137.5 ± 5.9	11.1	119.4	152.4
PH	CS15T	4way0Sib	112	135.3 ± 4.0	21.6	71.1	180.3
PH	CS15T	4way1Sib	219	134.3 ± 2.7	20.4	58.4	185.4
PH	CS15T	4way2sib	93	137.2 ± 4.1	19.8	66.0	180.3
PH	CS15T	4way3sib	513	135.9 ± 1.8	20.1	83.8	195.6
PH	CS15T	B73*olc1* x Tx703	138	136.2 ± 3.5	21.0	83.8	198.1
PH	CS15T	Tx772 x Tx906	127	123.4 ± 3.2	18.1	76.2	175.3
PH	CS15TP	LH195	7	145.5 ± 11.1	12.0	127.0	157.5
PH	CS15TP	PB80	7	149.1 ± 9.8	10.7	134.6	162.6
PH	CS15TP	PHV63	7	144.8 ± 10.2	11.0	127.0	154.9
PH	CS15TP	4way0Sib	40	137.8 ± 6.8	21.4	106.7	190.5
PH	CS15TP	4way1Sib	68	132.8 ± 5.2	21.6	88.9	190.5
PH	CS15TP	4way2sib	33	138.4 ± 9.8	27.5	76.2	188.0
PH	CS15TP	4way3sib	169	143.9 ± 4.1	26.8	71.1	195.6
PH	CS15TP	B73*olc1* x Tx703	27	141.0 ± 12.6	31.8	78.7	190.5
PH	CS15TP	Tx772 x Tx906	44	127.9 ± 5.9	19.3	88.9	175.3
EH	CS13N	LH195	36	53.9 ± 2.8	8.2	40.6	71.1
EH	CS13N	LH82	35	41.2 ± 3.1	8.9	22.9	61.0
EH	CS13N	PHV63	35	52.8 ± 2.6	7.5	35.6	63.5
EH	CS13N	4way0Sib	117	62.5 ± 2.6	14.3	22.9	91.4
EH	CS13N	4way1Sib	233	60.7 ± 1.8	16.2	20.3	106.7
EH	CS13N	4way2sib	103	61.4 ± 3.0	15.5	22.9	104.1
EH	CS13N	4way3sib	542	64.9 ± 1.2	14.6	20.3	106.7
EH	CS13N	B73*olc1* x Tx703	148	62.6 ± 2.5	15.3	17.8	96.5
EH	CS13N	Tx772 x Tx906	134	51.0 ± 2.3	13.5	20.3	86.4
EH	CS13T	LH195	33	49.4 ± 2.5	7.1	38.1	66.0
EH	CS13T	LH82	31	40.2 ± 2.2	6.0	30.5	53.3
EH	CS13T	PHV63	36	53.4 ± 1.9	5.5	40.6	63.5
EH	CS13T	4way0Sib	115	62.5 ± 2.7	14.3	27.9	99.1
EH	CS13T	4way1Sib	215	60.8 ± 1.8	13.2	22.9	94.0
EH	CS13T	4way2sib	99	59.9 ± 2.6	13.0	27.9	96.5
EH	CS13T	4way3sib	513	63.4 ± 1.2	13.6	25.4	101.6
EH	CS13T	B73*olc1* x Tx703	136	63.8 ± 2.5	14.8	33.0	99.1
EH	CS13T	Tx772 x Tx906	133	49.4 ± 2.1	12.5	25.4	78.7
EH	CS14I	LH195	24	44.6 ± 4.9	11.7	27.9	66.0
EH	CS14I	PB80	24	37.9 ± 2.8	6.7	25.4	50.8
EH	CS14I	PHV63	22	44.9 ± 5.7	13.0	22.9	73.7
EH	CS14I	4way0Sib	104	44.7 ± 2.5	12.8	15.2	78.7
EH	CS14I	4way1Sib	209	46.3 ± 2.0	14.7	17.8	96.5
EH	CS14I	4way2sib	87	45.7 ± 2.8	13.0	15.2	76.2
EH	CS14I	4way3sib	469	48.0 ± 1.2	13.7	7.6	101.6
EH	CS14I	B73*olc1* x Tx703	118	46.0 ± 2.4	13.0	20.3	86.4
EH	CS14I	Tx772 x Tx906	118	39.8 ± 2.2	11.8	15.2	76.2
EH	CS14D	LH195	23	47.4 ± 3.6	8.4	25.4	58.4
EH	CS14D	PB80	23	69.2 ± 3.7	8.6	50.8	88.9
EH	CS14D	PHV63	24	46.6 ± 3.3	7.8	33.0	66.0
EH	CS14D	4way0Sib	105	58.9 ± 3.1	15.8	20.3	96.5
EH	CS14D	4way1Sib	209	58.7 ± 2.3	17.2	20.3	106.7
EH	CS14D	4way2sib	91	61.8 ± 3.5	16.7	25.4	99.1
EH	CS14D	4way3sib	473	62.8 ± 1.6	17.8	2.5	109.2

Trait	Env	Check/Pop	N	Mean	Std. Dev.	Min	Max
EH	CS14D	B73*olc1* x Tx703	125	56.8 ± 3.1	17.3	22.9	104.1
EH	CS14D	Tx772 x Tx906	123	51.2 ± 2.5	14.1	22.9	83.8
EH	CS14N	LH195	16	41.3 ± 3.0	5.7	30.5	50.8
EH	CS14N	PB80	16	62.1 ± 4.6	8.7	43.2	71.1
EH	CS14N	PHV63	16	39.4 ± 4.5	8.5	27.9	53.3
EH	CS14N	4way0Sib	64	47.2 ± 3.9	15.5	10.2	73.7
EH	CS14N	4way1Sib	129	46.8 ± 2.4	13.9	15.2	88.9
EH	CS14N	4way2sib	49	47.1 ± 3.8	13.1	17.8	81.3
EH	CS14N	4way3sib	274	49.0 ± 1.8	15.2	12.7	94.0
EH	CS14N	B73*olc1* x Tx703	74	44.7 ± 3.0	13.1	5.1	76.2
EH	CS14N	Tx772 x Tx906	52	42.5 ± 4.3	15.5	10.2	81.3
EH	CS15T	LH195	16	42.1 ± 6.9	5.4	35.6	50.8
EH	CS15T	PB80	16	56.5 ± 3.7	6.9	48.3	71.1
EH	CS15T	PHV63	16	37.0 ± 4.3	8.0	25.4	50.8
EH	CS15T	4way0Sib	112	41.1 ± 2.5	13.4	2.5	71.1
EH	CS15T	4way1Sib	219	41.0 ± 1.7	12.7	17.8	76.2
EH	CS15T	4way2sib	93	43.3 ± 2.3	11.2	15.2	66.0
EH	CS15T	4way3sib	513	43.3 ± 1.0	12.1	12.7	81.3
EH	CS15T	B73*olc1* x Tx703	138	44.3 ± 2.3	13.8	15.2	83.8
EH	CS15T	Tx772 x Tx906	128	32.1 ± 2.1	12.1	10.2	111.8
EH	CS15TP	LH195	7	43.2 ± 5.4	5.9	35.6	50.8
EH	CS15TP	PB80	7	53.7 ± 4.6	5.0	48.3	63.5
EH	CS15TP	PHV63	7	41.0 ± 8.4	9.1	27.9	50.8
EH	CS15TP	4way0Sib	40	40.8 ± 4.3	13.5	17.8	68.6
EH	CS15TP	4way1Sib	68	39.1 ± 3.8	15.6	10.2	76.2
EH	CS15TP	4way2sib	33	42.4 ± 5.8	16.4	12.7	73.7
EH	CS15TP	4way3sib	169	46.1 ± 2.4	15.9	5.1	86.4
EH	CS15TP	B73*olc1* x Tx703	27	47.8 ± 8.3	20.9	2.5	86.4
EH	CS15TP	Tx772 x Tx906	44	30.5 ± 3.8	12.6	10.2	61.0
DTA	CS13N	LH195	34	84.7 ± 0.6	1.7	82.0	87.0
DTA	CS13N	LH82	35	78.0 ± 0.9	2.5	75.0	85.0
DTA	CS13N	PHV63	34	83.4 ± 0.7	2.0	78.0	91.0
DTA	CS13N	4way0Sib	116	82.2 ± 0.5	2.8	74.0	90.0
DTA	CS13N	4way1Sib	232	81.7 ± 0.4	2.9	73.0	90.0
DTA	CS13N	4way2sib	102	82.7 ± 0.6	3.0	75.0	91.0
DTA	CS13N	4way3sib	540	82.3 ± 0.2	2.9	72.0	92.0
DTA	CS13N	B73*olc1* x Tx703	148	81.9 ± 0.4	2.7	74.0	89.0
DTA	CS13N	Tx772 x Tx906	133	82.5 ± 0.4	2.5	76.0	90.0
DTA	CS13T	LH195	33	91.7 ± 0.3	0.7	90.0	93.0
DTA	CS13T	LH82	31	85.4 ± 0.3	0.8	84.0	87.0
DTA	CS13T	PHV63	36	89.6 ± 0.4	1.3	87.0	92.0
DTA	CS13T	4way0Sib	115	88.9 ± 0.5	2.8	83.0	95.0
DTA	CS13T	4way1Sib	215	88.8 ± 0.4	3.1	82.0	97.0
DTA	CS13T	4way2sib	100	90.0 ± 0.6	3.2	82.0	97.0
DTA	CS13T	4way3sib	513	89.3 ± 0.2	2.7	81.0	99.0
DTA	CS13T	B73*olc1* x Tx703	135	89.1 ± 0.4	2.3	84.0	94.0
DTA	CS13T	Tx772 x Tx906	133	89.5 ± 0.4	2.4	83.0	98.0
DTA	CS14I	LH195	24	80.9 ± 0.3	0.7	80.0	82.0
DTA	CS14I	PB80	24	83.3 ± 0.3	0.6	82.0	84.0
DTA	CS14I	PHV63	24	81.3 ± 2.0	4.7	68.0	87.0
DTA	CS14I	4way0Sib	104	81.0 ± 0.7	3.3	72.0	91.0

Trait	**Env**	**Check/Pop**	**N**	**Mean**	**Std. Dev.**	**Min**	**Max**
DTA	CS14I	4way1Sib	209	80.8 ± 0.4	2.9	74.0	88.0
DTA	CS14I	4way2sib	87	81.5 ± 0.6	2.9	74.0	87.0
DTA	CS14I	4way3sib	470	81.5 ± 0.3	3.1	70.0	95.0
DTA	CS14I	B73*olc1* x Tx703	118	81.6 ± 0.5	2.8	77.0	88.0
DTA	CS14I	Tx772 x Tx906	118	80.8 ± 0.6	3.2	76.0	93.0
DTA	CS14D	LH195	24	74.2 ± 1.2	2.8	71.0	85.0
DTA	CS14D	PB80	23	70.0 ± 1.4	3.1	67.0	82.0
DTA	CS14D	PHV63	24	71.8 ± 0.9	2.0	69.0	78.0
DTA	CS14D	4way0Sib	107	71.6 ± 0.7	3.4	64.0	82.0
DTA	CS14D	4way1Sib	211	71.2 ± 0.4	3.3	64.0	82.0
DTA	CS14D	4way2sib	91	71.1 ± 0.7	3.0	65.0	78.0
DTA	CS14D	4way3sib	477	71.4 ± 0.2	3.2	64.0	83.0
DTA	CS14D	B73*olc1* x Tx703	128	71.7 ± 0.7	4.1	64.0	84.0
DTA	CS14D	Tx772 x Tx906	122	71.0 ± 0.6	3.1	64.0	82.0
DTA	CS15T	LH195	16	80.7 ± 0.9	1.7	78.0	84.0
DTA	CS15T	PB80	16	78.1 ± 1.3	2.4	75.0	84.0
DTA	CS15T	PHV63	16	85.9 ± 3.9	7.2	79.0	99.0
DTA	CS15T	4way0Sib	112	78.0 ± 0.6	2.4	69.0	82.0
DTA	CS15T	4way1Sib	213	77.7 ± 0.4	3.2	69.0	88.0
DTA	CS15T	4way2sib	92	77.9 ± 0.7	3.6	68.0	93.0
DTA	CS15T	4way3sib	507	78.4 ± 0.3	3.3	71.0	97.0
DTA	CS15T	B73*olc1* x Tx703	136	78.2 ± 0.5	3.1	69.0	86.0
DTA	CS15T	Tx772 x Tx906	128	77.1 ± 0.5	3.1	69.0	88.0
DTA	CS15TP	LH195	7	81.7 ± 2.7	2.9	79.0	87.0
DTA	CS15TP	PB80	7	78.3 ± 1.8	2.0	76.0	81.0
DTA	CS15TP	PHV63	7	78.7 ± 1.9	2.1	76.0	82.0
DTA	CS15TP	4way0Sib	40	77.8 ± 1.1	3.4	71.0	86.0
DTA	CS15TP	4way1Sib	68	76.9 ± 1.0	4.2	70.0	87.0
DTA	CS15TP	4way2sib	33	79.4 ± 1.4	3.8	71.0	90.0
DTA	CS15TP	4way3sib	168	78.5 ± 0.6	3.8	68.0	91.0
DTA	CS15TP	B73*olc1* x Tx703	27	78.5 ± 1.6	4.1	72.0	88.0
DTA	CS15TP	Tx772 x Tx906	44	79.3 ± 1.5	4.8	72.0	94.0
DTS	CS13N	LH195	34	84.9 ± 0.7	1.9	82.0	89.0
DTS	CS13N	LH82	35	78.3 ± 1.0	2.9	75.0	85.0
DTS	CS13N	PHV63	34	83.2 ± 0.7	1.9	79.0	86.0
DTS	CS13N	4way0Sib	114	83.8 ± 0.5	2.8	76.0	90.0
DTS	CS13N	4way1Sib	230	83.3 ± 0.4	2.9	74.0	92.0
DTS	CS13N	4way2sib	100	83.8 ± 0.5	2.5	79.0	90.0
DTS	CS13N	4way3sib	532	83.9 ± 0.2	2.8	74.0	92.0
DTS	CS13N	B73*olc1* x Tx703	147	83.6 ± 0.4	2.6	74.0	90.0
DTS	CS13N	Tx772 x Tx906	129	84.2 ± 0.5	2.7	76.0	91.0
DTS	CS13T	LH195	33	92.1 ± 0.4	1.1	90.0	94.0
DTS	CS13T	LH82	31	85.4 ± 0.3	0.8	84.0	87.0
DTS	CS13T	PHV63	36	90.0 ± 0.5	1.4	87.0	93.0
DTS	CS13T	4way0Sib	115	37.2 ± 0.6	3.1	85.0	99.0
DTS	CS13T	4way1Sib	215	91.3 ± 0.5	3.6	83.0	100.0
DTS	CS13T	4way2sib	98	92.2 ± 0.7	3.6	83.0	100.0
DTS	CS13T	4way3sib	513	91.7 ± 0.3	3.4	82.0	101.0
DTS	CS13T	B73*olc1* x Tx703	135	91.8 ± 0.4	2.6	84.0	99.0
DTS	CS13T	Tx772 x Tx906	133	92.7 ± 0.5	2.9	85.0	101.0
DTS	CS14I	LH195	24	85.6 ± 0.7	1.6	83.0	90.0

Trait	Env	Check/Pop	N	Mean	Std. Dev.	Min	Max
DTS	CS14I	PB80	24	81.0 ± 0.5	1.1	79.0	83.0
DTS	CS14I	PHV63	24	85.0 ± 1.2	2.8	81.0	96.0
DTS	CS14I	4way0Sib	104	85.0 ± 0.8	4.0	75.0	95.0
DTS	CS14I	4way1Sib	209	84.8 ± 0.5	3.8	76.0	97.0
DTS	CS14I	4way2sib	87	85.6 ± 0.8	3.8	77.0	94.0
DTS	CS14I	4way3sib	467	85.6 ± 0.4	3.9	73.0	101.0
DTS	CS14I	B73*olc1* x Tx703	118	85.8 ± 0.6	3.5	79.0	95.0
DTS	CS14I	Tx772 x Tx906	117	84.8 ± 0.7	3.6	77.0	93.0
DTS	CS14D	LH195	24	75.2 ± 1.3	3.0	71.0	85.0
DTS	CS14D	PB80	23	71.7 ± 1.6	3.7	68.0	84.0
DTS	CS14D	PHV63	24	73.2 ± 1.1	2.5	70.0	78.0
DTS	CS14D	4way0Sib	104	74.7 ± 0.7	3.6	67.0	85.0
DTS	CS14D	4way1Sib	211	74.8 ± 0.5	3.6	66.0	86.0
DTS	CS14D	4way2sib	90	74.4 ± 0.7	3.3	67.0	84.0
DTS	CS14D	4way3sib	475	74.6 ± 0.3	3.3	66.0	86.0
DTS	CS14D	B73*olc1* x Tx703	128	75.3 ± 0.8	4.4	66.0	87.0
DTS	CS14D	Tx772 x Tx906	121	74.4 ± 0.6	3.3	68.0	86.0
DTS	CS15T	LH195	16	82.5 ± 1.2	2.3	80.0	88.0
DTS	CS15T	PB80	16	80.0 ± 1.5	2.7	76.0	86.0
DTS	CS15T	PHV63	16	85.9 ± 3.9	7.2	79.0	99.0
DTS	CS15T	4way0Sib	112	82.1 ± 0.7	3.6	74.0	98.0
DTS	CS15T	4way1Sib	219	81.4 ± 0.6	4.3	72.0	100.0
DTS	CS15T	4way2sib	93	81.9 ± 1.0	5.0	70.0	98.0
DTS	CS15T	4way3sib	511	82.2 ± 0.4	4.2	74.0	99.0
DTS	CS15T	B73*olc1* x Tx703	136	81.9 ± 0.7	4.2	72.0	94.0
DTS	CS15T	Tx772 x Tx906	127	81.1 ± 0.7	3.9	73.0	92.0
DTS	CS15TP	LH195	7	83.7 ± 4.9	5.3	78.0	91.0
DTS	CS15TP	PB80	7	81.1 ± 4.2	4.6	78.0	91.0
DTS	CS15TP	PHV63	7	83.4 ± 4.7	5.1	78.0	91.0
DTS	CS15TP	4way0Sib	40	81.5 ± 1.2	3.8	74.0	91.0
DTS	CS15TP	4way1Sib	67	80.8 ± 1.3	5.5	73.0	98.0
DTS	CS15TP	4way2sib	33	84.4 ± 2.0	5.6	73.0	99.0
DTS	CS15TP	4way3sib	168	81.9 ± 0.8	4.9	70.0	100.0
DTS	CS15TP	B73*olc1* x Tx703	26	82.0 ± 1.9	4.8	74.0	98.0
DTS	CS15TP	Tx772 x Tx906	43	83.0 ± 1.8	5.7	74.0	98.0
LR	CS13N	LH195	72	0.6 ± 0.1	0.5	0.0	2.0
LR	CS13N	LH82	70	0.6 ± 0.1	0.5	0.0	1.0
LR	CS13N	PHV63	70	1.0 ± 0.2	0.7	0.0	2.0
LR	CS13N	4way0Sib	234	1.0 ± 0.1	0.6	0.0	3.0
LR	CS13N	4way1Sib	464	1.0 ± 0.1	0.6	0.0	3.0
LR	CS13N	4way2sib	204	1.1 ± 0.1	0.6	0.0	3.0
LR	CS13N	4way3sib	1080	1.1 ± 0.0	0.6	0.0	3.0
LR	CS13N	B73*olc1* x Tx703	298	0.9 ± 0.1	0.5	0.0	3.0
LR	CS13N	Tx772 x Tx906	268	1.1 ± 0.1	0.7	0.0	3.0
LR	CS14D	LH195	48	0.4 ± 0.2	0.5	0.0	1.0
LR	CS14D	PB80	48	0.1 ± 0.0	0.3	0.0	1.0
LR	CS14D	PHV63	48	0.4 ± 0.1	0.5	0.0	1.0
LR	CS14D	4way0Sib	210	0.3 ± 0.1	0.5	0.0	2.0
LR	CS14D	4way1Sib	418	0.4 ± 0.1	0.5	0.0	3.0
LR	CS14D	4way2sib	182	0.4 ± 0.1	0.5	0.0	2.0
LR	CS14D	4way3sib	946	0.3 ± 0.0	0.5	0.0	2.0

Trait	Env	Check/Pop	N	Mean	Std. Dev.	Min	Max
LR	CS14D	B73*olc1* x Tx703	252	0.4 ± 0.1	0.6	0.0	2.0
LR	CS14D	Tx772 x Tx906	246	0.5 ± 0.1	0.6	0.0	2.0
LR	CS14I	LH195	48	0.5 ± 0.2	0.5	0.0	2.0
LR	CS14I	PB80	48	0.1 ± 0.1	0.3	0.0	1.0
LR	CS14I	PHV63	48	0.6 ± 0.2	0.8	0.0	3.0
LR	CS14I	4way0Sib	208	0.7 ± 0.1	0.9	0.0	3.0
LR	CS14I	4way1Sib	418	0.8 ± 0.1	0.8	0.0	3.0
LR	CS14I	4way2sib	174	0.7 ± 0.1	0.8	0.0	3.0
LR	CS14I	4way3sib	940	0.7 ± 0.1	0.9	0.0	3.0
LR	CS14I	B73*olc1* x Tx703	236	0.7 ± 0.1	0.8	0.0	3.0
LR	CS14I	Tx772 x Tx906	236	0.7 ± 0.1	0.8	0.0	3.0
LR	CS15T	LH195	6	1.0 ± 0.7	0.6	0.0	2.0
LR	CS15T	PB80	6	0.8 ± 0.8	0.8	0.0	2.0
LR	CS15T	PHV63	6	0.0 ± 0.0	0.0	0.0	0.0
LR	CS15T	4way0Sib	112	0.7 ± 0.2	0.9	0.0	3.0
LR	CS15T	4way1Sib	219	0.7 ± 0.1	0.9	0.0	3.0
LR	CS15T	4way2sib	93	0.7 ± 0.2	1.0	0.0	3.0
LR	CS15T	4way3sib	513	0.7 ± 0.1	0.9	0.0	3.0
LR	CS15T	B73*olc1* x Tx703	137	0.7 ± 0.2	0.9	0.0	3.0
LR	CS15T	Tx772 x Tx906	128	0.7 ± 0.2	0.9	0.0	3.0
LR	CS15TP	LH195	7	0.3 ± 0.5	0.5	0.0	1.0
LR	CS15TP	PB80	7	0.0 ± 0.0	0.0	0.0	0.0
LR	CS15TP	PHV63	7	0.6 ± 0.5	0.5	0.0	1.0
LR	CS15TP	4way0Sib	40	0.5 ± 0.2	0.7	0.0	2.0
LR	CS15TP	4way1Sib	68	0.5 ± 0.2	0.8	0.0	3.0
LR	CS15TP	4way2sib	33	0.9 ± 0.4	1.1	0.0	3.0
LR	CS15TP	4way3sib	169	0.6 ± 0.1	0.9	0.0	3.0
LR	CS15TP	B73*olc1* x Tx703	27	0.4 ± 0.3	0.8	0.0	3.0
LR	CS15TP	Tx772 x Tx906	44	0.5 ± 0.2	0.7	0.0	2.0

B3. BLUP estimates of parental lines, progeny, subpopulations and ex-PVPs across multiple environmental trial analysis for plant height (PH), ear height (EH), days to anthesis (DTA), days to silking (DTS) and leaf rolling (LR).

	PH (cm)	**EH (cm)**	**DTA (days)**	**DTS (days)**	**LR (0:3)**
B73*olc1*	184.2	70.4	82.2	84.1	0.6
Tx903	147.1	52.0	78.9	82.7	0.2
Tx772	143.9	42.1	78.1	82.4	0.4
Tx906	158.0	44.6	79.6	84.6	0.5
Progeny	155.8	51.4	80.1	83.2	0.7
LH195	153.5	44.3	82.1	83.9	0.4
PB80	162.3	58.0	80.4	80.5	0.2
LH82	119.5	31.1	76.4	77.8	0.2
PHV63	145.8	44.2	80.7	82.9	0.6
4way0Sib	156.6	51.7	79.9	83.1	0.7
4way1Sib	154.7	50.7	79.7	82.9	0.7
4way2sib	154.6	51.5	80.5	83.5	0.7
4way3sib	159.1	53.8	80.2	83.4	0.7
B73*olc1* x Tx703	154.7	52.3	80.1	83.4	0.6
Tx772 x Tx906	149.1	42.8	79.9	83.2	0.7

B4. All SNPs above 3-LOD in full population GWA study using the complete marker for plant height (PH), ear height (EH), days to anthesis (DTA) and days to silking (DTS). QTL were classified by group adjacent SNP that differ by less than 1 Mbps.

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
PH	PH_1	chr1_4040134	1	4040134	0.20	1.00E-03	3.00	0.56
PH	PH_1	chr1_4446759	1	4446759	0.20	8.22E-04	3.09	0.58
PH	PH_2	chr1_51853040	1	51853040	0.13	6.51E-04	3.19	0.60
PH	PH_2	chr1_51853044	1	51853044	0.13	6.51E-04	3.19	0.60
PH	PH_2	chr1_51853047	1	51853047	0.13	6.51E-04	3.19	0.60
PH	PH_3	chr1_65195157	1	65195157	0.16	2.12E-05	4.67	0.93
PH	PH_4	chr1_69865553	1	69865553	0.28	1.23E-04	3.91	0.76
PH	PH_4	chr1_69932745	1	69932745	0.46	5.20E-04	3.28	0.62
PH	PH_4	chr1_70516197	1	70516197	0.34	3.31E-04	3.48	0.66
PH	PH_4	chr1_70726321	1	70726321	0.15	4.52E-04	3.34	0.63
PH	PH_4	chr1_70726653	1	70726653	0.24	6.24E-04	3.20	0.60
PH	PH_5	chr1_80814365	1	80814365	0.22	4.14E-04	3.38	0.64
PH	PH_5	chr1_81076561	1	81076561	0.22	3.28E-04	3.48	0.66
PH	PH_6	chr1_82912116	1	82912116	0.18	3.37E-04	3.47	0.66
PH	PH_6	chr1_82912134	1	82912134	0.19	1.75E-04	3.76	0.72
PH	PH_7	chr1_86498097	1	86498097	0.20	5.76E-04	3.24	0.61
PH	PH_7	chr1_86585652	1	86585652	0.21	5.43E-04	3.27	0.62
PH	PH_7	chr1_86945200	1	86945200	0.22	7.78E-04	3.11	0.58
PH	PH_7	chr1_86945222	1	86945222	0.22	8.30E-04	3.08	0.57
PH	PH_8	chr1_89234735	1	89234735	0.26	4.41E-04	3.36	0.64
PH	PH_8	chr1_89234772	1	89234772	0.26	4.41E-04	3.36	0.64
PH	PH_8	chr1_89240426	1	89240426	0.27	3.28E-05	4.48	0.89
PH	PH_8	chr1_89240641	1	89240641	0.28	1.81E-04	3.74	0.72
PH	PH_8	chr1_89240714	1	89240714	0.27	9.70E-05	4.01	0.78
PH	PH_8	chr1_89830316	1	89830316	0.27	2.28E-06	5.64	1.15
PH	PH_8	chr1_90215425	1	90215425	0.26	1.38E-04	3.86	0.75
PH	PH_8	chr1_90215427	1	90215427	0.26	1.88E-04	3.73	0.72
PH	PH_8	chr1_90217035	1	90217035	0.27	9.94E-05	4.00	0.78
PH	PH_8	chr1_90323716	1	90323716	0.26	1.45E-04	3.84	0.74
PH	PH_9	chr1_90952442	1	90952442	0.49	7.18E-04	3.14	0.59
PH	PH_9	chr1_91191720	1	91191720	0.20	6.67E-04	3.18	0.60
PH	PH_9	chr1_91191837	1	91191837	0.21	7.74E-04	3.11	0.58
PH	PH_9	chr1_91247613	1	91247613	0.21	2.03E-04	3.69	0.71
PH	PH_9	chr1_91247624	1	91247624	0.21	2.03E-04	3.69	0.71

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
PH	PH_9	chr1_91247642	1	91247642	0.20	7.86E-04	3.10	0.58
PH	PH_10	chr1_251992124	1	251992124	0.45	7.63E-04	3.12	0.58
PH	PH_10	chr1_251992170	1	251992170	0.45	7.63E-04	3.12	0.58
PH	PH_10	chr1_251995145	1	251995145	0.44	1.78E-04	3.75	0.72
PH	PH_10	chr1_251995482	1	251995482	0.44	8.00E-04	3.10	0.58
PH	PH_11	chr1_253280955	1	253280955	0.32	7.65E-04	3.12	0.58
PH	PH_12	chr1_276987588	1	276987588	0.20	1.00E-03	3.00	0.56
PH	PH_13	chr2_26730200	2	26730200	0.17	7.90E-04	3.10	0.58
PH	PH_14	chr2_175707147	2	175707147	0.41	6.88E-04	3.16	0.59
PH	PH_15	chr2_211581902	2	211581902	0.48	6.79E-04	3.17	0.59
PH	PH_16	chr2_212745934	2	212745934	0.35	6.94E-04	3.16	0.59
PH	PH_17	chr2_216821100	2	216821100	0.47	9.04E-04	3.04	0.57
PH	PH_18	chr2_223778817	2	223778817	0.38	2.13E-04	3.67	0.71
PH	PH_19	chr3_10366959	3	10366959	0.45	1.52E-04	3.82	0.74
PH	PH_19	chr3_10387653	3	10387653	0.46	2.86E-04	3.54	0.68
PH	PH_19	chr3_10387700	3	10387700	0.44	5.18E-04	3.29	0.62
PH	PH_19	chr3_10452133	3	10452133	0.46	7.66E-05	4.12	0.81
PH	PH_19	chr3_10452135	3	10452135	0.46	7.66E-05	4.12	0.81
PH	PH_19	chr3_10455204	3	10455204	0.45	7.38E-05	4.13	0.81
PH	PH_19	chr3_10462628	3	10462628	0.20	2.07E-04	3.68	0.71
PH	PH_20	chr3_20806785	3	20806785	0.50	7.27E-04	3.14	0.59
PH	PH_21	chr3_30539128	3	30539128	0.07	5.44E-04	3.26	0.61
PH	PH_22	chr3_69204751	3	69204751	0.22	9.53E-04	3.02	0.56
PH	PH_22	chr3_69204769	3	69204769	0.22	8.36E-04	3.08	0.57
PH	PH_23	chr3_148797744	3	148797744	0.30	4.52E-04	3.34	0.63
PH	PH_23	chr3_148877069	3	148877069	0.28	8.94E-05	4.05	0.79
PH	PH_23	chr3_148877128	3	148877128	0.28	3.96E-04	3.40	0.65
PH	PH_23	chr3_148877130	3	148877130	0.28	3.96E-04	3.40	0.65
PH	PH_23	chr3_148877137	3	148877137	0.29	4.83E-04	3.32	0.63
PH	PH_23	chr3_148877155	3	148877155	0.29	4.83E-04	3.32	0.63
PH	PH_24	chr3_151971584	3	151971584	0.47	7.95E-04	3.10	0.58
PH	PH_24	chr3_151971622	3	151971622	0.47	8.52E-04	3.07	0.57
PH	PH_25	chr3_154075824	3	154075824	0.29	1.47E-05	4.83	0.97
PH	PH_25	chr3_154075870	3	154075870	0.25	6.36E-04	3.20	0.60
PH	PH_25	chr3_154075887	3	154075887	0.25	6.36E-04	3.20	0.60
PH	PH_25	chr3_154075890	3	154075890	0.25	6.36E-04	3.20	0.60
PH	PH_25	chr3_154076084	3	154076084	0.26	9.35E-04	3.03	0.56
PH	PH_25	chr3_154077726	3	154077726	0.27	2.80E-05	4.55	0.90

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
PH	PH_25	chr3_154124966	3	154124966	0.49	1.72E-04	3.76	0.73
PH	PH_25	chr3_154125085	3	154125085	0.49	1.29E-04	3.89	0.75
PH	PH_25	chr3_154409508	3	154409508	0.15	3.54E-04	3.45	0.66
PH	PH_25	chr3_154409545	3	154409545	0.29	6.35E-04	3.20	0.60
PH	PH_25	chr3_154563985	3	154563985	0.27	7.11E-04	3.15	0.59
PH	PH_25	chr3_154592422	3	154592422	0.29	6.53E-05	4.19	0.82
PH	PH_25	chr3_154592481	3	154592481	0.29	6.53E-05	4.19	0.82
PH	PH_25	chr3_154592489	3	154592489	0.29	6.53E-05	4.19	0.82
PH	PH_25	chr3_154625415	3	154625415	0.29	1.02E-04	3.99	0.78
PH	PH_25	chr3_154625420	3	154625420	0.29	4.63E-04	3.33	0.63
PH	PH_25	chr3_154661548	3	154661548	0.28	8.14E-05	4.09	0.80
PH	PH_25	chr3_154739847	3	154739847	0.29	1.28E-04	3.89	0.76
PH	PH_25	chr3_154981090	3	154981090	0.28	3.33E-04	3.48	0.66
PH	PH_25	chr3_154981137	3	154981137	0.27	7.43E-04	3.13	0.58
PH	PH_25	chr3_155091887	3	155091887	0.31	2.74E-04	3.56	0.68
PH	PH_25	chr3_155803339	3	155803339	0.48	1.93E-04	3.71	0.72
PH	PH_25	chr3_155803532	3	155803532	0.29	8.40E-06	5.08	1.02
PH	PH_25	chr3_155967126	3	155967126	0.28	3.57E-04	3.45	0.66
PH	PH_25	chr3_155967168	3	155967168	0.31	3.03E-04	3.52	0.67
PH	PH_25	chr3_156287541	3	156287541	0.28	3.04E-04	3.52	0.67
PH	PH_25	chr3_156287743	3	156287743	0.28	1.07E-04	3.97	0.77
PH	PH_25	chr3_156486164	3	156486164	0.28	1.61E-04	3.79	0.73
PH	PH_25	chr3_156799845	3	156799845	0.49	4.87E-04	3.31	0.63
PH	PH_25	chr3_156969980	3	156969980	0.49	6.27E-05	4.20	0.83
PH	PH_25	chr3_156969997	3	156969997	0.48	1.29E-04	3.89	0.75
PH	PH_25	chr3_157018380	3	157018380	0.21	7.96E-04	3.10	0.58
PH	PH_25	chr3_157051502	3	157051502	0.31	6.05E-04	3.22	0.60
PH	PH_25	chr3_157417448	3	157417448	0.30	1.18E-07	6.93	1.45
PH	PH_25	chr3_157568991	3	157568991	0.29	4.88E-06	5.31	1.08
PH	PH_25	chr3_157576226	3	157576226	0.30	1.36E-07	6.87	1.44
PH	PH_25	chr3_157576421	3	157576421	0.30	9.98E-08	7.00	1.47
PH	PH_25	chr3_157576589	3	157576589	0.28	1.84E-05	4.73	0.95
PH	PH_25	chr3_157576725	3	157576725	0.30	9.21E-07	6.04	1.25
PH	PH_25	chr3_157576733	3	157576733	0.29	4.41E-07	6.36	1.32
PH	PH_25	chr3_157578664	3	157578664	0.31	3.28E-06	5.48	1.12
PH	PH_25	chr3_157578666	3	157578666	0.31	4.93E-06	5.31	1.08
PH	PH_25	chr3_158348209	3	158348209	0.48	4.99E-05	4.30	0.85
PH	PH_25	chr3_158348357	3	158348357	0.26	2.49E-04	3.60	0.69

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
PH	PH_25	chr3_158451553	3	158451553	0.22	5.77E-04	3.24	0.61
PH	PH_25	chr3_158780416	3	158780416	0.23	8.15E-04	3.09	0.58
PH	PH_25	chr3_158780445	3	158780445	0.24	4.40E-04	3.36	0.64
PH	PH_25	chr3_158780918	3	158780918	0.30	6.60E-06	5.18	1.05
PH	PH_25	chr3_158890884	3	158890884	0.48	1.34E-06	5.87	1.21
PH	PH_25	chr3_158972316	3	158972316	0.48	6.36E-06	5.20	1.05
PH	PH_25	chr3_158973464	3	158973464	0.23	9.67E-04	3.01	0.56
PH	PH_25	chr3_159379133	3	159379133	0.25	9.38E-04	3.03	0.56
PH	PH_25	chr3_159385192	3	159385192	0.49	1.80E-05	4.75	0.95
PH	PH_25	chr3_159388105	3	159388105	0.29	6.47E-06	5.19	1.05
PH	PH_25	chr3_159678426	3	159678426	0.30	4.14E-05	4.38	0.87
PH	PH_25	chr3_159678466	3	159678466	0.30	5.32E-05	4.27	0.84
PH	PH_25	chr3_159678635	3	159678635	0.30	8.05E-05	4.09	0.80
PH	PH_25	chr3_159731276	3	159731276	0.26	7.69E-04	3.11	0.58
PH	PH_25	chr3_159800996	3	159800996	0.48	3.62E-06	5.44	1.11
PH	PH_25	chr3_159801043	3	159801043	0.28	5.36E-06	5.27	1.07
PH	PH_25	chr3_159801235	3	159801235	0.30	7.37E-06	5.13	1.04
PH	PH_25	chr3_159807447	3	159807447	0.29	1.09E-05	4.96	1.00
PH	PH_25	chr3_159810023	3	159810023	0.29	5.45E-05	4.26	0.84
PH	PH_25	chr3_159818701	3	159818701	0.49	2.03E-05	4.69	0.94
PH	PH_25	chr3_159820547	3	159820547	0.48	2.21E-05	4.66	0.93
PH	PH_25	chr3_159861750	3	159861750	0.24	3.15E-04	3.50	0.67
PH	PH_25	chr3_159868843	3	159868843	0.29	2.60E-06	5.58	1.14
PH	PH_25	chr3_160665463	3	160665463	0.50	2.40E-05	4.62	0.92
PH	PH_25	chr3_160666211	3	160666211	0.23	7.19E-04	3.14	0.59
PH	PH_25	chr3_161257076	3	161257076	0.29	1.24E-05	4.91	0.99
PH	PH_25	chr3_161257078	3	161257078	0.29	1.24E-05	4.91	0.99
PH	PH_25	chr3_161257090	3	161257090	0.29	1.24E-05	4.91	0.99
PH	PH_25	chr3_161257096	3	161257096	0.29	1.24E-05	4.91	0.99
PH	PH_25	chr3_161259908	3	161259908	0.29	2.40E-04	3.62	0.69
PH	PH_25	chr3_161369706	3	161369706	0.29	3.62E-05	4.44	0.88
PH	PH_25	chr3_161369763	3	161369763	0.29	1.32E-04	3.88	0.75
PH	PH_25	chr3_161369818	3	161369818	0.28	3.64E-05	4.44	0.88
PH	PH_25	chr3_161369881	3	161369881	0.29	1.75E-05	4.76	0.95
PH	PH_25	chr3_161573134	3	161573134	0.27	4.90E-06	5.31	1.08
PH	PH_25	chr3_161573148	3	161573148	0.22	8.65E-04	3.06	0.57
PH	PH_25	chr3_161573155	3	161573155	0.27	6.47E-06	5.19	1.05
PH	PH_25	chr3_161573221	3	161573221	0.27	1.58E-06	5.80	1.19

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
PH	PH_25	chr3_161573250	3	161573250	0.27	1.58E-06	5.80	1.19
PH	PH_25	chr3_161575037	3	161575037	0.29	2.85E-04	3.54	0.68
PH	PH_25	chr3_161575049	3	161575049	0.49	2.18E-06	5.66	1.16
PH	PH_25	chr3_161575068	3	161575068	0.49	1.70E-06	5.77	1.18
PH	PH_25	chr3_161575090	3	161575090	0.29	4.71E-04	3.33	0.63
PH	PH_25	chr3_161575111	3	161575111	0.50	4.79E-06	5.32	1.08
PH	PH_25	chr3_161575140	3	161575140	0.50	4.79E-06	5.32	1.08
PH	PH_25	chr3_161575170	3	161575170	0.34	3.67E-05	4.43	0.88
PH	PH_25	chr3_161576585	3	161576585	0.29	4.70E-05	4.33	0.85
PH	PH_25	chr3_161576642	3	161576642	0.25	2.77E-04	3.56	0.68
PH	PH_25	chr3_161638284	3	161638284	0.29	8.77E-06	5.06	1.02
PH	PH_25	chr3_161650139	3	161650139	0.30	2.99E-05	4.53	0.90
PH	PH_25	chr3_161650198	3	161650198	0.23	8.82E-04	3.05	0.57
PH	PH_25	chr3_161650243	3	161650243	0.29	8.13E-06	5.09	1.03
PH	PH_25	chr3_161650452	3	161650452	0.28	1.19E-05	4.92	0.99
PH	PH_25	chr3_161650457	3	161650457	0.25	1.83E-04	3.74	0.72
PH	PH_25	chr3_161650485	3	161650485	0.25	3.42E-04	3.47	0.66
PH	PH_25	chr3_161650544	3	161650544	0.23	1.04E-04	3.98	0.78
PH	PH_25	chr3_162063874	3	162063874	0.27	6.45E-04	3.19	0.60
PH	PH_25	chr3_162179943	3	162179943	0.25	9.57E-04	3.02	0.56
PH	PH_25	chr3_162180254	3	162180254	0.24	7.34E-04	3.13	0.59
PH	PH_26	chr3_163638820	3	163638820	0.26	3.64E-04	3.44	0.65
PH	PH_26	chr3_163638850	3	163638850	0.26	4.05E-04	3.39	0.64
PH	PH_26	chr3_163638859	3	163638859	0.26	3.64E-04	3.44	0.65
PH	PH_26	chr3_163638861	3	163638861	0.26	3.64E-04	3.44	0.65
PH	PH_26	chr3_163638863	3	163638863	0.26	4.05E-04	3.39	0.64
PH	PH_26	chr3_163638879	3	163638879	0.26	4.05E-04	3.39	0.64
PH	PH_26	chr3_163638882	3	163638882	0.26	4.05E-04	3.39	0.64
PH	PH_26	chr3_163638892	3	163638892	0.26	4.05E-04	3.39	0.64
PH	PH_26	chr3_164192755	3	164192755	0.23	9.99E-04	3.00	0.56
PH	PH_26	chr3_164587464	3	164587464	0.47	2.20E-04	3.66	0.70
PH	PH_26	chr3_164884616	3	164884616	0.24	1.54E-04	3.81	0.74
PH	PH_26	chr3_164978091	3	164978091	0.23	5.36E-04	3.27	0.62
PH	PH_26	chr3_164978680	3	164978680	0.24	6.17E-04	3.21	0.60
PH	PH_26	chr3_165017930	3	165017930	0.29	3.47E-04	3.46	0.66
PH	PH_26	chr3_165017969	3	165017969	0.29	9.87E-04	3.01	0.56
PH	PH_26	chr3_165021955	3	165021955	0.48	9.60E-04	3.02	0.56
PH	PH_26	chr3_165174695	3	165174695	0.28	8.91E-04	3.05	0.57

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
PH	PH_26	chr3_165175866	3	165175866	0.28	4.53E-04	3.34	0.63
PH	PH_26	chr3_165178733	3	165178733	0.24	3.80E-04	3.42	0.65
PH	PH_26	chr3_165178754	3	165178754	0.24	3.80E-04	3.42	0.65
PH	PH_26	chr3_165178771	3	165178771	0.29	3.46E-04	3.46	0.66
PH	PH_26	chr3_165412700	3	165412700	0.46	8.08E-04	3.09	0.58
PH	PH_26	chr3_165412702	3	165412702	0.46	7.83E-04	3.11	0.58
PH	PH_26	chr3_165446755	3	165446755	0.12	7.44E-04	3.13	0.58
PH	PH_26	chr3_165446990	3	165446990	0.24	9.61E-04	3.02	0.56
PH	PH_26	chr3_165458009	3	165458009	0.26	9.01E-04	3.05	0.57
PH	PH_27	chr3_186928178	3	186928178	0.47	9.30E-04	3.03	0.56
PH	PH_27	chr3_186928196	3	186928196	0.47	9.30E-04	3.03	0.56
PH	PH_28	chr3_220857274	3	220857274	0.20	4.30E-04	3.37	0.64
PH	PH_28	chr3_221547147	3	221547147	0.34	2.56E-04	3.59	0.69
PH	PH_28	chr3_221615024	3	221615024	0.22	9.83E-04	3.01	0.56
PH	PH_28	chr3_221615051	3	221615051	0.22	9.83E-04	3.01	0.56
PH	PH_29	chr6_38115718	6	38115718	0.26	9.68E-04	3.01	0.56
PH	PH_29	chr6_38115749	6	38115749	0.26	9.68E-04	3.01	0.56
PH	PH_30	chr7_1569310	7	1569310	0.48	8.34E-04	3.08	0.57
PH	PH_30	chr7_1569316	7	1569316	0.48	8.34E-04	3.08	0.57
PH	PH_30	chr7_1569319	7	1569319	0.48	8.34E-04	3.08	0.57
PH	PH_30	chr7_1627743	7	1627743	0.45	9.91E-04	3.00	0.56
PH	PH_30	chr7_1627758	7	1627758	0.45	9.91E-04	3.00	0.56
PH	PH_30	chr7_1629033	7	1629033	0.47	4.95E-04	3.31	0.62
PH	PH_30	chr7_1919250	7	1919250	0.48	4.76E-04	3.32	0.63
PH	PH_30	chr7_1919267	7	1919267	0.48	4.99E-04	3.30	0.62
PH	PH_30	chr7_1919271	7	1919271	0.48	4.99E-04	3.30	0.62
PH	PH_30	chr7_1919319	7	1919319	0.47	3.80E-04	3.42	0.65
PH	PH_30	chr7_1924503	7	1924503	0.49	7.41E-04	3.13	0.59
PH	PH_31	chr7_161859807	7	161859807	0.28	7.25E-04	3.14	0.59
PH	PH_32	chr8_138525988	8	138525988	0.25	8.49E-04	3.07	0.57
PH	PH_33	chr8_174407940	8	174407940	0.16	1.88E-04	3.73	0.72
PH	PH_34	chr9_105081037	9	105081037	0.46	5.79E-04	3.24	0.61
PH	PH_34	chr9_105081043	9	105081043	0.29	1.84E-04	3.74	0.72
PH	PH_34	chr9_105081122	9	105081122	0.43	3.66E-04	3.44	0.65
PH	PH_34	chr9_105081143	9	105081143	0.43	4.73E-04	3.33	0.63
PH	PH_34	chr9_105081332	9	105081332	0.44	9.57E-04	3.02	0.56
PH	PH_35	chr9_137787462	9	137787462	0.14	1.97E-04	3.71	0.71
PH	PH_35	chr9_138752303	9	138752303	0.46	8.61E-04	3.07	0.57

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
PH	PH_36	chr9_145514218	9	145514218	0.07	4.48E-05	4.35	0.86
PH	PH_37	chr10_140989987	10	140989987	0.23	3.52E-04	3.45	0.66
PH	PH_37	chr10_141235016	10	141235016	0.21	3.91E-04	3.41	0.65
PH	PH_38	chr10_147901736	10	147901736	0.27	5.49E-04	3.26	0.61
PH	PH_38	chr10_147901752	10	147901752	0.26	6.29E-04	3.20	0.60
PH	PH_38	chr10_147902196	10	147902196	0.26	8.67E-04	3.06	0.57
PH	PH_38	chr10_148085986	10	148085986	0.26	8.16E-04	3.09	0.58
EH	EH_1	chr1_4446759	1	4446759	0.20	1.00E-03	3.00	0.54
EH	EH_1	chr1_4603919	1	4603919	0.44	6.37E-04	3.20	0.59
EH	EH_1	chr1_4743760	1	4743760	0.41	3.11E-04	3.51	0.66
EH	EH_1	chr1_4743914	1	4743914	0.44	3.98E-05	4.40	0.85
EH	EH_1	chr1_4744136	1	4744136	0.41	2.11E-04	3.68	0.69
EH	EH_1	chr1_4744144	1	4744144	0.41	1.77E-04	3.75	0.71
EH	EH_1	chr1_4760662	1	4760662	0.44	7.54E-04	3.12	0.57
EH	EH_1	chr1_4760704	1	4760704	0.44	8.90E-04	3.05	0.56
EH	EH_1	chr1_4771786	1	4771786	0.42	2.20E-04	3.66	0.69
EH	EH_2	chr1_17519583	1	17519583	0.16	7.77E-04	3.11	0.57
EH	EH_3	chr1_26913595	1	26913595	0.32	7.92E-04	3.10	0.57
EH	EH_3	chr1_26913599	1	26913599	0.38	3.41E-04	3.47	0.65
EH	EH_4	chr1_46455966	1	46455966	0.27	2.16E-04	3.67	0.69
EH	EH_4	chr1_46455973	1	46455973	0.27	2.16E-04	3.67	0.69
EH	EH_5	chr1_296175139	1	296175139	0.36	5.42E-05	4.27	0.82
EH	EH_6	chr2_27763768	2	27763768	0.18	5.41E-04	3.27	0.60
EH	EH_7	chr2_66712204	2	66712204	0.42	3.83E-04	3.42	0.64
EH	EH_8	chr2_199207556	2	199207556	0.50	8.92E-04	3.05	0.56
EH	EH_9	chr2_216821100	2	216821100	0.47	5.25E-04	3.28	0.61
EH	EH_9	chr2_216821129	2	216821129	0.47	6.98E-04	3.16	0.58
EH	EH_10	chr3_10366959	3	10366959	0.45	3.06E-04	3.51	0.66
EH	EH_10	chr3_10387653	3	10387653	0.46	1.97E-04	3.70	0.70
EH	EH_10	chr3_10387700	3	10387700	0.44	5.52E-04	3.26	0.60
EH	EH_11	chr3_20806785	3	20806785	0.50	4.04E-04	3.39	0.63
EH	EH_12	chr3_30539128	3	30539128	0.07	1.68E-04	3.77	0.71
EH	EH_13	chr3_148797744	3	148797744	0.30	1.97E-04	3.71	0.70
EH	EH_13	chr3_148877069	3	148877069	0.28	1.87E-04	3.73	0.70
EH	EH_13	chr3_148877128	3	148877128	0.28	3.73E-04	3.43	0.64
EH	EH_13	chr3_148877130	3	148877130	0.28	3.73E-04	3.43	0.64
EH	EH_13	chr3_148877137	3	148877137	0.29	1.32E-04	3.88	0.74
EH	EH_13	chr3_148877155	3	148877155	0.29	1.32E-04	3.88	0.74

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
EH	EH_13	chr3_148974530	3	148974530	0.49	7.03E-04	3.15	0.58
EH	EH_13	chr3_148974537	3	148974537	0.49	3.61E-04	3.44	0.64
EH	EH_13	chr3_148975376	3	148975376	0.48	5.71E-04	3.24	0.60
EH	EH_13	chr3_148975403	3	148975403	0.49	7.31E-04	3.14	0.57
EH	EH_13	chr3_148975409	3	148975409	0.49	7.31E-04	3.14	0.57
EH	EH_13	chr3_148975431	3	148975431	0.49	5.11E-04	3.29	0.61
EH	EH_13	chr3_148975438	3	148975438	0.49	5.11E-04	3.29	0.61
EH	EH_13	chr3_149250622	3	149250622	0.29	5.84E-04	3.23	0.60
EH	EH_13	chr3_149250630	3	149250630	0.29	8.08E-04	3.09	0.57
EH	EH_13	chr3_149398810	3	149398810	0.29	3.06E-04	3.51	0.66
EH	EH_14	chr3_151355894	3	151355894	0.49	6.06E-04	3.22	0.59
EH	EH_14	chr3_151818007	3	151818007	0.48	1.93E-04	3.72	0.70
EH	EH_14	chr3_151971584	3	151971584	0.47	3.91E-04	3.41	0.63
EH	EH_14	chr3_151971622	3	151971622	0.47	5.36E-04	3.27	0.60
EH	EH_14	chr3_151971975	3	151971975	0.48	6.13E-04	3.21	0.59
EH	EH_14	chr3_152057126	3	152057126	0.48	5.65E-04	3.25	0.60
EH	EH_15	chr3_153764074	3	153764074	0.50	1.03E-04	3.99	0.76
EH	EH_15	chr3_154075824	3	154075824	0.29	4.59E-08	7.34	1.52
EH	EH_15	chr3_154075870	3	154075870	0.25	3.28E-06	5.48	1.10
EH	EH_15	chr3_154075887	3	154075887	0.25	3.28E-06	5.48	1.10
EH	EH_15	chr3_154075890	3	154075890	0.25	3.28E-06	5.48	1.10
EH	EH_15	chr3_154076084	3	154076084	0.26	2.63E-07	6.58	1.34
EH	EH_15	chr3_154077726	3	154077726	0.27	6.03E-09	8.22	1.72
EH	EH_15	chr3_154124966	3	154124966	0.49	3.80E-05	4.42	0.86
EH	EH_15	chr3_154125085	3	154125085	0.49	3.42E-05	4.47	0.87
EH	EH_15	chr3_154250578	3	154250578	0.13	4.28E-04	3.37	0.63
EH	EH_15	chr3_154408191	3	154408191	0.35	9.25E-04	3.03	0.55
EH	EH_15	chr3_154408488	3	154408488	0.49	9.15E-04	3.04	0.55
EH	EH_15	chr3_154409508	3	154409508	0.15	7.49E-08	7.13	1.47
EH	EH_15	chr3_154409545	3	154409545	0.29	7.02E-07	6.15	1.25
EH	EH_15	chr3_154561425	3	154561425	0.27	1.55E-04	3.81	0.72
EH	EH_15	chr3_154563862	3	154563862	0.27	4.40E-04	3.36	0.62
EH	EH_15	chr3_154563985	3	154563985	0.27	1.33E-05	4.88	0.96
EH	EH_15	chr3_154592422	3	154592422	0.29	5.28E-08	7.28	1.50
EH	EH_15	chr3_154592481	3	154592481	0.29	5.28E-08	7.28	1.50
EH	EH_15	chr3_154592487	3	154592487	0.18	4.81E-04	3.32	0.61
EH	EH_15	chr3_154592489	3	154592489	0.29	5.28E-08	7.28	1.50
EH	EH_15	chr3_154625415	3	154625415	0.29	4.55E-09	8.34	1.75

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
EH	EH_15	chr3_154625420	3	154625420	0.29	1.45E-08	7.84	1.63
EH	EH_15	chr3_154627523	3	154627523	0.28	4.71E-07	6.33	1.29
EH	EH_15	chr3_154627556	3	154627556	0.28	5.45E-07	6.26	1.27
EH	EH_15	chr3_154627560	3	154627560	0.28	2.30E-06	5.64	1.13
EH	EH_15	chr3_154650534	3	154650534	0.28	4.32E-08	7.36	1.52
EH	EH_15	chr3_154650575	3	154650575	0.28	2.06E-07	6.69	1.37
EH	EH_15	chr3_154650638	3	154650638	0.28	4.22E-04	3.37	0.63
EH	EH_15	chr3_154655030	3	154655030	0.29	1.60E-07	6.80	1.39
EH	EH_15	chr3_154655098	3	154655098	0.28	1.93E-06	5.71	1.15
EH	EH_15	chr3_154655116	3	154655116	0.28	1.93E-06	5.71	1.15
EH	EH_15	chr3_154661548	3	154661548	0.28	2.78E-08	7.56	1.57
EH	EH_15	chr3_154732521	3	154732521	0.28	2.23E-06	5.65	1.13
EH	EH_15	chr3_154739343	3	154739343	0.25	1.01E-05	5.00	0.99
EH	EH_15	chr3_154739847	3	154739847	0.29	8.74E-09	8.06	1.68
EH	EH_15	chr3_154739888	3	154739888	0.27	9.47E-07	6.02	1.22
EH	EH_15	chr3_154980602	3	154980602	0.28	8.99E-04	3.05	0.56
EH	EH_15	chr3_154980617	3	154980617	0.28	6.85E-04	3.16	0.58
EH	EH_15	chr3_154981090	3	154981090	0.28	4.44E-08	7.35	1.52
EH	EH_15	chr3_154981137	3	154981137	0.27	3.27E-07	6.48	1.32
EH	EH_15	chr3_155091887	3	155091887	0.31	1.13E-08	7.95	1.66
EH	EH_15	chr3_155317564	3	155317564	0.28	1.96E-06	5.71	1.15
EH	EH_15	chr3_155803297	3	155803297	0.31	2.12E-04	3.67	0.69
EH	EH_15	chr3_155803339	3	155803339	0.48	6.75E-07	6.17	1.25
EH	EH_15	chr3_155803532	3	155803532	0.29	1.81E-10	9.74	2.07
EH	EH_15	chr3_155967126	3	155967126	0.28	1.03E-07	6.99	1.44
EH	EH_15	chr3_155967168	3	155967168	0.31	1.89E-08	7.72	1.61
EH	EH_15	chr3_156275693	3	156275693	0.27	2.44E-04	3.61	0.68
EH	EH_15	chr3_156287541	3	156287541	0.28	9.12E-09	8.04	1.68
EH	EH_15	chr3_156287743	3	156287743	0.28	4.05E-09	8.39	1.76
EH	EH_15	chr3_156287758	3	156287758	0.48	1.09E-05	4.96	0.98
EH	EH_15	chr3_156287774	3	156287774	0.26	2.58E-04	3.59	0.67
EH	EH_15	chr3_156304805	3	156304805	0.50	8.84E-04	3.05	0.56
EH	EH_15	chr3_156304807	3	156304807	0.27	7.88E-04	3.10	0.57
EH	EH_15	chr3_156304839	3	156304839	0.50	8.84E-04	3.05	0.56
EH	EH_15	chr3_156486164	3	156486164	0.28	9.75E-09	8.01	1.67
EH	EH_15	chr3_156799657	3	156799657	0.27	2.38E-04	3.62	0.68
EH	EH_15	chr3_156799845	3	156799845	0.49	7.08E-08	7.15	1.47
EH	EH_15	chr3_156800034	3	156800034	0.48	7.15E-05	4.15	0.80

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
EH	EH_15	chr3_156939575	3	156939575	0.26	1.51E-04	3.82	0.72
EH	EH_15	chr3_156939584	3	156939584	0.28	2.66E-04	3.58	0.67
EH	EH_15	chr3_156969980	3	156969980	0.49	9.87E-07	6.01	1.21
EH	EH_15	chr3_156969997	3	156969997	0.48	2.36E-06	5.63	1.13
EH	EH_15	chr3_157018356	3	157018356	0.26	2.06E-04	3.69	0.69
EH	EH_15	chr3_157018359	3	157018359	0.26	2.06E-04	3.69	0.69
EH	EH_15	chr3_157018365	3	157018365	0.26	2.06E-04	3.69	0.69
EH	EH_15	chr3_157018380	3	157018380	0.21	1.76E-04	3.75	0.71
EH	EH_15	chr3_157051502	3	157051502	0.31	7.22E-08	7.14	1.47
EH	EH_15	chr3_157417448	3	157417448	0.30	3.57E-13	12.45	2.71
EH	EH_15	chr3_157568991	3	157568991	0.29	5.90E-11	10.23	2.19
EH	EH_15	chr3_157569114	3	157569114	0.17	1.78E-06	5.75	1.16
EH	EH_15	chr3_157576226	3	157576226	0.30	1.20E-12	11.92	2.59
EH	EH_15	chr3_157576421	3	157576421	0.30	1.27E-11	10.89	2.34
EH	EH_15	chr3_157576589	3	157576589	0.28	1.39E-10	9.86	2.10
EH	EH_15	chr3_157576725	3	157576725	0.30	6.75E-12	11.17	2.41
EH	EH_15	chr3_157576733	3	157576733	0.29	6.35E-12	11.20	2.42
EH	EH_15	chr3_157578664	3	157578664	0.31	8.50E-11	10.07	2.15
EH	EH_15	chr3_157578666	3	157578666	0.31	1.38E-10	9.86	2.10
EH	EH_15	chr3_157587467	3	157587467	0.26	4.69E-05	4.33	0.84
EH	EH_15	chr3_157773525	3	157773525	0.35	8.91E-04	3.05	0.56
EH	EH_15	chr3_157918560	3	157918560	0.23	2.03E-04	3.69	0.70
EH	EH_15	chr3_157938112	3	157938112	0.23	6.62E-04	3.18	0.58
EH	EH_15	chr3_158348209	3	158348209	0.48	1.03E-09	8.99	1.90
EH	EH_15	chr3_158348357	3	158348357	0.26	3.61E-07	6.44	1.31
EH	EH_15	chr3_158444445	3	158444445	0.26	6.26E-05	4.20	0.81
EH	EH_15	chr3_158451553	3	158451553	0.22	1.14E-04	3.94	0.75
EH	EH_15	chr3_158521181	3	158521181	0.26	7.26E-05	4.14	0.79
EH	EH_15	chr3_158780416	3	158780416	0.23	6.12E-05	4.21	0.81
EH	EH_15	chr3_158780445	3	158780445	0.24	1.36E-06	5.87	1.18
EH	EH_15	chr3_158780918	3	158780918	0.30	8.51E-14	13.07	2.86
EH	EH_15	chr3_158781033	3	158781033	0.27	4.64E-07	6.33	1.29
EH	EH_15	chr3_158790476	3	158790476	0.27	1.54E-07	6.81	1.40
EH	EH_15	chr3_158890884	3	158890884	0.48	3.09E-13	12.51	2.73
EH	EH_15	chr3_158901755	3	158901755	0.22	2.68E-04	3.57	0.67
EH	EH_15	chr3_158901791	3	158901791	0.49	6.76E-04	3.17	0.58
EH	EH_15	chr3_158972316	3	158972316	0.48	9.68E-13	12.01	2.61
EH	EH_15	chr3_158973464	3	158973464	0.23	1.71E-05	4.77	0.93

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
EH	EH_15	chr3_159379133	3	159379133	0.25	2.22E-06	5.65	1.13
EH	EH_15	chr3_159385192	3	159385192	0.49	6.27E-13	12.20	2.65
EH	EH_15	chr3_159385285	3	159385285	0.26	8.36E-06	5.08	1.00
EH	EH_15	chr3_159385286	3	159385286	0.26	8.36E-06	5.08	1.00
EH	EH_15	chr3_159385309	3	159385309	0.26	9.63E-06	5.02	0.99
EH	EH_15	chr3_159388105	3	159388105	0.29	1.67E-12	11.78	2.55
EH	EH_15	chr3_159678426	3	159678426	0.30	4.08E-12	11.39	2.46
EH	EH_15	chr3_159678466	3	159678466	0.30	2.19E-11	10.66	2.29
EH	EH_15	chr3_159678604	3	159678604	0.24	3.23E-05	4.49	0.87
EH	EH_15	chr3_159678635	3	159678635	0.30	1.16E-10	9.94	2.12
EH	EH_15	chr3_159678650	3	159678650	0.24	4.14E-05	4.38	0.85
EH	EH_15	chr3_159680509	3	159680509	0.25	7.82E-04	3.11	0.57
EH	EH_15	chr3_159800933	3	159800933	0.25	4.11E-06	5.39	1.07
EH	EH_15	chr3_159800996	3	159800996	0.48	4.16E-11	10.38	2.22
EH	EH_15	chr3_159801043	3	159801043	0.28	5.51E-13	12.26	2.67
EH	EH_15	chr3_159801068	3	159801068	0.26	7.20E-05	4.14	0.80
EH	EH_15	chr3_159801074	3	159801074	0.26	8.38E-05	4.08	0.78
EH	EH_15	chr3_159801091	3	159801091	0.22	1.89E-04	3.72	0.70
EH	EH_15	chr3_159801092	3	159801092	0.22	1.70E-04	3.77	0.71
EH	EH_15	chr3_159801235	3	159801235	0.30	5.60E-11	10.25	2.19
EH	EH_15	chr3_159801239	3	159801239	0.26	6.40E-06	5.19	1.03
EH	EH_15	chr3_159807179	3	159807179	0.26	9.56E-05	4.02	0.77
EH	EH_15	chr3_159807447	3	159807447	0.29	4.98E-12	11.30	2.44
EH	EH_15	chr3_159810023	3	159810023	0.29	4.85E-10	9.31	1.97
EH	EH_15	chr3_159818313	3	159818313	0.26	6.89E-04	3.16	0.58
EH	EH_15	chr3_159818316	3	159818316	0.24	4.46E-04	3.35	0.62
EH	EH_15	chr3_159818326	3	159818326	0.25	1.63E-04	3.79	0.72
EH	EH_15	chr3_159818698	3	159818698	0.23	8.71E-04	3.06	0.56
EH	EH_15	chr3_159818701	3	159818701	0.49	4.29E-09	8.37	1.75
EH	EH_15	chr3_159820547	3	159820547	0.48	7.99E-10	9.10	1.92
EH	EH_15	chr3_159861750	3	159861750	0.24	6.89E-05	4.16	0.80
EH	EH_15	chr3_159868843	3	159868843	0.29	3.02E-11	10.52	2.26
EH	EH_15	chr3_159870399	3	159870399	0.19	6.61E-04	3.18	0.58
EH	EH_15	chr3_159870623	3	159870623	0.27	2.37E-04	3.63	0.68
EH	EH_15	chr3_160665462	3	160665462	0.26	1.79E-04	3.75	0.71
EH	EH_15	chr3_160665463	3	160665463	0.50	3.43E-11	10.46	2.24
EH	EH_15	chr3_160665476	3	160665476	0.23	4.95E-04	3.31	0.61
EH	EH_15	chr3_160665487	3	160665487	0.23	7.11E-04	3.15	0.58

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
EH	EH_15	chr3_161252051	3	161252051	0.28	7.21E-04	3.14	0.58
EH	EH_15	chr3_161257076	3	161257076	0.29	5.38E-09	8.27	1.73
EH	EH_15	chr3_161257078	3	161257078	0.29	5.38E-09	8.27	1.73
EH	EH_15	chr3_161257090	3	161257090	0.29	5.38E-09	8.27	1.73
EH	EH_15	chr3_161257096	3	161257096	0.29	5.38E-09	8.27	1.73
EH	EH_15	chr3_161259908	3	161259908	0.29	1.76E-08	7.75	1.61
EH	EH_15	chr3_161364532	3	161364532	0.37	5.40E-04	3.27	0.60
EH	EH_15	chr3_161369706	3	161369706	0.29	6.17E-09	8.21	1.72
EH	EH_15	chr3_161369763	3	161369763	0.29	4.08E-08	7.39	1.53
EH	EH_15	chr3_161369771	3	161369771	0.25	4.30E-04	3.37	0.62
EH	EH_15	chr3_161369773	3	161369773	0.24	4.56E-04	3.34	0.62
EH	EH_15	chr3_161369818	3	161369818	0.28	4.55E-09	8.34	1.75
EH	EH_15	chr3_161369881	3	161369881	0.29	7.13E-09	8.15	1.70
EH	EH_15	chr3_161563412	3	161563412	0.23	9.31E-04	3.03	0.55
EH	EH_15	chr3_161563431	3	161563431	0.23	4.16E-04	3.38	0.63
EH	EH_15	chr3_161563433	3	161563433	0.23	8.12E-04	3.09	0.56
EH	EH_15	chr3_161563441	3	161563441	0.23	4.16E-04	3.38	0.63
EH	EH_15	chr3_161573134	3	161573134	0.27	2.76E-09	8.56	1.80
EH	EH_15	chr3_161573148	3	161573148	0.22	1.96E-04	3.71	0.70
EH	EH_15	chr3_161573155	3	161573155	0.27	3.12E-09	8.51	1.79
EH	EH_15	chr3_161573221	3	161573221	0.27	7.55E-10	9.12	1.93
EH	EH_15	chr3_161573250	3	161573250	0.27	7.55E-10	9.12	1.93
EH	EH_15	chr3_161575037	3	161575037	0.29	5.80E-07	6.24	1.27
EH	EH_15	chr3_161575049	3	161575049	0.49	1.06E-08	7.98	1.66
EH	EH_15	chr3_161575068	3	161575068	0.49	7.87E-09	8.10	1.69
EH	EH_15	chr3_161575090	3	161575090	0.29	8.60E-07	6.07	1.23
EH	EH_15	chr3_161575111	3	161575111	0.50	1.54E-08	7.81	1.63
EH	EH_15	chr3_161575140	3	161575140	0.50	1.54E-08	7.81	1.63
EH	EH_15	chr3_161576585	3	161576585	0.29	5.90E-04	3.23	0.59
EH	EH_15	chr3_161576642	3	161576642	0.25	1.66E-04	3.78	0.71
EH	EH_15	chr3_161638284	3	161638284	0.29	8.31E-10	9.08	1.92
EH	EH_15	chr3_161650139	3	161650139	0.30	4.54E-08	7.34	1.52
EH	EH_15	chr3_161650198	3	161650198	0.23	4.79E-04	3.32	0.61
EH	EH_15	chr3_161650243	3	161650243	0.29	3.44E-08	7.46	1.55
EH	EH_15	chr3_161650452	3	161650452	0.28	8.07E-09	8.09	1.69
EH	EH_15	chr3_161650457	3	161650457	0.25	3.41E-04	3.47	0.65
EH	EH_15	chr3_161650485	3	161650485	0.25	5.49E-04	3.26	0.60
EH	EH_15	chr3_161650544	3	161650544	0.23	9.44E-04	3.03	0.55

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
EH	EH_15	chr3_161732785	3	161732785	0.30	1.06E-06	5.97	1.21
EH	EH_15	chr3_162034696	3	162034696	0.29	5.23E-05	4.28	0.83
EH	EH_15	chr3_162034773	3	162034773	0.29	3.78E-04	3.42	0.64
EH	EH_15	chr3_162034810	3	162034810	0.29	3.78E-04	3.42	0.64
EH	EH_15	chr3_162034827	3	162034827	0.29	3.78E-04	3.42	0.64
EH	EH_15	chr3_162034831	3	162034831	0.29	3.78E-04	3.42	0.64
EH	EH_15	chr3_162063874	3	162063874	0.27	4.77E-04	3.32	0.61
EH	EH_15	chr3_162064220	3	162064220	0.49	1.69E-04	3.77	0.71
EH	EH_15	chr3_162097279	3	162097279	0.48	1.58E-04	3.80	0.72
EH	EH_15	chr3_162178810	3	162178810	0.24	6.68E-04	3.17	0.58
EH	EH_15	chr3_162179943	3	162179943	0.25	1.04E-04	3.98	0.76
EH	EH_15	chr3_162180147	3	162180147	0.24	7.96E-04	3.10	0.57
EH	EH_15	chr3_162180254	3	162180254	0.24	7.96E-05	4.10	0.79
EH	EH_15	chr3_162317866	3	162317866	0.29	6.40E-04	3.19	0.59
EH	EH_15	chr3_162318161	3	162318161	0.49	1.97E-04	3.71	0.70
EH	EH_15	chr3_162318227	3	162318227	0.49	2.20E-04	3.66	0.69
EH	EH_15	chr3_162318357	3	162318357	0.49	9.57E-04	3.02	0.55
EH	EH_15	chr3_162599378	3	162599378	0.29	4.67E-04	3.33	0.62
EH	EH_15	chr3_162599393	3	162599393	0.29	5.14E-04	3.29	0.61
EH	EH_15	chr3_162606680	3	162606680	0.48	7.18E-04	3.14	0.58
EH	EH_15	chr3_162696410	3	162696410	0.49	6.28E-05	4.20	0.81
EH	EH_16	chr3_164524652	3	164524652	0.48	8.29E-06	5.08	1.00
EH	EH_16	chr3_164581009	3	164581009	0.29	7.72E-05	4.11	0.79
EH	EH_16	chr3_164581079	3	164581079	0.29	6.27E-05	4.20	0.81
EH	EH_16	chr3_164581105	3	164581105	0.28	9.33E-04	3.03	0.55
EH	EH_16	chr3_164587783	3	164587783	0.30	3.39E-04	3.47	0.65
EH	EH_16	chr3_164587790	3	164587790	0.30	1.93E-04	3.71	0.70
EH	EH_16	chr3_164587830	3	164587830	0.29	6.71E-04	3.17	0.58
EH	EH_16	chr3_164587832	3	164587832	0.29	6.71E-04	3.17	0.58
EH	EH_16	chr3_164587844	3	164587844	0.29	1.16E-04	3.94	0.75
EH	EH_16	chr3_164588707	3	164588707	0.29	2.12E-04	3.67	0.69
EH	EH_16	chr3_164884616	3	164884616	0.24	6.89E-04	3.16	0.58
EH	EH_16	chr3_164975717	3	164975717	0.29	3.86E-04	3.41	0.63
EH	EH_16	chr3_164978022	3	164978022	0.29	4.65E-04	3.33	0.62
EH	EH_16	chr3_164978025	3	164978025	0.29	1.18E-04	3.93	0.75
EH	EH_16	chr3_164978057	3	164978057	0.28	2.25E-04	3.65	0.69
EH	EH_16	chr3_164978680	3	164978680	0.24	7.58E-04	3.12	0.57
EH	EH_16	chr3_164978728	3	164978728	0.29	6.31E-04	3.20	0.59

Trait	**QTL**	**SNP**	**Chr**	**Position**	**maf**	**P-value**	**LOD**	**Var explained**
EH	EH_16	chr3_165017930	3	165017930	0.29	8.79E-05	4.06	0.78
EH	EH_16	chr3_165017969	3	165017969	0.29	2.97E-04	3.53	0.66
EH	EH_16	chr3_165021955	3	165021955	0.48	2.94E-05	4.53	0.88
EH	EH_16	chr3_165021985	3	165021985	0.48	5.92E-05	4.23	0.81
EH	EH_16	chr3_165168084	3	165168084	0.48	1.00E-04	4.00	0.76
EH	EH_16	chr3_165174695	3	165174695	0.28	3.15E-05	4.50	0.87
EH	EH_16	chr3_165174761	3	165174761	0.28	2.26E-05	4.65	0.91
EH	EH_16	chr3_165175552	3	165175552	0.28	1.92E-05	4.72	0.92
EH	EH_16	chr3_165175866	3	165175866	0.28	1.53E-05	4.81	0.94
EH	EH_16	chr3_165178733	3	165178733	0.24	5.23E-04	3.28	0.61
EH	EH_16	chr3_165178754	3	165178754	0.24	5.23E-04	3.28	0.61
EH	EH_16	chr3_165178771	3	165178771	0.29	9.95E-06	5.00	0.99
EH	EH_16	chr3_165446755	3	165446755	0.12	1.34E-05	4.87	0.96
EH	EH_16	chr3_165446990	3	165446990	0.24	5.95E-04	3.23	0.59
EH	EH_16	chr3_165457973	3	165457973	0.49	3.98E-05	4.40	0.85
EH	EH_16	chr3_165457997	3	165457997	0.49	3.82E-05	4.42	0.86
EH	EH_16	chr3_165458009	3	165458009	0.26	1.96E-05	4.71	0.92
EH	EH_16	chr3_165458062	3	165458062	0.31	2.50E-04	3.60	0.68
EH	EH_16	chr3_165458089	3	165458089	0.31	1.39E-04	3.86	0.73
EH	EH_16	chr3_165458092	3	165458092	0.31	1.39E-04	3.86	0.73
EH	EH_16	chr3_165458421	3	165458421	0.31	7.32E-05	4.14	0.79
EH	EH_16	chr3_165458422	3	165458422	0.31	6.38E-05	4.20	0.81
EH	EH_16	chr3_165458450	3	165458450	0.31	3.06E-04	3.51	0.66
EH	EH_16	chr3_165458453	3	165458453	0.31	1.65E-04	3.78	0.72
EH	EH_16	chr3_165458456	3	165458456	0.31	1.37E-04	3.86	0.73
EH	EH_16	chr3_165458515	3	165458515	0.48	5.37E-05	4.27	0.82
EH	EH_16	chr3_165458612	3	165458612	0.50	1.23E-05	4.91	0.97
EH	EH_16	chr3_165704521	3	165704521	0.28	3.47E-05	4.46	0.87
EH	EH_16	chr3_165722971	3	165722971	0.48	2.00E-05	4.70	0.92
EH	EH_16	chr3_165728239	3	165728239	0.29	1.34E-04	3.87	0.74
EH	EH_16	chr3_165858588	3	165858588	0.28	4.83E-05	4.32	0.83
EH	EH_16	chr3_165858627	3	165858627	0.28	3.26E-04	3.49	0.65
EH	EH_16	chr3_165862973	3	165862973	0.28	2.25E-04	3.65	0.69
EH	EH_16	chr3_165879324	3	165879324	0.25	3.49E-04	3.46	0.64
EH	EH_16	chr3_166200130	3	166200130	0.28	5.29E-04	3.28	0.61
EH	EH_17	chr3_168492756	3	168492756	0.25	9.57E-04	3.02	0.55
EH	EH_18	chr3_220856968	3	220856968	0.48	4.49E-04	3.35	0.62
EH	EH_18	chr3_220857274	3	220857274	0.20	1.01E-04	3.99	0.76

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
EH	EH_18	chr3_221183243	3	221183243	0.20	4.88E-04	3.31	0.61
EH	EH_18	chr3_221301543	3	221301543	0.32	3.49E-04	3.46	0.64
EH	EH_18	chr3_221403281	3	221403281	0.21	8.16E-05	4.09	0.78
EH	EH_18	chr3_221546970	3	221546970	0.22	7.49E-05	4.13	0.79
EH	EH_18	chr3_221547147	3	221547147	0.34	3.19E-05	4.50	0.87
EH	EH_18	chr3_221609405	3	221609405	0.22	9.20E-04	3.04	0.55
EH	EH_18	chr3_221615024	3	221615024	0.22	3.97E-04	3.40	0.63
EH	EH_18	chr3_221615051	3	221615051	0.22	3.97E-04	3.40	0.63
EH	EH_18	chr3_221634905	3	221634905	0.24	6.58E-04	3.18	0.58
EH	EH_19	chr3_222671336	3	222671336	0.48	9.10E-04	3.04	0.55
EH	EH_19	chr3_222671354	3	222671354	0.23	2.39E-04	3.62	0.68
EH	EH_19	chr3_222794249	3	222794249	0.22	1.57E-04	3.81	0.72
EH	EH_19	chr3_222794266	3	222794266	0.22	1.57E-04	3.81	0.72
EH	EH_19	chr3_223306062	3	223306062	0.24	7.44E-04	3.13	0.57
EH	EH_20	chr5_21528310	5	21528310	0.50	3.61E-05	4.44	0.86
EH	EH_21	chr5_198204637	5	198204637	0.45	8.09E-04	3.09	0.57
EH	EH_21	chr5_198204657	5	198204657	0.45	4.52E-04	3.34	0.62
EH	EH_22	chr6_163875983	6	163875983	0.47	2.50E-04	3.60	0.68
EH	EH_23	chr7_22681508	7	22681508	0.44	7.54E-05	4.12	0.79
EH	EH_23	chr7_22681584	7	22681584	0.46	1.01E-03	3.00	0.54
EH	EH_24	chr7_113153042	7	113153042	0.46	9.09E-04	3.04	0.55
EH	EH_25	chr8_108496728	8	108496728	0.48	3.31E-04	3.48	0.65
EH	EH_26	chr8_116869259	8	116869259	0.49	4.13E-04	3.38	0.63
EH	EH_26	chr8_116869267	8	116869267	0.29	5.49E-04	3.26	0.60
EH	EH_26	chr8_116869290	8	116869290	0.29	4.67E-04	3.33	0.62
EH	EH_26	chr8_116871164	8	116871164	0.49	6.75E-04	3.17	0.58
EH	EH_27	chr8_145967972	8	145967972	0.23	8.36E-04	3.08	0.56
EH	EH_27	chr8_145970799	8	145970799	0.23	2.87E-04	3.54	0.66
EH	EH_27	chr8_146154127	8	146154127	0.21	9.29E-04	3.03	0.55
EH	EH_27	chr8_146559715	8	146559715	0.50	6.35E-04	3.20	0.59
EH	EH_28	chr9_116356316	9	116356316	0.16	4.37E-04	3.36	0.62
DTA	DTA_1	chr1_5590402	1	5590402	0.25	4.32E-04	3.36	0.58
DTA	DTA_1	chr1_5610218	1	5610218	0.24	4.71E-04	3.33	0.58
DTA	DTA_2	chr1_27122661	1	27122661	0.01	1.05E-04	3.98	0.71
DTA	DTA_3	chr1_37136833	1	37136833	0.30	8.08E-04	3.09	0.53
DTA	DTA_4	chr1_45116508	1	45116508	0.46	7.22E-04	3.14	0.54
DTA	DTA_5	chr1_46628742	1	46628742	0.34	8.95E-04	3.05	0.52
DTA	DTA_5	chr1_46628767	1	46628767	0.33	5.47E-05	4.26	0.77

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTA	DTA_5	chr1_46924318	1	46924318	0.32	7.77E-04	3.11	0.53
DTA	DTA_6	chr1_48999976	1	48999976	0.45	3.79E-04	3.42	0.59
DTA	DTA_7	chr1_52095418	1	52095418	0.45	4.84E-04	3.32	0.57
DTA	DTA_7	chr1_52457692	1	52457692	0.23	9.44E-04	3.03	0.51
DTA	DTA_7	chr1_52605441	1	52605441	0.23	2.04E-04	3.69	0.65
DTA	DTA_7	chr1_52608062	1	52608062	0.23	5.50E-04	3.26	0.56
DTA	DTA_8	chr1_61946214	1	61946214	0.33	5.49E-04	3.26	0.56
DTA	DTA_8	chr1_62329140	1	62329140	0.39	1.44E-04	3.84	0.68
DTA	DTA_9	chr1_276325709	1	276325709	0.29	2.23E-04	3.65	0.64
DTA	DTA_9	chr1_276362724	1	276362724	0.29	6.46E-04	3.19	0.55
DTA	DTA_9	chr1_276682794	1	276682794	0.30	6.61E-04	3.18	0.55
DTA	DTA_10	chr1_296175139	1	296175139	0.36	3.18E-04	3.50	0.61
DTA	DTA_11	chr2_50809075	2	50809075	0.01	8.22E-04	3.09	0.53
DTA	DTA_12	chr3_146607524	3	146607524	0.49	3.70E-04	3.43	0.60
DTA	DTA_12	chr3_146723136	3	146723136	0.29	3.11E-04	3.51	0.61
DTA	DTA_12	chr3_147328863	3	147328863	0.50	5.36E-04	3.27	0.56
DTA	DTA_12	chr3_147745260	3	147745260	0.29	9.55E-04	3.02	0.51
DTA	DTA_13	chr3_148975376	3	148975376	0.48	2.25E-04	3.65	0.64
DTA	DTA_13	chr3_149249611	3	149249611	0.50	1.85E-04	3.73	0.66
DTA	DTA_13	chr3_149249613	3	149249613	0.50	1.85E-04	3.73	0.66
DTA	DTA_13	chr3_149250047	3	149250047	0.48	9.68E-04	3.01	0.51
DTA	DTA_13	chr3_149250050	3	149250050	0.48	9.54E-04	3.02	0.51
DTA	DTA_13	chr3_149250059	3	149250059	0.48	4.28E-04	3.37	0.58
DTA	DTA_13	chr3_149250622	3	149250622	0.29	3.18E-04	3.50	0.61
DTA	DTA_13	chr3_149250630	3	149250630	0.29	2.69E-04	3.57	0.63
DTA	DTA_13	chr3_149398810	3	149398810	0.29	3.86E-04	3.41	0.59
DTA	DTA_14	chr3_153764074	3	153764074	0.50	6.11E-07	6.21	1.18
DTA	DTA_14	chr3_153770646	3	153770646	0.44	3.61E-04	3.44	0.60
DTA	DTA_14	chr3_153771141	3	153771141	0.20	1.05E-05	4.98	0.92
DTA	DTA_14	chr3_153771151	3	153771151	0.20	1.33E-04	3.88	0.69
DTA	DTA_14	chr3_153771171	3	153771171	0.21	3.07E-04	3.51	0.61
DTA	DTA_14	chr3_153783006	3	153783006	0.44	1.54E-04	3.81	0.67
DTA	DTA_14	chr3_154017208	3	154017208	0.21	1.80E-04	3.74	0.66
DTA	DTA_14	chr3_154017236	3	154017236	0.20	1.23E-04	3.91	0.70
DTA	DTA_14	chr3_154075824	3	154075824	0.29	5.11E-07	6.29	1.19
DTA	DTA_14	chr3_154075870	3	154075870	0.25	6.15E-06	5.21	0.97
DTA	DTA_14	chr3_154075887	3	154075887	0.25	6.15E-06	5.21	0.97
DTA	DTA_14	chr3_154075890	3	154075890	0.25	6.15E-06	5.21	0.97

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTA	DTA_14	chr3_154076084	3	154076084	0.26	2.01E-06	5.70	1.07
DTA	DTA_14	chr3_154077726	3	154077726	0.27	1.33E-07	6.88	1.32
DTA	DTA_14	chr3_154124966	3	154124966	0.49	4.34E-06	5.36	1.00
DTA	DTA_14	chr3_154125085	3	154125085	0.49	3.83E-06	5.42	1.01
DTA	DTA_14	chr3_154250578	3	154250578	0.13	9.23E-04	3.04	0.52
DTA	DTA_14	chr3_154408191	3	154408191	0.35	2.47E-08	7.61	1.48
DTA	DTA_14	chr3_154408279	3	154408279	0.20	4.54E-05	4.34	0.78
DTA	DTA_14	chr3_154409508	3	154409508	0.15	3.32E-07	6.48	1.23
DTA	DTA_14	chr3_154409545	3	154409545	0.29	1.54E-08	7.81	1.52
DTA	DTA_14	chr3_154563862	3	154563862	0.27	3.84E-04	3.42	0.59
DTA	DTA_14	chr3_154563985	3	154563985	0.27	5.71E-04	3.24	0.56
DTA	DTA_14	chr3_154576317	3	154576317	0.32	1.93E-05	4.71	0.86
DTA	DTA_14	chr3_154576332	3	154576332	0.32	1.93E-05	4.71	0.86
DTA	DTA_14	chr3_154576346	3	154576346	0.32	1.93E-05	4.71	0.86
DTA	DTA_14	chr3_154592422	3	154592422	0.29	3.87E-08	7.41	1.43
DTA	DTA_14	chr3_154592481	3	154592481	0.29	3.87E-08	7.41	1.43
DTA	DTA_14	chr3_154592489	3	154592489	0.29	3.87E-08	7.41	1.43
DTA	DTA_14	chr3_154625415	3	154625415	0.29	2.33E-09	8.63	1.70
DTA	DTA_14	chr3_154625420	3	154625420	0.29	3.08E-09	8.51	1.67
DTA	DTA_14	chr3_154627523	3	154627523	0.28	5.91E-09	8.23	1.61
DTA	DTA_14	chr3_154627556	3	154627556	0.28	6.54E-09	8.18	1.60
DTA	DTA_14	chr3_154627560	3	154627560	0.28	6.82E-09	8.17	1.60
DTA	DTA_14	chr3_154650534	3	154650534	0.28	6.45E-09	8.19	1.60
DTA	DTA_14	chr3_154650575	3	154650575	0.28	2.77E-08	7.56	1.47
DTA	DTA_14	chr3_154650655	3	154650655	0.43	5.27E-04	3.28	0.57
DTA	DTA_14	chr3_154655030	3	154655030	0.29	1.24E-07	6.91	1.33
DTA	DTA_14	chr3_154655098	3	154655098	0.28	4.05E-07	6.39	1.22
DTA	DTA_14	chr3_154655116	3	154655116	0.28	4.05E-07	6.39	1.22
DTA	DTA_14	chr3_154661548	3	154661548	0.28	3.25E-07	6.49	1.24
DTA	DTA_14	chr3_154732521	3	154732521	0.28	2.73E-07	6.56	1.25
DTA	DTA_14	chr3_154739343	3	154739343	0.25	6.14E-05	4.21	0.76
DTA	DTA_14	chr3_154739847	3	154739847	0.29	1.63E-07	6.79	1.30
DTA	DTA_14	chr3_154739888	3	154739888	0.27	9.45E-07	6.02	1.14
DTA	DTA_14	chr3_154981090	3	154981090	0.28	1.18E-05	4.93	0.91
DTA	DTA_14	chr3_154981137	3	154981137	0.27	4.18E-06	5.38	1.00
DTA	DTA_14	chr3_155091887	3	155091887	0.31	4.31E-09	8.37	1.64
DTA	DTA_14	chr3_155317564	3	155317564	0.28	4.67E-06	5.33	0.99
DTA	DTA_14	chr3_155803339	3	155803339	0.48	8.04E-09	8.09	1.58

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTA	DTA_14	chr3_155803532	3	155803532	0.29	2.94E-09	8.53	1.68
DTA	DTA_14	chr3_155967126	3	155967126	0.28	9.04E-08	7.04	1.35
DTA	DTA_14	chr3_155967168	3	155967168	0.31	1.62E-07	6.79	1.30
DTA	DTA_14	chr3_156275693	3	156275693	0.27	4.88E-05	4.31	0.78
DTA	DTA_14	chr3_156287541	3	156287541	0.28	9.03E-08	7.04	1.36
DTA	DTA_14	chr3_156287743	3	156287743	0.28	4.97E-08	7.30	1.41
DTA	DTA_14	chr3_156287758	3	156287758	0.48	5.19E-10	9.29	1.84
DTA	DTA_14	chr3_156287774	3	156287774	0.26	1.35E-04	3.87	0.69
DTA	DTA_14	chr3_156287801	3	156287801	0.26	1.81E-04	3.74	0.66
DTA	DTA_14	chr3_156304726	3	156304726	0.22	2.64E-05	4.58	0.83
DTA	DTA_14	chr3_156304807	3	156304807	0.27	2.76E-04	3.56	0.62
DTA	DTA_14	chr3_156304837	3	156304837	0.21	1.98E-04	3.70	0.65
DTA	DTA_14	chr3_156434695	3	156434695	0.21	5.64E-04	3.25	0.56
DTA	DTA_14	chr3_156434769	3	156434769	0.21	6.08E-04	3.22	0.55
DTA	DTA_14	chr3_156434777	3	156434777	0.21	6.08E-04	3.22	0.55
DTA	DTA_14	chr3_156486164	3	156486164	0.28	4.25E-09	8.37	1.64
DTA	DTA_14	chr3_156799657	3	156799657	0.27	4.62E-05	4.34	0.78
DTA	DTA_14	chr3_156799845	3	156799845	0.49	7.47E-11	10.13	2.02
DTA	DTA_14	chr3_156799970	3	156799970	0.23	6.95E-06	5.16	0.95
DTA	DTA_14	chr3_156800034	3	156800034	0.48	3.94E-08	7.40	1.43
DTA	DTA_14	chr3_156939575	3	156939575	0.26	3.00E-06	5.52	1.03
DTA	DTA_14	chr3_156939584	3	156939584	0.28	1.02E-06	5.99	1.13
DTA	DTA_14	chr3_156969980	3	156969980	0.49	9.82E-12	11.01	2.22
DTA	DTA_14	chr3_156969997	3	156969997	0.48	4.05E-11	10.39	2.08
DTA	DTA_14	chr3_157018356	3	157018356	0.26	7.00E-06	5.15	0.95
DTA	DTA_14	chr3_157018359	3	157018359	0.26	7.00E-06	5.15	0.95
DTA	DTA_14	chr3_157018365	3	157018365	0.26	7.00E-06	5.15	0.95
DTA	DTA_14	chr3_157018380	3	157018380	0.21	6.83E-06	5.17	0.96
DTA	DTA_14	chr3_157051502	3	157051502	0.31	1.93E-09	8.72	1.72
DTA	DTA_14	chr3_157417448	3	157417448	0.30	2.58E-12	11.59	2.34
DTA	DTA_14	chr3_157568991	3	157568991	0.29	8.23E-11	10.08	2.01
DTA	DTA_14	chr3_157569114	3	157569114	0.17	3.51E-09	8.45	1.66
DTA	DTA_14	chr3_157576226	3	157576226	0.30	8.01E-14	13.10	2.68
DTA	DTA_14	chr3_157576421	3	157576421	0.30	1.81E-11	10.74	2.16
DTA	DTA_14	chr3_157576589	3	157576589	0.28	7.30E-12	11.14	2.24
DTA	DTA_14	chr3_157576725	3	157576725	0.30	9.98E-12	11.00	2.21
DTA	DTA_14	chr3_157576733	3	157576733	0.29	1.27E-12	11.90	2.41
DTA	DTA_14	chr3_157578664	3	157578664	0.31	1.16E-11	10.94	2.20

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTA	DTA_14	chr3_157578666	3	157578666	0.31	8.67E-12	11.06	2.23
DTA	DTA_14	chr3_157587430	3	157587430	0.36	8.07E-04	3.09	0.53
DTA	DTA_14	chr3_157587467	3	157587467	0.26	7.30E-06	5.14	0.95
DTA	DTA_14	chr3_157773525	3	157773525	0.35	8.34E-05	4.08	0.73
DTA	DTA_14	chr3_157918560	3	157918560	0.23	2.34E-06	5.63	1.05
DTA	DTA_14	chr3_157938112	3	157938112	0.23	2.41E-05	4.62	0.84
DTA	DTA_14	chr3_157941470	3	157941470	0.23	6.04E-06	5.22	0.97
DTA	DTA_14	chr3_158049977	3	158049977	0.30	8.18E-05	4.09	0.73
DTA	DTA_14	chr3_158049997	3	158049997	0.30	8.18E-05	4.09	0.73
DTA	DTA_14	chr3_158050012	3	158050012	0.30	8.18E-05	4.09	0.73
DTA	DTA_14	chr3_158348209	3	158348209	0.48	1.21E-11	10.92	2.20
DTA	DTA_14	chr3_158348267	3	158348267	0.30	1.66E-06	5.78	1.09
DTA	DTA_14	chr3_158348357	3	158348357	0.26	4.48E-07	6.35	1.21
DTA	DTA_14	chr3_158444445	3	158444445	0.26	1.67E-05	4.78	0.88
DTA	DTA_14	chr3_158451553	3	158451553	0.22	5.56E-06	5.25	0.98
DTA	DTA_14	chr3_158521181	3	158521181	0.26	8.63E-07	6.06	1.15
DTA	DTA_14	chr3_158650511	3	158650511	0.44	7.19E-04	3.14	0.54
DTA	DTA_14	chr3_158780416	3	158780416	0.23	1.17E-08	7.93	1.55
DTA	DTA_14	chr3_158780445	3	158780445	0.24	7.37E-09	8.13	1.59
DTA	DTA_14	chr3_158780918	3	158780918	0.30	1.12E-14	13.95	2.87
DTA	DTA_14	chr3_158781033	3	158781033	0.27	6.15E-08	7.21	1.39
DTA	DTA_14	chr3_158790476	3	158790476	0.27	2.58E-08	7.59	1.47
DTA	DTA_14	chr3_158890884	3	158890884	0.48	2.59E-21	20.59	4.38
DTA	DTA_14	chr3_158901755	3	158901755	0.22	1.73E-08	7.76	1.51
DTA	DTA_14	chr3_158972316	3	158972316	0.48	6.25E-17	16.20	3.38
DTA	DTA_14	chr3_158973464	3	158973464	0.23	8.70E-09	8.06	1.57
DTA	DTA_14	chr3_159379133	3	159379133	0.25	2.34E-06	5.63	1.05
DTA	DTA_14	chr3_159380236	3	159380236	0.44	6.76E-04	3.17	0.54
DTA	DTA_14	chr3_159380239	3	159380239	0.44	3.68E-04	3.43	0.60
DTA	DTA_14	chr3_159380250	3	159380250	0.44	6.76E-04	3.17	0.54
DTA	DTA_14	chr3_159380253	3	159380253	0.44	6.76E-04	3.17	0.54
DTA	DTA_14	chr3_159381162	3	159381162	0.46	7.29E-04	3.14	0.54
DTA	DTA_14	chr3_159385192	3	159385192	0.49	2.64E-18	17.58	3.69
DTA	DTA_14	chr3_159385285	3	159385285	0.26	6.17E-06	5.21	0.97
DTA	DTA_14	chr3_159385286	3	159385286	0.26	6.17E-06	5.21	0.97
DTA	DTA_14	chr3_159385309	3	159385309	0.26	7.40E-06	5.13	0.95
DTA	DTA_14	chr3_159388105	3	159388105	0.29	1.17E-16	15.93	3.31
DTA	DTA_14	chr3_159678385	3	159678385	0.46	3.47E-04	3.46	0.60

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTA	DTA_14	chr3_159678426	3	159678426	0.30	4.39E-19	18.36	3.87
DTA	DTA_14	chr3_159678466	3	159678466	0.30	6.62E-19	18.18	3.82
DTA	DTA_14	chr3_159678604	3	159678604	0.24	7.74E-07	6.11	1.16
DTA	DTA_14	chr3_159678635	3	159678635	0.30	7.55E-18	17.12	3.58
DTA	DTA_14	chr3_159678650	3	159678650	0.24	1.01E-06	5.99	1.13
DTA	DTA_14	chr3_159680509	3	159680509	0.25	7.59E-06	5.12	0.95
DTA	DTA_14	chr3_159731276	3	159731276	0.26	8.98E-07	6.05	1.14
DTA	DTA_14	chr3_159800933	3	159800933	0.25	1.19E-06	5.92	1.12
DTA	DTA_14	chr3_159800996	3	159800996	0.48	7.65E-15	14.12	2.91
DTA	DTA_14	chr3_159801043	3	159801043	0.28	6.02E-16	15.22	3.15
DTA	DTA_14	chr3_159801068	3	159801068	0.26	2.83E-06	5.55	1.04
DTA	DTA_14	chr3_159801074	3	159801074	0.26	4.09E-06	5.39	1.00
DTA	DTA_14	chr3_159801091	3	159801091	0.22	1.61E-07	6.79	1.30
DTA	DTA_14	chr3_159801092	3	159801092	0.22	2.52E-07	6.60	1.26
DTA	DTA_14	chr3_159801235	3	159801235	0.30	9.07E-17	16.04	3.34
DTA	DTA_14	chr3_159801239	3	159801239	0.26	1.45E-06	5.84	1.10
DTA	DTA_14	chr3_159807179	3	159807179	0.26	6.17E-06	5.21	0.97
DTA	DTA_14	chr3_159807447	3	159807447	0.29	1.86E-18	17.73	3.72
DTA	DTA_14	chr3_159810023	3	159810023	0.29	6.77E-15	14.17	2.92
DTA	DTA_14	chr3_159818313	3	159818313	0.26	2.82E-05	4.55	0.83
DTA	DTA_14	chr3_159818316	3	159818316	0.24	9.28E-05	4.03	0.72
DTA	DTA_14	chr3_159818326	3	159818326	0.25	2.67E-05	4.57	0.83
DTA	DTA_14	chr3_159818698	3	159818698	0.23	1.10E-07	6.96	1.34
DTA	DTA_14	chr3_159818701	3	159818701	0.49	1.94E-16	15.71	3.26
DTA	DTA_14	chr3_159819875	3	159819875	0.23	3.58E-05	4.45	0.81
DTA	DTA_14	chr3_159819880	3	159819880	0.23	1.06E-05	4.98	0.92
DTA	DTA_14	chr3_159820547	3	159820547	0.48	1.82E-15	14.74	3.05
DTA	DTA_14	chr3_159861750	3	159861750	0.24	3.48E-07	6.46	1.23
DTA	DTA_14	chr3_159868843	3	159868843	0.29	1.03E-17	16.99	3.55
DTA	DTA_14	chr3_159870280	3	159870280	0.29	2.26E-06	5.65	1.06
DTA	DTA_14	chr3_159870399	3	159870399	0.19	5.95E-05	4.23	0.76
DTA	DTA_14	chr3_159870526	3	159870526	0.26	8.65E-05	4.06	0.73
DTA	DTA_14	chr3_159870623	3	159870623	0.27	3.50E-06	5.46	1.02
DTA	DTA_14	chr3_159873162	3	159873162	0.23	3.77E-05	4.42	0.80
DTA	DTA_14	chr3_160665462	3	160665462	0.26	2.85E-07	6.54	1.25
DTA	DTA_14	chr3_160665463	3	160665463	0.50	1.10E-15	14.96	3.10
DTA	DTA_14	chr3_160665476	3	160665476	0.23	8.52E-06	5.07	0.94
DTA	DTA_14	chr3_160665487	3	160665487	0.23	2.90E-05	4.54	0.83

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTA	DTA_14	chr3_160666211	3	160666211	0.23	8.55E-06	5.07	0.94
DTA	DTA_14	chr3_161251937	3	161251937	0.28	2.61E-04	3.58	0.63
DTA	DTA_14	chr3_161251987	3	161251987	0.27	4.69E-04	3.33	0.58
DTA	DTA_14	chr3_161251989	3	161251989	0.27	5.18E-04	3.29	0.57
DTA	DTA_14	chr3_161252051	3	161252051	0.28	6.95E-05	4.16	0.75
DTA	DTA_14	chr3_161257076	3	161257076	0.29	2.73E-11	10.56	2.12
DTA	DTA_14	chr3_161257078	3	161257078	0.29	2.73E-11	10.56	2.12
DTA	DTA_14	chr3_161257090	3	161257090	0.29	2.73E-11	10.56	2.12
DTA	DTA_14	chr3_161257096	3	161257096	0.29	2.73E-11	10.56	2.12
DTA	DTA_14	chr3_161259908	3	161259908	0.29	4.62E-14	13.34	2.73
DTA	DTA_14	chr3_161364532	3	161364532	0.37	4.10E-07	6.39	1.21
DTA	DTA_14	chr3_161364604	3	161364604	0.45	3.85E-07	6.41	1.22
DTA	DTA_14	chr3_161369706	3	161369706	0.29	1.39E-13	12.86	2.63
DTA	DTA_14	chr3_161369763	3	161369763	0.29	1.29E-12	11.89	2.41
DTA	DTA_14	chr3_161369771	3	161369771	0.25	4.20E-04	3.38	0.59
DTA	DTA_14	chr3_161369773	3	161369773	0.24	6.73E-04	3.17	0.54
DTA	DTA_14	chr3_161369818	3	161369818	0.28	1.05E-13	12.98	2.65
DTA	DTA_14	chr3_161369881	3	161369881	0.29	2.96E-14	13.53	2.77
DTA	DTA_14	chr3_161563404	3	161563404	0.45	4.03E-04	3.39	0.59
DTA	DTA_14	chr3_161563412	3	161563412	0.23	9.48E-05	4.02	0.72
DTA	DTA_14	chr3_161563431	3	161563431	0.23	9.17E-05	4.04	0.72
DTA	DTA_14	chr3_161563433	3	161563433	0.23	1.20E-04	3.92	0.70
DTA	DTA_14	chr3_161563441	3	161563441	0.23	9.17E-05	4.04	0.72
DTA	DTA_14	chr3_161563491	3	161563491	0.22	2.73E-05	4.56	0.83
DTA	DTA_14	chr3_161565616	3	161565616	0.23	1.20E-04	3.92	0.70
DTA	DTA_14	chr3_161565632	3	161565632	0.23	1.27E-04	3.90	0.69
DTA	DTA_14	chr3_161565647	3	161565647	0.23	1.27E-04	3.90	0.69
DTA	DTA_14	chr3_161573134	3	161573134	0.27	2.68E-10	9.57	1.90
DTA	DTA_14	chr3_161573148	3	161573148	0.22	1.62E-04	3.79	0.67
DTA	DTA_14	chr3_161573155	3	161573155	0.27	1.34E-10	9.87	1.97
DTA	DTA_14	chr3_161573221	3	161573221	0.27	2.68E-11	10.57	2.12
DTA	DTA_14	chr3_161573250	3	161573250	0.27	2.68E-11	10.57	2.12
DTA	DTA_14	chr3_161573899	3	161573899	0.45	3.73E-04	3.43	0.60
DTA	DTA_14	chr3_161575037	3	161575037	0.29	2.62E-10	9.58	1.90
DTA	DTA_14	chr3_161575049	3	161575049	0.49	6.09E-09	8.22	1.61
DTA	DTA_14	chr3_161575068	3	161575068	0.49	3.63E-09	8.44	1.66
DTA	DTA_14	chr3_161575090	3	161575090	0.29	3.57E-10	9.45	1.87
DTA	DTA_14	chr3_161575111	3	161575111	0.50	6.52E-08	7.19	1.39

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTA	DTA_14	chr3_161575140	3	161575140	0.50	6.52E-08	7.19	1.39
DTA	DTA_14	chr3_161576642	3	161576642	0.25	9.12E-04	3.04	0.52
DTA	DTA_14	chr3_161638284	3	161638284	0.29	1.61E-13	12.79	2.61
DTA	DTA_14	chr3_161650139	3	161650139	0.30	2.39E-11	10.62	2.13
DTA	DTA_14	chr3_161650158	3	161650158	0.22	4.35E-05	4.36	0.79
DTA	DTA_14	chr3_161650198	3	161650198	0.23	8.46E-07	6.07	1.15
DTA	DTA_14	chr3_161650243	3	161650243	0.29	2.22E-10	9.65	1.92
DTA	DTA_14	chr3_161650452	3	161650452	0.28	8.67E-11	10.06	2.01
DTA	DTA_14	chr3_161650457	3	161650457	0.25	4.46E-04	3.35	0.58
DTA	DTA_14	chr3_161650485	3	161650485	0.25	6.57E-04	3.18	0.55
DTA	DTA_14	chr3_161650544	3	161650544	0.23	8.36E-06	5.08	0.94
DTA	DTA_14	chr3_161732785	3	161732785	0.30	6.15E-13	12.21	2.48
DTA	DTA_14	chr3_161847127	3	161847127	0.23	5.95E-04	3.23	0.56
DTA	DTA_14	chr3_161969350	3	161969350	0.23	2.69E-04	3.57	0.63
DTA	DTA_14	chr3_161971165	3	161971165	0.17	2.10E-06	5.68	1.06
DTA	DTA_14	chr3_161971196	3	161971196	0.24	5.91E-04	3.23	0.56
DTA	DTA_14	chr3_162034696	3	162034696	0.29	2.45E-06	5.61	1.05
DTA	DTA_14	chr3_162034773	3	162034773	0.29	3.24E-07	6.49	1.24
DTA	DTA_14	chr3_162034810	3	162034810	0.29	3.24E-07	6.49	1.24
DTA	DTA_14	chr3_162034827	3	162034827	0.29	3.24E-07	6.49	1.24
DTA	DTA_14	chr3_162034831	3	162034831	0.29	3.24E-07	6.49	1.24
DTA	DTA_14	chr3_162064220	3	162064220	0.49	2.41E-05	4.62	0.84
DTA	DTA_14	chr3_162096206	3	162096206	0.29	7.98E-06	5.10	0.94
DTA	DTA_14	chr3_162097205	3	162097205	0.47	3.87E-04	3.41	0.59
DTA	DTA_14	chr3_162097279	3	162097279	0.48	1.81E-04	3.74	0.66
DTA	DTA_14	chr3_162178736	3	162178736	0.31	9.16E-04	3.04	0.52
DTA	DTA_14	chr3_162179943	3	162179943	0.25	2.56E-04	3.59	0.63
DTA	DTA_14	chr3_162180147	3	162180147	0.24	1.79E-04	3.75	0.66
DTA	DTA_14	chr3_162317866	3	162317866	0.29	4.58E-06	5.34	0.99
DTA	DTA_14	chr3_162318161	3	162318161	0.49	1.62E-04	3.79	0.67
DTA	DTA_14	chr3_162318227	3	162318227	0.49	2.91E-04	3.54	0.62
DTA	DTA_14	chr3_162318357	3	162318357	0.49	5.01E-04	3.30	0.57
DTA	DTA_14	chr3_162318376	3	162318376	0.49	5.89E-04	3.23	0.56
DTA	DTA_14	chr3_162437820	3	162437820	0.29	7.50E-05	4.13	0.74
DTA	DTA_14	chr3_162587602	3	162587602	0.49	5.71E-04	3.24	0.56
DTA	DTA_14	chr3_162589163	3	162589163	0.29	1.97E-05	4.70	0.86
DTA	DTA_14	chr3_162597295	3	162597295	0.19	4.41E-04	3.36	0.58
DTA	DTA_14	chr3_162597473	3	162597473	0.30	4.71E-05	4.33	0.78

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTA	DTA_14	chr3_162597560	3	162597560	0.31	6.95E-05	4.16	0.75
DTA	DTA_14	chr3_162599378	3	162599378	0.29	5.79E-06	5.24	0.97
DTA	DTA_14	chr3_162599393	3	162599393	0.29	8.11E-06	5.09	0.94
DTA	DTA_14	chr3_162600084	3	162600084	0.29	1.84E-06	5.74	1.08
DTA	DTA_14	chr3_162600110	3	162600110	0.33	6.48E-05	4.19	0.75
DTA	DTA_14	chr3_162606680	3	162606680	0.48	1.94E-05	4.71	0.86
DTA	DTA_14	chr3_162606704	3	162606704	0.48	1.09E-05	4.96	0.91
DTA	DTA_14	chr3_162696407	3	162696407	0.24	2.53E-04	3.60	0.63
DTA	DTA_14	chr3_162696410	3	162696410	0.49	1.95E-05	4.71	0.86
DTA	DTA_14	chr3_162831149	3	162831149	0.30	7.92E-05	4.10	0.73
DTA	DTA_14	chr3_162831181	3	162831181	0.30	1.18E-04	3.93	0.70
DTA	DTA_15	chr3_164524652	3	164524652	0.48	4.24E-06	5.37	1.00
DTA	DTA_15	chr3_164581009	3	164581009	0.29	5.45E-06	5.26	0.98
DTA	DTA_15	chr3_164581079	3	164581079	0.29	6.03E-07	6.22	1.18
DTA	DTA_15	chr3_164581105	3	164581105	0.28	3.62E-04	3.44	0.60
DTA	DTA_15	chr3_164581160	3	164581160	0.28	6.52E-04	3.19	0.55
DTA	DTA_15	chr3_164587783	3	164587783	0.30	9.22E-06	5.04	0.93
DTA	DTA_15	chr3_164587790	3	164587790	0.30	5.58E-06	5.25	0.97
DTA	DTA_15	chr3_164587830	3	164587830	0.29	7.99E-06	5.10	0.94
DTA	DTA_15	chr3_164587832	3	164587832	0.29	7.99E-06	5.10	0.94
DTA	DTA_15	chr3_164587844	3	164587844	0.29	4.81E-06	5.32	0.99
DTA	DTA_15	chr3_164588707	3	164588707	0.29	4.96E-05	4.30	0.78
DTA	DTA_15	chr3_164589520	3	164589520	0.24	1.35E-04	3.87	0.69
DTA	DTA_15	chr3_164975381	3	164975381	0.30	2.21E-05	4.66	0.85
DTA	DTA_15	chr3_164975717	3	164975717	0.29	5.21E-06	5.28	0.98
DTA	DTA_15	chr3_164978022	3	164978022	0.29	4.68E-05	4.33	0.78
DTA	DTA_15	chr3_164978025	3	164978025	0.29	1.23E-05	4.91	0.90
DTA	DTA_15	chr3_164978057	3	164978057	0.28	3.49E-05	4.46	0.81
DTA	DTA_15	chr3_164978728	3	164978728	0.29	1.25E-05	4.90	0.90
DTA	DTA_15	chr3_164979640	3	164979640	0.30	6.30E-06	5.20	0.96
DTA	DTA_15	chr3_164979656	3	164979656	0.44	4.54E-04	3.34	0.58
DTA	DTA_15	chr3_165017930	3	165017930	0.29	1.99E-06	5.70	1.07
DTA	DTA_15	chr3_165017969	3	165017969	0.29	1.79E-05	4.75	0.87
DTA	DTA_15	chr3_165021955	3	165021955	0.48	1.03E-05	4.99	0.92
DTA	DTA_15	chr3_165021985	3	165021985	0.48	2.56E-05	4.59	0.84
DTA	DTA_15	chr3_165168084	3	165168084	0.48	2.31E-05	4.64	0.85
DTA	DTA_15	chr3_165174695	3	165174695	0.28	2.87E-05	4.54	0.83
DTA	DTA_15	chr3_165174761	3	165174761	0.28	2.32E-05	4.64	0.85

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTA	DTA_15	chr3_165175552	3	165175552	0.28	1.79E-05	4.75	0.87
DTA	DTA_15	chr3_165175866	3	165175866	0.28	5.18E-04	3.29	0.57
DTA	DTA_15	chr3_165178771	3	165178771	0.29	2.22E-05	4.65	0.85
DTA	DTA_15	chr3_165446990	3	165446990	0.24	7.34E-04	3.13	0.54
DTA	DTA_15	chr3_165458009	3	165458009	0.26	7.15E-04	3.15	0.54
DTA	DTA_15	chr3_165458089	3	165458089	0.31	8.55E-04	3.07	0.52
DTA	DTA_15	chr3_165458092	3	165458092	0.31	8.55E-04	3.07	0.52
DTA	DTA_15	chr3_165458515	3	165458515	0.48	7.85E-05	4.10	0.74
DTA	DTA_15	chr3_165458612	3	165458612	0.50	3.09E-05	4.51	0.82
DTA	DTA_15	chr3_165704466	3	165704466	0.22	1.03E-04	3.99	0.71
DTA	DTA_15	chr3_165704521	3	165704521	0.28	3.03E-05	4.52	0.82
DTA	DTA_15	chr3_165722971	3	165722971	0.48	1.65E-04	3.78	0.67
DTA	DTA_15	chr3_165728239	3	165728239	0.29	4.07E-05	4.39	0.79
DTA	DTA_15	chr3_165858588	3	165858588	0.28	2.88E-04	3.54	0.62
DTA	DTA_15	chr3_165862378	3	165862378	0.23	2.91E-04	3.54	0.62
DTA	DTA_15	chr3_165862389	3	165862389	0.23	2.91E-04	3.54	0.62
DTA	DTA_15	chr3_165862414	3	165862414	0.23	2.91E-04	3.54	0.62
DTA	DTA_15	chr3_165862973	3	165862973	0.28	5.62E-05	4.25	0.77
DTA	DTA_15	chr3_165879324	3	165879324	0.25	3.06E-04	3.51	0.61
DTA	DTA_15	chr3_165903092	3	165903092	0.23	1.06E-04	3.97	0.71
DTA	DTA_15	chr3_166151739	3	166151739	0.29	6.21E-04	3.21	0.55
DTA	DTA_15	chr3_166151763	3	166151763	0.22	2.33E-05	4.63	0.85
DTA	DTA_15	chr3_166200169	3	166200169	0.22	4.88E-04	3.31	0.57
DTA	DTA_15	chr3_166200209	3	166200209	0.22	4.88E-04	3.31	0.57
DTA	DTA_15	chr3_166206434	3	166206434	0.23	7.15E-05	4.15	0.74
DTA	DTA_15	chr3_166206471	3	166206471	0.23	7.15E-05	4.15	0.74
DTA	DTA_15	chr3_166206478	3	166206478	0.22	8.35E-05	4.08	0.73
DTA	DTA_15	chr3_166430306	3	166430306	0.30	8.49E-05	4.07	0.73
DTA	DTA_15	chr3_166430331	3	166430331	0.29	2.01E-04	3.70	0.65
DTA	DTA_15	chr3_166430359	3	166430359	0.30	8.49E-05	4.07	0.73
DTA	DTA_15	chr3_167394795	3	167394795	0.27	6.07E-04	3.22	0.55
DTA	DTA_15	chr3_167394810	3	167394810	0.27	6.07E-04	3.22	0.55
DTA	DTA_15	chr3_167394822	3	167394822	0.27	6.07E-04	3.22	0.55
DTA	DTA_15	chr3_167431049	3	167431049	0.26	4.67E-04	3.33	0.58
DTA	DTA_16	chr3_168629919	3	168629919	0.23	8.74E-04	3.06	0.52
DTA	DTA_16	chr3_168629926	3	168629926	0.23	8.74E-04	3.06	0.52
DTA	DTA_16	chr3_168629931	3	168629931	0.26	6.54E-04	3.18	0.55
DTA	DTA_16	chr3_168629983	3	168629983	0.24	4.89E-04	3.31	0.57

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTA	DTA_16	chr3_169080083	3	169080083	0.25	6.67E-04	3.18	0.55
DTA	DTA_17	chr3_205970789	3	205970789	0.22	8.25E-04	3.08	0.53
DTA	DTA_17	chr3_205970811	3	205970811	0.22	7.94E-04	3.10	0.53
DTA	DTA_17	chr3_206193036	3	206193036	0.22	2.72E-04	3.57	0.62
DTA	DTA_17	chr3_206196179	3	206196179	0.23	8.97E-04	3.05	0.52
DTA	DTA_17	chr3_206196213	3	206196213	0.23	8.97E-04	3.05	0.52
DTA	DTA_17	chr3_206196248	3	206196248	0.23	9.52E-04	3.02	0.51
DTA	DTA_17	chr3_206196324	3	206196324	0.23	7.11E-04	3.15	0.54
DTA	DTA_17	chr3_206586257	3	206586257	0.22	1.22E-04	3.91	0.70
DTA	DTA_17	chr3_206846979	3	206846979	0.20	3.14E-05	4.50	0.82
DTA	DTA_17	chr3_206847034	3	206847034	0.20	3.14E-05	4.50	0.82
DTA	DTA_17	chr3_206847070	3	206847070	0.19	1.74E-04	3.76	0.66
DTA	DTA_17	chr3_206847075	3	206847075	0.19	1.74E-04	3.76	0.66
DTA	DTA_17	chr3_206847106	3	206847106	0.19	1.74E-04	3.76	0.66
DTA	DTA_17	chr3_206847130	3	206847130	0.19	1.74E-04	3.76	0.66
DTA	DTA_17	chr3_206847136	3	206847136	0.19	1.74E-04	3.76	0.66
DTA	DTA_17	chr3_206848101	3	206848101	0.20	4.17E-04	3.38	0.59
DTA	DTA_17	chr3_206943785	3	206943785	0.19	5.10E-05	4.29	0.77
DTA	DTA_17	chr3_206952964	3	206952964	0.18	6.82E-04	3.17	0.54
DTA	DTA_17	chr3_206953158	3	206953158	0.18	4.38E-04	3.36	0.58
DTA	DTA_17	chr3_206953193	3	206953193	0.18	7.55E-04	3.12	0.53
DTA	DTA_17	chr3_206957744	3	206957744	0.20	9.42E-04	3.03	0.51
DTA	DTA_17	chr3_206958973	3	206958973	0.17	7.57E-04	3.12	0.53
DTA	DTA_17	chr3_206959062	3	206959062	0.17	7.59E-04	3.12	0.53
DTA	DTA_17	chr3_206959086	3	206959086	0.17	7.59E-04	3.12	0.53
DTA	DTA_17	chr3_207151139	3	207151139	0.20	2.27E-04	3.64	0.64
DTA	DTA_17	chr3_207151171	3	207151171	0.20	2.70E-04	3.57	0.63
DTA	DTA_17	chr3_207151227	3	207151227	0.21	1.46E-04	3.83	0.68
DTA	DTA_17	chr3_207151231	3	207151231	0.21	1.23E-04	3.91	0.70
DTA	DTA_17	chr3_207151266	3	207151266	0.20	6.80E-05	4.17	0.75
DTA	DTA_17	chr3_207178337	3	207178337	0.20	9.34E-05	4.03	0.72
DTA	DTA_17	chr3_207178370	3	207178370	0.20	1.81E-04	3.74	0.66
DTA	DTA_17	chr3_207250765	3	207250765	0.20	4.30E-04	3.37	0.58
DTA	DTA_17	chr3_207250860	3	207250860	0.20	7.01E-05	4.15	0.75
DTA	DTA_17	chr3_207250878	3	207250878	0.20	5.29E-05	4.28	0.77
DTA	DTA_17	chr3_207252776	3	207252776	0.20	4.60E-04	3.34	0.58
DTA	DTA_17	chr3_207766422	3	207766422	0.19	3.36E-04	3.47	0.61
DTA	DTA_17	chr3_207768822	3	207768822	0.20	4.17E-04	3.38	0.59

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTA	DTA_17	chr3_207772297	3	207772297	0.20	4.53E-04	3.34	0.58
DTA	DTA_17	chr3_207901009	3	207901009	0.19	2.47E-04	3.61	0.63
DTA	DTA_17	chr3_207901044	3	207901044	0.19	2.47E-04	3.61	0.63
DTA	DTA_17	chr3_207988505	3	207988505	0.19	2.92E-04	3.54	0.62
DTA	DTA_17	chr3_208034892	3	208034892	0.19	1.13E-04	3.95	0.70
DTA	DTA_17	chr3_208034904	3	208034904	0.19	1.97E-04	3.71	0.65
DTA	DTA_17	chr3_208038720	3	208038720	0.19	9.10E-04	3.04	0.52
DTA	DTA_17	chr3_208467111	3	208467111	0.21	6.95E-04	3.16	0.54
DTA	DTA_17	chr3_208543150	3	208543150	0.19	8.06E-04	3.09	0.53
DTA	DTA_17	chr3_208543193	3	208543193	0.20	8.38E-04	3.08	0.53
DTA	DTA_17	chr3_208617442	3	208617442	0.20	3.10E-04	3.51	0.61
DTA	DTA_17	chr3_208617481	3	208617481	0.20	3.10E-04	3.51	0.61
DTA	DTA_17	chr3_208618864	3	208618864	0.20	2.58E-04	3.59	0.63
DTA	DTA_17	chr3_208625340	3	208625340	0.21	1.61E-05	4.79	0.88
DTA	DTA_17	chr3_208700687	3	208700687	0.21	4.13E-04	3.38	0.59
DTA	DTA_17	chr3_208700703	3	208700703	0.21	4.13E-04	3.38	0.59
DTA	DTA_17	chr3_208789438	3	208789438	0.22	2.83E-04	3.55	0.62
DTA	DTA_17	chr3_208789510	3	208789510	0.22	3.81E-04	3.42	0.59
DTA	DTA_17	chr3_208791772	3	208791772	0.22	7.52E-04	3.12	0.53
DTA	DTA_17	chr3_208791795	3	208791795	0.22	4.65E-04	3.33	0.58
DTA	DTA_17	chr3_208889291	3	208889291	0.22	4.04E-04	3.39	0.59
DTA	DTA_17	chr3_208889321	3	208889321	0.22	5.88E-04	3.23	0.56
DTA	DTA_17	chr3_208889447	3	208889447	0.20	3.00E-04	3.52	0.62
DTA	DTA_17	chr3_208889458	3	208889458	0.21	5.14E-04	3.29	0.57
DTA	DTA_17	chr3_208890431	3	208890431	0.20	6.72E-04	3.17	0.54
DTA	DTA_17	chr3_208890441	3	208890441	0.20	6.78E-04	3.17	0.54
DTA	DTA_17	chr3_208916795	3	208916795	0.21	3.97E-05	4.40	0.80
DTA	DTA_17	chr3_208969488	3	208969488	0.21	7.63E-04	3.12	0.53
DTA	DTA_17	chr3_209009289	3	209009289	0.21	9.60E-04	3.02	0.51
DTA	DTA_17	chr3_209009319	3	209009319	0.21	9.26E-04	3.03	0.52
DTA	DTA_17	chr3_209009436	3	209009436	0.21	2.02E-04	3.70	0.65
DTA	DTA_17	chr3_209009471	3	209009471	0.21	3.83E-04	3.42	0.59
DTA	DTA_17	chr3_209010840	3	209010840	0.21	5.59E-04	3.25	0.56
DTA	DTA_17	chr3_209014053	3	209014053	0.22	9.15E-04	3.04	0.52
DTA	DTA_17	chr3_209024427	3	209024427	0.22	5.08E-04	3.29	0.57
DTA	DTA_17	chr3_209024481	3	209024481	0.21	4.55E-04	3.34	0.58
DTA	DTA_17	chr3_209734137	3	209734137	0.22	7.68E-04	3.11	0.53
DTA	DTA_18	chr3_220844514	3	220844514	0.20	5.16E-04	3.29	0.57

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTA	DTA_19	chr5_18583394	5	18583394	0.01	5.96E-04	3.23	0.56
DTA	DTA_20	chr6_149671374	6	149671374	0.18	1.77E-04	3.75	0.66
DTA	DTA_21	chr8_22685323	8	22685323	0.50	3.66E-04	3.44	0.60
DTA	DTA_22	chr8_79126904	8	79126904	0.20	7.52E-04	3.12	0.53
DTA	DTA_22	chr8_79126916	8	79126916	0.21	9.64E-04	3.02	0.51
DTA	DTA_23	chr8_111111523	8	111111523	0.01	3.29E-04	3.48	0.61
DTA	DTA_24	chr8_130926879	8	130926879	0.23	2.41E-04	3.62	0.64
DTA	DTA_24	chr8_131334405	8	131334405	0.24	7.43E-04	3.13	0.54
DTA	DTA_24	chr8_132170923	8	132170923	0.24	1.67E-04	3.78	0.67
DTA	DTA_24	chr8_132170951	8	132170951	0.24	1.06E-04	3.98	0.71
DTA	DTA_24	chr8_132170954	8	132170954	0.24	1.07E-04	3.97	0.71
DTA	DTA_24	chr8_132170972	8	132170972	0.24	1.07E-04	3.97	0.71
DTA	DTA_25	chr8_133566383	8	133566383	0.26	8.62E-04	3.06	0.52
DTA	DTA_25	chr8_133949014	8	133949014	0.24	5.72E-04	3.24	0.56
DTA	DTA_25	chr8_133949077	8	133949077	0.24	2.63E-04	3.58	0.63
DTA	DTA_25	chr8_134005625	8	134005625	0.21	1.61E-04	3.79	0.67
DTA	DTA_25	chr8_134006372	8	134006372	0.23	1.62E-04	3.79	0.67
DTA	DTA_25	chr8_134229264	8	134229264	0.24	1.99E-04	3.70	0.65
DTA	DTA_25	chr8_134229576	8	134229576	0.24	1.13E-04	3.95	0.70
DTA	DTA_25	chr8_134230097	8	134230097	0.24	4.71E-05	4.33	0.78
DTA	DTA_25	chr8_134230103	8	134230103	0.24	3.96E-05	4.40	0.80
DTA	DTA_25	chr8_134378632	8	134378632	0.24	3.36E-04	3.47	0.61
DTA	DTA_25	chr8_134378654	8	134378654	0.24	4.04E-04	3.39	0.59
DTA	DTA_25	chr8_134529676	8	134529676	0.24	6.62E-04	3.18	0.55
DTA	DTA_25	chr8_135154178	8	135154178	0.24	5.16E-04	3.29	0.57
DTA	DTA_26	chr8_168682612	8	168682612	0.47	6.60E-05	4.18	0.75
DTA	DTA_27	chr9_26817330	9	26817330	0.33	5.78E-04	3.24	0.56
DTA	DTA_28	chr9_33066876	9	33066876	0.33	4.32E-04	3.36	0.58
DTA	DTA_29	chr9_34242075	9	34242075	0.43	9.99E-04	3.00	0.51
DTA	DTA_29	chr9_34242135	9	34242135	0.43	9.99E-04	3.00	0.51
DTA	DTA_30	chr9_37406020	9	37406020	0.43	6.94E-04	3.16	0.54
DTA	DTA_30	chr9_37520739	9	37520739	0.34	6.11E-04	3.21	0.55
DTA	DTA_30	chr9_37520761	9	37520761	0.34	7.87E-04	3.10	0.53
DTA	DTA_30	chr9_37700056	9	37700056	0.42	5.10E-04	3.29	0.57
DTA	DTA_30	chr9_37792364	9	37792364	0.33	2.92E-04	3.53	0.62
DTA	DTA_30	chr9_37792370	9	37792370	0.33	2.92E-04	3.53	0.62
DTA	DTA_30	chr9_37792422	9	37792422	0.43	6.35E-04	3.20	0.55
DTA	DTA_30	chr9_37792430	9	37792430	0.43	6.35E-04	3.20	0.55

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTA	DTA_31	chr9_39339965	9	39339965	0.49	8.11E-04	3.09	0.53
DTA	DTA_32	chr9_40600623	9	40600623	0.33	7.00E-04	3.15	0.54
DTA	DTA_32	chr9_40600728	9	40600728	0.42	4.29E-04	3.37	0.58
DTA	DTA_32	chr9_40746897	9	40746897	0.33	1.39E-04	3.86	0.68
DTA	DTA_32	chr9_40746927	9	40746927	0.33	7.41E-04	3.13	0.54
DTA	DTA_32	chr9_40746932	9	40746932	0.33	7.41E-04	3.13	0.54
DTA	DTA_32	chr9_41118915	9	41118915	0.42	2.78E-04	3.56	0.62
DTA	DTA_32	chr9_41118922	9	41118922	0.42	1.81E-04	3.74	0.66
DTA	DTA_32	chr9_41520164	9	41520164	0.34	7.84E-04	3.11	0.53
DTA	DTA_32	chr9_41520878	9	41520878	0.33	7.76E-04	3.11	0.53
DTA	DTA_32	chr9_41754537	9	41754537	0.34	3.70E-04	3.43	0.60
DTA	DTA_33	chr9_42760498	9	42760498	0.42	1.81E-04	3.74	0.66
DTA	DTA_33	chr9_42840883	9	42840883	0.43	6.17E-04	3.21	0.55
DTA	DTA_33	chr9_42840886	9	42840886	0.43	6.78E-04	3.17	0.54
DTA	DTA_33	chr9_42840888	9	42840888	0.43	6.78E-04	3.17	0.54
DTA	DTA_33	chr9_43274338	9	43274338	0.33	7.65E-04	3.12	0.53
DTA	DTA_33	chr9_43274364	9	43274364	0.33	9.77E-04	3.01	0.51
DTA	DTA_33	chr9_43274375	9	43274375	0.33	4.99E-04	3.30	0.57
DTA	DTA_34	chr9_44376006	9	44376006	0.32	6.99E-04	3.16	0.54
DTA	DTA_34	chr9_44376029	9	44376029	0.32	6.56E-04	3.18	0.55
DTA	DTA_34	chr9_44376063	9	44376063	0.32	6.56E-04	3.18	0.55
DTA	DTA_35	chr9_55272158	9	55272158	0.42	7.48E-04	3.13	0.54
DTA	DTA_36	chr9_58143240	9	58143240	0.34	1.00E-03	3.00	0.51
DTA	DTA_37	chr9_74531283	9	74531283	0.43	4.07E-04	3.39	0.59
DTA	DTA_38	chr9_142823994	9	142823994	0.01	7.63E-05	4.12	0.74
DTA	DTA_38	chr9_142824003	9	142824003	0.01	7.63E-05	4.12	0.74
DTA	DTA_38	chr9_142824007	9	142824007	0.01	7.63E-05	4.12	0.74
DTA	DTA_38	chr9_142824025	9	142824025	0.01	7.63E-05	4.12	0.74
DTA	DTA_38	chr9_142824028	9	142824028	0.01	7.63E-05	4.12	0.74
DTA	DTA_38	chr9_142864265	9	142864265	0.25	5.78E-04	3.24	0.56
DTA	DTA_38	chr9_143178223	9	143178223	0.22	1.00E-03	3.00	0.51
DTA	DTA_38	chr9_143906355	9	143906355	0.46	5.85E-04	3.23	0.56
DTA	DTA_38	chr9_143952985	9	143952985	0.25	8.80E-05	4.06	0.73
DTA	DTA_38	chr9_143952997	9	143952997	0.25	8.80E-05	4.06	0.73
DTA	DTA_38	chr9_143955414	9	143955414	0.39	9.76E-04	3.01	0.51
DTA	DTA_38	chr9_144036312	9	144036312	0.25	5.33E-04	3.27	0.56
DTA	DTA_38	chr9_144525073	9	144525073	0.27	3.09E-05	4.51	0.82
DTA	DTA_38	chr9_144525127	9	144525127	0.27	3.44E-05	4.46	0.81

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTA	DTA_38	chr9_144525131	9	144525131	0.27	5.09E-05	4.29	0.77
DTA	DTA_38	chr9_144525309	9	144525309	0.26	7.03E-05	4.15	0.75
DTA	DTA_38	chr9_144785234	9	144785234	0.25	4.51E-04	3.35	0.58
DTA	DTA_38	chr9_144785253	9	144785253	0.25	4.51E-04	3.35	0.58
DTA	DTA_38	chr9_144882669	9	144882669	0.27	2.44E-04	3.61	0.63
DTA	DTA_38	chr9_144882687	9	144882687	0.27	9.57E-05	4.02	0.72
DTA	DTA_38	chr9_144882703	9	144882703	0.27	2.44E-04	3.61	0.63
DTA	DTA_38	chr9_144924016	9	144924016	0.01	1.46E-04	3.84	0.68
DTA	DTA_38	chr9_144993643	9	144993643	0.26	7.10E-04	3.15	0.54
DTA	DTA_38	chr9_145514123	9	145514123	0.01	5.81E-05	4.24	0.76
DTA	DTA_38	chr9_145514129	9	145514129	0.01	5.81E-05	4.24	0.76
DTA	DTA_38	chr9_145514132	9	145514132	0.01	5.81E-05	4.24	0.76
DTA	DTA_38	chr9_145514135	9	145514135	0.01	5.81E-05	4.24	0.76
DTA	DTA_38	chr9_145514151	9	145514151	0.01	5.81E-05	4.24	0.76
DTA	DTA_38	chr9_146227374	9	146227374	0.01	1.05E-04	3.98	0.71
DTA	DTA_38	chr9_146228046	9	146228046	0.01	4.71E-05	4.33	0.78
DTA	DTA_38	chr9_146340995	9	146340995	0.01	9.44E-05	4.02	0.72
DTA	DTA_38	chr9_146341061	9	146341061	0.01	5.94E-04	3.23	0.56
DTA	DTA_38	chr9_146341171	9	146341171	0.01	3.79E-05	4.42	0.80
DTA	DTA_38	chr9_146341173	9	146341173	0.01	3.79E-05	4.42	0.80
DTA	DTA_39	chr10_13788786	10	13788786	0.49	9.15E-04	3.04	0.52
DTS	DTS_1	chr1_38725154	1	38725154	0.28	8.53E-04	3.07	0.57
DTS	DTS_2	chr1_48999976	1	48999976	0.45	5.27E-04	3.28	0.62
DTS	DTS_3	chr1_50952023	1	50952023	0.25	9.27E-04	3.03	0.56
DTS	DTS_3	chr1_51293990	1	51293990	0.44	1.01E-03	3.00	0.56
DTS	DTS_3	chr1_51325088	1	51325088	0.46	1.26E-04	3.90	0.76
DTS	DTS_3	chr1_52095418	1	52095418	0.45	1.91E-04	3.72	0.72
DTS	DTS_3	chr1_52097024	1	52097024	0.21	8.80E-04	3.06	0.57
DTS	DTS_3	chr1_52099224	1	52099224	0.23	4.57E-04	3.34	0.63
DTS	DTS_3	chr1_52161058	1	52161058	0.45	2.35E-04	3.63	0.70
DTS	DTS_3	chr1_52161074	1	52161074	0.45	2.49E-04	3.60	0.69
DTS	DTS_3	chr1_52195291	1	52195291	0.22	2.04E-04	3.69	0.71
DTS	DTS_3	chr1_52195333	1	52195333	0.22	2.04E-04	3.69	0.71
DTS	DTS_3	chr1_52253383	1	52253383	0.22	8.88E-04	3.05	0.57
DTS	DTS_3	chr1_52457692	1	52457692	0.23	3.94E-04	3.40	0.65
DTS	DTS_3	chr1_52457711	1	52457711	0.23	7.31E-04	3.14	0.59
DTS	DTS_3	chr1_52605441	1	52605441	0.23	3.49E-05	4.46	0.88
DTS	DTS_3	chr1_52608062	1	52608062	0.23	5.72E-04	3.24	0.61

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTS	DTS_3	chr1_52608097	1	52608097	0.23	8.80E-04	3.06	0.57
DTS	DTS_3	chr1_52608182	1	52608182	0.22	2.56E-04	3.59	0.69
DTS	DTS_4	chr1_290111513	1	290111513	0.25	8.77E-04	3.06	0.57
DTS	DTS_4	chr1_290111534	1	290111534	0.25	8.26E-04	3.08	0.58
DTS	DTS_4	chr1_290111553	1	290111553	0.25	8.77E-04	3.06	0.57
DTS	DTS_4	chr1_290195564	1	290195564	0.25	8.18E-04	3.09	0.58
DTS	DTS_4	chr1_290195595	1	290195595	0.15	1.24E-04	3.91	0.76
DTS	DTS_5	chr2_17095344	2	17095344	0.31	9.24E-04	3.03	0.57
DTS	DTS_5	chr2_17100784	2	17100784	0.30	4.78E-04	3.32	0.63
DTS	DTS_6	chr2_226226273	2	226226273	0.30	7.83E-04	3.11	0.58
DTS	DTS_7	chr3_153764074	3	153764074	0.50	1.21E-06	5.92	1.22
DTS	DTS_7	chr3_153771141	3	153771141	0.20	1.46E-04	3.84	0.74
DTS	DTS_7	chr3_153771151	3	153771151	0.20	2.97E-04	3.53	0.67
DTS	DTS_7	chr3_153771171	3	153771171	0.21	5.90E-04	3.23	0.61
DTS	DTS_7	chr3_153783006	3	153783006	0.44	8.60E-04	3.07	0.57
DTS	DTS_7	chr3_154017208	3	154017208	0.21	9.78E-04	3.01	0.56
DTS	DTS_7	chr3_154017236	3	154017236	0.20	5.10E-04	3.29	0.62
DTS	DTS_7	chr3_154075824	3	154075824	0.29	2.50E-06	5.60	1.15
DTS	DTS_7	chr3_154075870	3	154075870	0.25	1.69E-04	3.77	0.73
DTS	DTS_7	chr3_154075887	3	154075887	0.25	1.69E-04	3.77	0.73
DTS	DTS_7	chr3_154075890	3	154075890	0.25	1.69E-04	3.77	0.73
DTS	DTS_7	chr3_154076084	3	154076084	0.26	7.09E-05	4.15	0.81
DTS	DTS_7	chr3_154077726	3	154077726	0.27	4.99E-06	5.30	1.08
DTS	DTS_7	chr3_154124966	3	154124966	0.49	8.76E-06	5.06	1.02
DTS	DTS_7	chr3_154125085	3	154125085	0.49	4.46E-06	5.35	1.09
DTS	DTS_7	chr3_154408191	3	154408191	0.35	1.01E-06	6.00	1.24
DTS	DTS_7	chr3_154408279	3	154408279	0.20	1.61E-04	3.79	0.73
DTS	DTS_7	chr3_154409508	3	154409508	0.15	4.15E-06	5.38	1.10
DTS	DTS_7	chr3_154409545	3	154409545	0.29	6.63E-06	5.18	1.05
DTS	DTS_7	chr3_154576317	3	154576317	0.32	3.70E-04	3.43	0.65
DTS	DTS_7	chr3_154576332	3	154576332	0.32	3.70E-04	3.43	0.65
DTS	DTS_7	chr3_154576346	3	154576346	0.32	3.70E-04	3.43	0.65
DTS	DTS_7	chr3_154592422	3	154592422	0.29	2.81E-06	5.55	1.14
DTS	DTS_7	chr3_154592481	3	154592481	0.29	2.81E-06	5.55	1.14
DTS	DTS_7	chr3_154592489	3	154592489	0.29	2.81E-06	5.55	1.14
DTS	DTS_7	chr3_154625415	3	154625415	0.29	4.38E-06	5.36	1.09
DTS	DTS_7	chr3_154625420	3	154625420	0.29	3.78E-06	5.42	1.11
DTS	DTS_7	chr3_154627523	3	154627523	0.28	1.85E-07	6.73	1.41

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTS	DTS_7	chr3_154627556	3	154627556	0.28	2.28E-07	6.64	1.39
DTS	DTS_7	chr3_154627560	3	154627560	0.28	3.26E-07	6.49	1.35
DTS	DTS_7	chr3_154650534	3	154650534	0.28	2.39E-07	6.62	1.38
DTS	DTS_7	chr3_154650575	3	154650575	0.28	9.15E-07	6.04	1.25
DTS	DTS_7	chr3_154655030	3	154655030	0.29	5.94E-06	5.23	1.06
DTS	DTS_7	chr3_154655098	3	154655098	0.28	1.19E-05	4.92	0.99
DTS	DTS_7	chr3_154655116	3	154655116	0.28	1.19E-05	4.92	0.99
DTS	DTS_7	chr3_154661548	3	154661548	0.28	1.49E-05	4.83	0.97
DTS	DTS_7	chr3_154732521	3	154732521	0.28	3.53E-06	5.45	1.11
DTS	DTS_7	chr3_154739343	3	154739343	0.25	5.83E-04	3.23	0.61
DTS	DTS_7	chr3_154739847	3	154739847	0.29	2.14E-05	4.67	0.93
DTS	DTS_7	chr3_154739888	3	154739888	0.27	2.58E-05	4.59	0.91
DTS	DTS_7	chr3_154981090	3	154981090	0.28	3.22E-04	3.49	0.67
DTS	DTS_7	chr3_154981137	3	154981137	0.27	8.34E-05	4.08	0.80
DTS	DTS_7	chr3_155091887	3	155091887	0.31	2.43E-06	5.61	1.15
DTS	DTS_7	chr3_155317564	3	155317564	0.28	3.87E-05	4.41	0.87
DTS	DTS_7	chr3_155803339	3	155803339	0.48	1.21E-07	6.92	1.45
DTS	DTS_7	chr3_155803532	3	155803532	0.29	4.10E-07	6.39	1.33
DTS	DTS_7	chr3_155967126	3	155967126	0.28	6.43E-06	5.19	1.05
DTS	DTS_7	chr3_155967168	3	155967168	0.31	5.72E-06	5.24	1.06
DTS	DTS_7	chr3_156071095	3	156071095	0.33	1.19E-04	3.92	0.76
DTS	DTS_7	chr3_156275693	3	156275693	0.27	2.57E-04	3.59	0.69
DTS	DTS_7	chr3_156287541	3	156287541	0.28	1.40E-05	4.85	0.97
DTS	DTS_7	chr3_156287743	3	156287743	0.28	1.10E-05	4.96	1.00
DTS	DTS_7	chr3_156287758	3	156287758	0.48	8.05E-08	7.09	1.49
DTS	DTS_7	chr3_156304726	3	156304726	0.22	3.04E-04	3.52	0.67
DTS	DTS_7	chr3_156434695	3	156434695	0.21	6.51E-04	3.19	0.60
DTS	DTS_7	chr3_156486164	3	156486164	0.28	6.30E-07	6.20	1.29
DTS	DTS_7	chr3_156799845	3	156799845	0.49	2.38E-08	7.62	1.62
DTS	DTS_7	chr3_156799970	3	156799970	0.23	3.76E-05	4.42	0.88
DTS	DTS_7	chr3_156800034	3	156800034	0.48	8.82E-09	8.05	1.72
DTS	DTS_7	chr3_156969980	3	156969980	0.49	8.52E-10	9.07	1.96
DTS	DTS_7	chr3_156969997	3	156969997	0.48	2.77E-09	8.56	1.84
DTS	DTS_7	chr3_157018356	3	157018356	0.26	2.16E-04	3.67	0.71
DTS	DTS_7	chr3_157018359	3	157018359	0.26	2.16E-04	3.67	0.71
DTS	DTS_7	chr3_157018365	3	157018365	0.26	2.16E-04	3.67	0.71
DTS	DTS_7	chr3_157018380	3	157018380	0.21	2.26E-04	3.65	0.70
DTS	DTS_7	chr3_157051502	3	157051502	0.31	1.86E-05	4.73	0.95

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTS	DTS_7	chr3_157417448	3	157417448	0.30	2.22E-07	6.65	1.39
DTS	DTS_7	chr3_157568991	3	157568991	0.29	1.33E-06	5.88	1.21
DTS	DTS_7	chr3_157569114	3	157569114	0.17	2.49E-05	4.60	0.92
DTS	DTS_7	chr3_157576226	3	157576226	0.30	2.20E-08	7.66	1.63
DTS	DTS_7	chr3_157576421	3	157576421	0.30	3.81E-07	6.42	1.34
DTS	DTS_7	chr3_157576589	3	157576589	0.28	5.51E-08	7.26	1.53
DTS	DTS_7	chr3_157576725	3	157576725	0.30	1.80E-07	6.74	1.41
DTS	DTS_7	chr3_157576733	3	157576733	0.29	4.98E-08	7.30	1.54
DTS	DTS_7	chr3_157578664	3	157578664	0.31	4.76E-07	6.32	1.31
DTS	DTS_7	chr3_157578666	3	157578666	0.31	4.15E-07	6.38	1.33
DTS	DTS_7	chr3_157587467	3	157587467	0.26	2.10E-04	3.68	0.71
DTS	DTS_7	chr3_157918560	3	157918560	0.23	3.74E-06	5.43	1.11
DTS	DTS_7	chr3_157938112	3	157938112	0.23	5.38E-06	5.27	1.07
DTS	DTS_7	chr3_157941470	3	157941470	0.23	1.43E-05	4.84	0.97
DTS	DTS_7	chr3_158049977	3	158049977	0.30	3.68E-04	3.43	0.65
DTS	DTS_7	chr3_158049997	3	158049997	0.30	3.68E-04	3.43	0.65
DTS	DTS_7	chr3_158050012	3	158050012	0.30	3.68E-04	3.43	0.65
DTS	DTS_7	chr3_158348209	3	158348209	0.48	1.89E-08	7.72	1.64
DTS	DTS_7	chr3_158348267	3	158348267	0.30	8.85E-05	4.05	0.79
DTS	DTS_7	chr3_158348357	3	158348357	0.26	4.57E-05	4.34	0.86
DTS	DTS_7	chr3_158444445	3	158444445	0.26	3.14E-04	3.50	0.67
DTS	DTS_7	chr3_158451553	3	158451553	0.22	3.67E-05	4.44	0.88
DTS	DTS_7	chr3_158521181	3	158521181	0.26	4.54E-05	4.34	0.86
DTS	DTS_7	chr3_158780416	3	158780416	0.23	5.64E-08	7.25	1.53
DTS	DTS_7	chr3_158780445	3	158780445	0.24	9.36E-08	7.03	1.48
DTS	DTS_7	chr3_158780918	3	158780918	0.30	1.89E-10	9.72	2.12
DTS	DTS_7	chr3_158781033	3	158781033	0.27	5.60E-05	4.25	0.84
DTS	DTS_7	chr3_158790476	3	158790476	0.27	2.98E-05	4.53	0.90
DTS	DTS_7	chr3_158890884	3	158890884	0.48	1.24E-16	15.91	3.62
DTS	DTS_7	chr3_158901755	3	158901755	0.22	4.62E-08	7.34	1.55
DTS	DTS_7	chr3_158972316	3	158972316	0.48	3.07E-14	13.51	3.03
DTS	DTS_7	chr3_158973464	3	158973464	0.23	1.27E-10	9.90	2.16
DTS	DTS_7	chr3_159379133	3	159379133	0.25	3.24E-04	3.49	0.67
DTS	DTS_7	chr3_159380134	3	159380134	0.45	4.23E-04	3.37	0.64
DTS	DTS_7	chr3_159380154	3	159380154	0.45	5.12E-04	3.29	0.62
DTS	DTS_7	chr3_159380236	3	159380236	0.44	6.00E-04	3.22	0.61
DTS	DTS_7	chr3_159380239	3	159380239	0.44	3.12E-04	3.51	0.67
DTS	DTS_7	chr3_159380250	3	159380250	0.44	6.00E-04	3.22	0.61

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTS	DTS_7	chr3_159380253	3	159380253	0.44	6.00E-04	3.22	0.61
DTS	DTS_7	chr3_159381121	3	159381121	0.46	9.04E-04	3.04	0.57
DTS	DTS_7	chr3_159381162	3	159381162	0.46	4.97E-04	3.30	0.62
DTS	DTS_7	chr3_159385192	3	159385192	0.49	8.38E-14	13.08	2.93
DTS	DTS_7	chr3_159385285	3	159385285	0.26	3.79E-04	3.42	0.65
DTS	DTS_7	chr3_159385286	3	159385286	0.26	3.79E-04	3.42	0.65
DTS	DTS_7	chr3_159385309	3	159385309	0.26	5.41E-04	3.27	0.62
DTS	DTS_7	chr3_159388105	3	159388105	0.29	3.21E-13	12.49	2.78
DTS	DTS_7	chr3_159678385	3	159678385	0.46	3.67E-04	3.44	0.65
DTS	DTS_7	chr3_159678426	3	159678426	0.30	1.34E-13	12.87	2.88
DTS	DTS_7	chr3_159678466	3	159678466	0.30	2.61E-13	12.58	2.81
DTS	DTS_7	chr3_159678604	3	159678604	0.24	5.26E-04	3.28	0.62
DTS	DTS_7	chr3_159678635	3	159678635	0.30	5.14E-13	12.29	2.73
DTS	DTS_7	chr3_159678650	3	159678650	0.24	6.07E-04	3.22	0.61
DTS	DTS_7	chr3_159731276	3	159731276	0.26	4.69E-07	6.33	1.32
DTS	DTS_7	chr3_159800933	3	159800933	0.25	7.84E-04	3.11	0.58
DTS	DTS_7	chr3_159800996	3	159800996	0.48	3.64E-12	11.44	2.53
DTS	DTS_7	chr3_159801043	3	159801043	0.28	2.72E-11	10.57	2.32
DTS	DTS_7	chr3_159801091	3	159801091	0.22	2.56E-07	6.59	1.38
DTS	DTS_7	chr3_159801092	3	159801092	0.22	5.79E-07	6.24	1.29
DTS	DTS_7	chr3_159801235	3	159801235	0.30	1.15E-11	10.94	2.41
DTS	DTS_7	chr3_159801239	3	159801239	0.26	2.41E-04	3.62	0.70
DTS	DTS_7	chr3_159807447	3	159807447	0.29	3.96E-13	12.40	2.76
DTS	DTS_7	chr3_159810023	3	159810023	0.29	1.08E-10	9.97	2.18
DTS	DTS_7	chr3_159810124	3	159810124	0.46	9.64E-04	3.02	0.56
DTS	DTS_7	chr3_159818326	3	159818326	0.25	1.39E-05	4.86	0.98
DTS	DTS_7	chr3_159818698	3	159818698	0.23	3.87E-07	6.41	1.33
DTS	DTS_7	chr3_159818701	3	159818701	0.49	5.20E-11	10.28	2.25
DTS	DTS_7	chr3_159819875	3	159819875	0.23	1.62E-05	4.79	0.96
DTS	DTS_7	chr3_159819880	3	159819880	0.23	7.63E-06	5.12	1.04
DTS	DTS_7	chr3_159820547	3	159820547	0.48	9.47E-11	10.02	2.19
DTS	DTS_7	chr3_159861750	3	159861750	0.24	4.74E-07	6.32	1.31
DTS	DTS_7	chr3_159868843	3	159868843	0.29	9.99E-12	11.00	2.42
DTS	DTS_7	chr3_159873162	3	159873162	0.23	1.60E-05	4.80	0.96
DTS	DTS_7	chr3_160665462	3	160665462	0.26	3.71E-04	3.43	0.65
DTS	DTS_7	chr3_160665463	3	160665463	0.50	1.96E-10	9.71	2.11
DTS	DTS_7	chr3_160665476	3	160665476	0.23	8.43E-05	4.07	0.80
DTS	DTS_7	chr3_160665487	3	160665487	0.23	1.38E-04	3.86	0.75

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTS	DTS_7	chr3_160666211	3	160666211	0.23	5.11E-05	4.29	0.85
DTS	DTS_7	chr3_161257076	3	161257076	0.29	1.41E-07	6.85	1.44
DTS	DTS_7	chr3_161257078	3	161257078	0.29	1.41E-07	6.85	1.44
DTS	DTS_7	chr3_161257090	3	161257090	0.29	1.41E-07	6.85	1.44
DTS	DTS_7	chr3_161257096	3	161257096	0.29	1.41E-07	6.85	1.44
DTS	DTS_7	chr3_161259908	3	161259908	0.29	2.63E-08	7.58	1.61
DTS	DTS_7	chr3_161364532	3	161364532	0.37	1.75E-04	3.76	0.73
DTS	DTS_7	chr3_161364604	3	161364604	0.45	1.45E-04	3.84	0.74
DTS	DTS_7	chr3_161369706	3	161369706	0.29	1.33E-09	8.88	1.91
DTS	DTS_7	chr3_161369763	3	161369763	0.29	3.62E-09	8.44	1.81
DTS	DTS_7	chr3_161369818	3	161369818	0.28	1.06E-09	8.97	1.94
DTS	DTS_7	chr3_161369881	3	161369881	0.29	7.63E-10	9.12	1.97
DTS	DTS_7	chr3_161563412	3	161563412	0.23	5.44E-04	3.26	0.62
DTS	DTS_7	chr3_161563431	3	161563431	0.23	7.93E-04	3.10	0.58
DTS	DTS_7	chr3_161563433	3	161563433	0.23	6.14E-04	3.21	0.60
DTS	DTS_7	chr3_161563441	3	161563441	0.23	7.93E-04	3.10	0.58
DTS	DTS_7	chr3_161563491	3	161563491	0.22	6.56E-04	3.18	0.60
DTS	DTS_7	chr3_161573134	3	161573134	0.27	8.27E-08	7.08	1.49
DTS	DTS_7	chr3_161573148	3	161573148	0.22	9.53E-04	3.02	0.56
DTS	DTS_7	chr3_161573155	3	161573155	0.27	2.79E-08	7.55	1.60
DTS	DTS_7	chr3_161573221	3	161573221	0.27	5.54E-09	8.26	1.77
DTS	DTS_7	chr3_161573250	3	161573250	0.27	5.54E-09	8.26	1.77
DTS	DTS_7	chr3_161575037	3	161575037	0.29	2.05E-07	6.69	1.40
DTS	DTS_7	chr3_161575049	3	161575049	0.49	3.59E-06	5.44	1.11
DTS	DTS_7	chr3_161575068	3	161575068	0.49	1.63E-06	5.79	1.19
DTS	DTS_7	chr3_161575090	3	161575090	0.29	3.11E-07	6.51	1.36
DTS	DTS_7	chr3_161575111	3	161575111	0.50	7.29E-06	5.14	1.04
DTS	DTS_7	chr3_161575140	3	161575140	0.50	7.29E-06	5.14	1.04
DTS	DTS_7	chr3_161576642	3	161576642	0.25	2.55E-04	3.59	0.69
DTS	DTS_7	chr3_161638284	3	161638284	0.29	1.13E-10	9.95	2.17
DTS	DTS_7	chr3_161638332	3	161638332	0.41	6.28E-04	3.20	0.60
DTS	DTS_7	chr3_161638336	3	161638336	0.41	6.28E-04	3.20	0.60
DTS	DTS_7	chr3_161650139	3	161650139	0.30	5.74E-09	8.24	1.76
DTS	DTS_7	chr3_161650158	3	161650158	0.22	4.08E-06	5.39	1.10
DTS	DTS_7	chr3_161650198	3	161650198	0.23	4.31E-08	7.37	1.56
DTS	DTS_7	chr3_161650243	3	161650243	0.29	6.24E-08	7.21	1.52
DTS	DTS_7	chr3_161650452	3	161650452	0.28	2.02E-09	8.70	1.87
DTS	DTS_7	chr3_161650457	3	161650457	0.25	2.35E-05	4.63	0.92

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTS	DTS_7	chr3_161650485	3	161650485	0.25	5.59E-05	4.25	0.84
DTS	DTS_7	chr3_161650544	3	161650544	0.23	1.20E-07	6.92	1.45
DTS	DTS_7	chr3_161732785	3	161732785	0.30	6.31E-10	9.20	1.99
DTS	DTS_7	chr3_161969350	3	161969350	0.23	9.55E-05	4.02	0.79
DTS	DTS_7	chr3_161971196	3	161971196	0.24	4.65E-04	3.33	0.63
DTS	DTS_7	chr3_162034696	3	162034696	0.29	4.34E-04	3.36	0.64
DTS	DTS_7	chr3_162034773	3	162034773	0.29	6.98E-05	4.16	0.82
DTS	DTS_7	chr3_162034810	3	162034810	0.29	6.98E-05	4.16	0.82
DTS	DTS_7	chr3_162034827	3	162034827	0.29	6.98E-05	4.16	0.82
DTS	DTS_7	chr3_162034831	3	162034831	0.29	6.98E-05	4.16	0.82
DTS	DTS_7	chr3_162096206	3	162096206	0.29	1.21E-05	4.92	0.99
DTS	DTS_7	chr3_162178736	3	162178736	0.31	2.29E-04	3.64	0.70
DTS	DTS_7	chr3_162179721	3	162179721	0.46	8.70E-04	3.06	0.57
DTS	DTS_7	chr3_162179722	3	162179722	0.46	8.70E-04	3.06	0.57
DTS	DTS_7	chr3_162179943	3	162179943	0.25	1.30E-04	3.89	0.76
DTS	DTS_7	chr3_162180147	3	162180147	0.24	1.28E-04	3.89	0.76
DTS	DTS_7	chr3_162180254	3	162180254	0.24	5.82E-04	3.24	0.61
DTS	DTS_7	chr3_162317866	3	162317866	0.29	1.05E-04	3.98	0.78
DTS	DTS_7	chr3_162318161	3	162318161	0.49	9.25E-04	3.03	0.57
DTS	DTS_7	chr3_162437820	3	162437820	0.29	8.17E-05	4.09	0.80
DTS	DTS_7	chr3_162589163	3	162589163	0.29	1.53E-05	4.81	0.97
DTS	DTS_7	chr3_162597473	3	162597473	0.30	8.36E-05	4.08	0.80
DTS	DTS_7	chr3_162597560	3	162597560	0.31	8.78E-05	4.06	0.79
DTS	DTS_7	chr3_162599378	3	162599378	0.29	4.57E-05	4.34	0.86
DTS	DTS_7	chr3_162599393	3	162599393	0.29	5.44E-05	4.26	0.84
DTS	DTS_7	chr3_162600084	3	162600084	0.29	1.18E-06	5.93	1.22
DTS	DTS_7	chr3_162600110	3	162600110	0.33	3.79E-04	3.42	0.65
DTS	DTS_7	chr3_162606680	3	162606680	0.48	2.39E-04	3.62	0.70
DTS	DTS_7	chr3_162606704	3	162606704	0.48	2.53E-04	3.60	0.69
DTS	DTS_7	chr3_162696407	3	162696407	0.24	8.33E-04	3.08	0.58
DTS	DTS_7	chr3_162696410	3	162696410	0.49	1.42E-04	3.85	0.75
DTS	DTS_7	chr3_162831149	3	162831149	0.30	2.90E-04	3.54	0.68
DTS	DTS_7	chr3_162831181	3	162831181	0.30	3.35E-04	3.47	0.66
DTS	DTS_8	chr3_164524652	3	164524652	0.48	4.07E-04	3.39	0.64
DTS	DTS_8	chr3_164525227	3	164525227	0.44	3.81E-04	3.42	0.65
DTS	DTS_8	chr3_164581009	3	164581009	0.29	5.75E-06	5.24	1.06
DTS	DTS_8	chr3_164581079	3	164581079	0.29	3.65E-07	6.44	1.34
DTS	DTS_8	chr3_164581105	3	164581105	0.28	4.77E-04	3.32	0.63

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTS	DTS_8	chr3_164581160	3	164581160	0.28	7.72E-04	3.11	0.58
DTS	DTS_8	chr3_164587783	3	164587783	0.30	3.44E-06	5.46	1.12
DTS	DTS_8	chr3_164587790	3	164587790	0.30	1.82E-06	5.74	1.18
DTS	DTS_8	chr3_164587830	3	164587830	0.29	3.25E-06	5.49	1.12
DTS	DTS_8	chr3_164587832	3	164587832	0.29	3.25E-06	5.49	1.12
DTS	DTS_8	chr3_164587844	3	164587844	0.29	1.45E-06	5.84	1.20
DTS	DTS_8	chr3_164588707	3	164588707	0.29	1.37E-05	4.86	0.98
DTS	DTS_8	chr3_164589520	3	164589520	0.24	2.01E-04	3.70	0.71
DTS	DTS_8	chr3_164975381	3	164975381	0.30	4.19E-05	4.38	0.87
DTS	DTS_8	chr3_164975717	3	164975717	0.29	2.66E-05	4.57	0.91
DTS	DTS_8	chr3_164978022	3	164978022	0.29	1.28E-05	4.89	0.98
DTS	DTS_8	chr3_164978025	3	164978025	0.29	3.49E-06	5.46	1.11
DTS	DTS_8	chr3_164978057	3	164978057	0.28	2.78E-05	4.56	0.91
DTS	DTS_8	chr3_164978680	3	164978680	0.24	8.01E-04	3.10	0.58
DTS	DTS_8	chr3_164978728	3	164978728	0.29	2.03E-05	4.69	0.94
DTS	DTS_8	chr3_164979640	3	164979640	0.30	6.83E-06	5.17	1.05
DTS	DTS_8	chr3_165017930	3	165017930	0.29	1.39E-06	5.86	1.21
DTS	DTS_8	chr3_165017969	3	165017969	0.29	6.01E-06	5.22	1.06
DTS	DTS_8	chr3_165021955	3	165021955	0.48	1.72E-04	3.76	0.73
DTS	DTS_8	chr3_165021985	3	165021985	0.48	2.88E-04	3.54	0.68
DTS	DTS_8	chr3_165168084	3	165168084	0.48	6.58E-05	4.18	0.82
DTS	DTS_8	chr3_165174695	3	165174695	0.28	1.46E-05	4.84	0.97
DTS	DTS_8	chr3_165174761	3	165174761	0.28	1.79E-05	4.75	0.95
DTS	DTS_8	chr3_165175552	3	165175552	0.28	3.02E-05	4.52	0.90
DTS	DTS_8	chr3_165175866	3	165175866	0.28	9.20E-04	3.04	0.57
DTS	DTS_8	chr3_165178733	3	165178733	0.24	3.83E-04	3.42	0.65
DTS	DTS_8	chr3_165178754	3	165178754	0.24	3.83E-04	3.42	0.65
DTS	DTS_8	chr3_165178771	3	165178771	0.29	1.28E-05	4.89	0.98
DTS	DTS_8	chr3_165446755	3	165446755	0.12	7.57E-04	3.12	0.58
DTS	DTS_8	chr3_165457973	3	165457973	0.49	2.87E-04	3.54	0.68
DTS	DTS_8	chr3_165457997	3	165457997	0.49	2.76E-04	3.56	0.68
DTS	DTS_8	chr3_165458009	3	165458009	0.26	5.41E-04	3.27	0.62
DTS	DTS_8	chr3_165458515	3	165458515	0.48	1.06E-04	3.97	0.78
DTS	DTS_8	chr3_165458612	3	165458612	0.50	1.05E-04	3.98	0.78
DTS	DTS_8	chr3_165704466	3	165704466	0.22	7.39E-05	4.13	0.81
DTS	DTS_8	chr3_165704521	3	165704521	0.28	1.99E-05	4.70	0.94
DTS	DTS_8	chr3_165722971	3	165722971	0.48	4.89E-04	3.31	0.63
DTS	DTS_8	chr3_165728239	3	165728239	0.29	6.22E-05	4.21	0.83

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTS	DTS_8	chr3_165730806	3	165730806	0.24	8.35E-04	3.08	0.57
DTS	DTS_8	chr3_165858588	3	165858588	0.28	6.87E-04	3.16	0.59
DTS	DTS_8	chr3_165862378	3	165862378	0.23	1.90E-04	3.72	0.72
DTS	DTS_8	chr3_165862389	3	165862389	0.23	1.90E-04	3.72	0.72
DTS	DTS_8	chr3_165862414	3	165862414	0.23	1.90E-04	3.72	0.72
DTS	DTS_8	chr3_165862973	3	165862973	0.28	1.64E-04	3.79	0.73
DTS	DTS_8	chr3_166151763	3	166151763	0.22	1.81E-04	3.74	0.72
DTS	DTS_8	chr3_166200130	3	166200130	0.28	7.97E-04	3.10	0.58
DTS	DTS_8	chr3_166206434	3	166206434	0.23	1.99E-04	3.70	0.71
DTS	DTS_8	chr3_166206471	3	166206471	0.23	1.99E-04	3.70	0.71
DTS	DTS_8	chr3_166206478	3	166206478	0.22	3.64E-04	3.44	0.65
DTS	DTS_8	chr3_166430237	3	166430237	0.28	4.79E-04	3.32	0.63
DTS	DTS_8	chr3_166430285	3	166430285	0.28	5.13E-04	3.29	0.62
DTS	DTS_8	chr3_166430306	3	166430306	0.30	7.36E-05	4.13	0.81
DTS	DTS_8	chr3_166430331	3	166430331	0.29	1.06E-04	3.97	0.77
DTS	DTS_8	chr3_166430359	3	166430359	0.30	7.36E-05	4.13	0.81
DTS	DTS_8	chr3_166450172	3	166450172	0.46	9.87E-04	3.01	0.56
DTS	DTS_8	chr3_166450332	3	166450332	0.27	9.79E-04	3.01	0.56
DTS	DTS_8	chr3_166451880	3	166451880	0.27	2.17E-04	3.66	0.71
DTS	DTS_8	chr3_166482619	3	166482619	0.28	5.62E-04	3.25	0.61
DTS	DTS_8	chr3_166482627	3	166482627	0.29	4.39E-04	3.36	0.64
DTS	DTS_8	chr3_166482663	3	166482663	0.28	5.62E-04	3.25	0.61
DTS	DTS_8	chr3_166691373	3	166691373	0.28	5.76E-04	3.24	0.61
DTS	DTS_8	chr3_166692440	3	166692440	0.27	6.53E-05	4.19	0.82
DTS	DTS_8	chr3_166799753	3	166799753	0.27	6.57E-04	3.18	0.60
DTS	DTS_8	chr3_166997981	3	166997981	0.50	9.22E-04	3.04	0.57
DTS	DTS_8	chr3_167394795	3	167394795	0.27	4.05E-05	4.39	0.87
DTS	DTS_8	chr3_167394810	3	167394810	0.27	4.05E-05	4.39	0.87
DTS	DTS_8	chr3_167394822	3	167394822	0.27	4.05E-05	4.39	0.87
DTS	DTS_8	chr3_167431049	3	167431049	0.26	7.40E-06	5.13	1.04
DTS	DTS_8	chr3_167446823	3	167446823	0.26	3.06E-04	3.51	0.67
DTS	DTS_8	chr3_167446844	3	167446844	0.26	2.21E-04	3.65	0.70
DTS	DTS_9	chr3_168629919	3	168629919	0.23	8.10E-04	3.09	0.58
DTS	DTS_9	chr3_168629926	3	168629926	0.23	8.10E-04	3.09	0.58
DTS	DTS_9	chr3_168629983	3	168629983	0.24	9.16E-04	3.04	0.57
DTS	DTS_9	chr3_168697077	3	168697077	0.26	3.21E-04	3.49	0.67
DTS	DTS_9	chr3_168837075	3	168837075	0.25	7.85E-04	3.11	0.58
DTS	DTS_9	chr3_169080486	3	169080486	0.24	8.85E-04	3.05	0.57

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTS	DTS_10	chr3_205695524	3	205695524	0.22	5.78E-04	3.24	0.61
DTS	DTS_10	chr3_205695577	3	205695577	0.22	5.78E-04	3.24	0.61
DTS	DTS_10	chr3_205970789	3	205970789	0.22	2.75E-04	3.56	0.68
DTS	DTS_10	chr3_205970811	3	205970811	0.22	2.29E-04	3.64	0.70
DTS	DTS_10	chr3_206153771	3	206153771	0.22	9.53E-04	3.02	0.56
DTS	DTS_10	chr3_206193036	3	206193036	0.22	4.30E-04	3.37	0.64
DTS	DTS_10	chr3_206195670	3	206195670	0.22	7.11E-04	3.15	0.59
DTS	DTS_10	chr3_206196324	3	206196324	0.23	9.23E-05	4.03	0.79
DTS	DTS_10	chr3_206552052	3	206552052	0.22	1.23E-04	3.91	0.76
DTS	DTS_10	chr3_206586257	3	206586257	0.22	1.43E-04	3.85	0.75
DTS	DTS_10	chr3_206846979	3	206846979	0.20	7.00E-04	3.16	0.59
DTS	DTS_10	chr3_206847034	3	206847034	0.20	7.00E-04	3.16	0.59
DTS	DTS_10	chr3_206847070	3	206847070	0.19	7.57E-04	3.12	0.58
DTS	DTS_10	chr3_206847075	3	206847075	0.19	7.57E-04	3.12	0.58
DTS	DTS_10	chr3_206847106	3	206847106	0.19	7.57E-04	3.12	0.58
DTS	DTS_10	chr3_206847130	3	206847130	0.19	7.57E-04	3.12	0.58
DTS	DTS_10	chr3_206847136	3	206847136	0.19	7.57E-04	3.12	0.58
DTS	DTS_10	chr3_206943785	3	206943785	0.19	8.24E-05	4.08	0.80
DTS	DTS_10	chr3_206953158	3	206953158	0.18	3.90E-04	3.41	0.65
DTS	DTS_10	chr3_206953193	3	206953193	0.18	4.38E-04	3.36	0.64
DTS	DTS_10	chr3_207151139	3	207151139	0.20	8.98E-04	3.05	0.57
DTS	DTS_10	chr3_207151171	3	207151171	0.20	8.51E-04	3.07	0.57
DTS	DTS_10	chr3_207151227	3	207151227	0.21	8.15E-04	3.09	0.58
DTS	DTS_10	chr3_207151231	3	207151231	0.21	7.48E-04	3.13	0.59
DTS	DTS_10	chr3_207151266	3	207151266	0.20	3.86E-04	3.41	0.65
DTS	DTS_10	chr3_207178337	3	207178337	0.20	1.03E-04	3.99	0.78
DTS	DTS_10	chr3_207178370	3	207178370	0.20	2.22E-04	3.65	0.70
DTS	DTS_10	chr3_207250765	3	207250765	0.20	7.70E-04	3.11	0.58
DTS	DTS_10	chr3_207250860	3	207250860	0.20	9.29E-05	4.03	0.79
DTS	DTS_10	chr3_207250878	3	207250878	0.20	8.32E-05	4.08	0.80
DTS	DTS_10	chr3_207755713	3	207755713	0.19	1.00E-03	3.00	0.56
DTS	DTS_10	chr3_207766422	3	207766422	0.19	6.94E-05	4.16	0.82
DTS	DTS_10	chr3_207768822	3	207768822	0.20	1.17E-04	3.93	0.77
DTS	DTS_10	chr3_207772297	3	207772297	0.20	8.30E-04	3.08	0.58
DTS	DTS_10	chr3_207901009	3	207901009	0.19	3.31E-04	3.48	0.66
DTS	DTS_10	chr3_207901044	3	207901044	0.19	3.31E-04	3.48	0.66
DTS	DTS_10	chr3_207988505	3	207988505	0.19	3.78E-04	3.42	0.65
DTS	DTS_10	chr3_208034892	3	208034892	0.19	1.92E-04	3.72	0.72

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTS	DTS_10	chr3_208034904	3	208034904	0.19	3.56E-04	3.45	0.66
DTS	DTS_10	chr3_208266797	3	208266797	0.20	5.27E-04	3.28	0.62
DTS	DTS_10	chr3_208404237	3	208404237	0.19	6.14E-04	3.21	0.60
DTS	DTS_10	chr3_208467111	3	208467111	0.21	3.64E-04	3.44	0.65
DTS	DTS_10	chr3_208537135	3	208537135	0.18	8.65E-04	3.06	0.57
DTS	DTS_10	chr3_208543150	3	208543150	0.19	6.82E-04	3.17	0.59
DTS	DTS_10	chr3_208543193	3	208543193	0.20	4.42E-04	3.35	0.64
DTS	DTS_10	chr3_208612881	3	208612881	0.20	1.80E-04	3.74	0.72
DTS	DTS_10	chr3_208612887	3	208612887	0.20	1.80E-04	3.74	0.72
DTS	DTS_10	chr3_208612892	3	208612892	0.20	1.80E-04	3.74	0.72
DTS	DTS_10	chr3_208612897	3	208612897	0.20	1.80E-04	3.74	0.72
DTS	DTS_10	chr3_208612904	3	208612904	0.20	1.80E-04	3.74	0.72
DTS	DTS_10	chr3_208614921	3	208614921	0.19	3.82E-04	3.42	0.65
DTS	DTS_10	chr3_208617392	3	208617392	0.19	5.64E-04	3.25	0.61
DTS	DTS_10	chr3_208617442	3	208617442	0.20	1.02E-04	3.99	0.78
DTS	DTS_10	chr3_208617481	3	208617481	0.20	1.02E-04	3.99	0.78
DTS	DTS_10	chr3_208618864	3	208618864	0.20	6.53E-05	4.19	0.82
DTS	DTS_10	chr3_208625340	3	208625340	0.21	1.34E-04	3.87	0.75
DTS	DTS_10	chr3_208916795	3	208916795	0.21	3.35E-04	3.48	0.66
DTS	DTS_10	chr3_208969488	3	208969488	0.21	9.82E-04	3.01	0.56
DTS	DTS_10	chr3_209009436	3	209009436	0.21	4.38E-04	3.36	0.64
DTS	DTS_10	chr3_209009471	3	209009471	0.21	3.66E-04	3.44	0.65
DTS	DTS_10	chr3_209010840	3	209010840	0.21	2.47E-04	3.61	0.69
DTS	DTS_10	chr3_209011664	3	209011664	0.21	5.58E-04	3.25	0.61
DTS	DTS_10	chr3_209024427	3	209024427	0.22	7.48E-04	3.13	0.59
DTS	DTS_10	chr3_209024481	3	209024481	0.21	8.60E-04	3.07	0.57
DTS	DTS_10	chr3_209734137	3	209734137	0.22	3.33E-04	3.48	0.66
DTS	DTS_11	chr4_194718012	4	194718012	0.15	1.00E-03	3.00	0.56
DTS	DTS_12	chr5_4308923	5	4308923	0.38	1.99E-04	3.70	0.71
DTS	DTS_13	chr5_18583394	5	18583394	0.01	1.06E-04	3.97	0.78
DTS	DTS_14	chr5_186960498	5	186960498	0.22	7.32E-04	3.14	0.59
DTS	DTS_14	chr5_186971839	5	186971839	0.26	9.62E-04	3.02	0.56
DTS	DTS_14	chr5_187083530	5	187083530	0.28	9.46E-04	3.02	0.56
DTS	DTS_14	chr5_187083543	5	187083543	0.27	6.61E-04	3.18	0.60
DTS	DTS_15	chr6_149671374	6	149671374	0.18	4.56E-04	3.34	0.63
DTS	DTS_16	chr6_151823130	6	151823130	0.28	1.14E-04	3.94	0.77
DTS	DTS_16	chr6_152250291	6	152250291	0.29	9.73E-04	3.01	0.56
DTS	DTS_16	chr6_152304450	6	152304450	0.28	3.09E-04	3.51	0.67

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTS	DTS_16	chr6_152304479	6	152304479	0.29	5.00E-04	3.30	0.62
DTS	DTS_17	chr7_151202724	7	151202724	0.25	6.70E-04	3.17	0.60
DTS	DTS_17	chr7_151384678	7	151384678	0.27	1.48E-04	3.83	0.74
DTS	DTS_17	chr7_152006225	7	152006225	0.25	3.81E-04	3.42	0.65
DTS	DTS_18	chr8_130926879	8	130926879	0.23	4.32E-04	3.36	0.64
DTS	DTS_18	chr8_131334405	8	131334405	0.24	6.79E-04	3.17	0.59
DTS	DTS_18	chr8_131335535	8	131335535	0.24	9.50E-04	3.02	0.56
DTS	DTS_18	chr8_132170951	8	132170951	0.24	9.88E-04	3.01	0.56
DTS	DTS_18	chr8_132525678	8	132525678	0.24	7.93E-04	3.10	0.58
DTS	DTS_18	chr8_132525745	8	132525745	0.24	5.66E-04	3.25	0.61
DTS	DTS_18	chr8_132525919	8	132525919	0.23	2.09E-04	3.68	0.71
DTS	DTS_19	chr8_133566383	8	133566383	0.26	1.68E-04	3.77	0.73
DTS	DTS_19	chr8_133566410	8	133566410	0.26	2.33E-04	3.63	0.70
DTS	DTS_19	chr8_133566422	8	133566422	0.26	2.33E-04	3.63	0.70
DTS	DTS_19	chr8_133949014	8	133949014	0.24	5.95E-04	3.23	0.61
DTS	DTS_19	chr8_134006372	8	134006372	0.23	4.04E-04	3.39	0.64
DTS	DTS_19	chr8_134012311	8	134012311	0.24	6.37E-04	3.20	0.60
DTS	DTS_19	chr8_134229264	8	134229264	0.24	4.84E-04	3.32	0.63
DTS	DTS_19	chr8_134229576	8	134229576	0.24	1.18E-04	3.93	0.77
DTS	DTS_19	chr8_134230097	8	134230097	0.24	9.54E-05	4.02	0.79
DTS	DTS_19	chr8_134230103	8	134230103	0.24	8.26E-05	4.08	0.80
DTS	DTS_19	chr8_134378632	8	134378632	0.24	5.94E-04	3.23	0.61
DTS	DTS_19	chr8_134378654	8	134378654	0.24	6.69E-04	3.17	0.60
DTS	DTS_19	chr8_135154178	8	135154178	0.24	2.77E-04	3.56	0.68
DTS	DTS_20	chr8_168682612	8	168682612	0.47	6.94E-04	3.16	0.59
DTS	DTS_21	chr9_26817330	9	26817330	0.33	2.79E-04	3.55	0.68
DTS	DTS_21	chr9_26817897	9	26817897	0.32	3.21E-04	3.49	0.67
DTS	DTS_21	chr9_26817900	9	26817900	0.32	2.22E-04	3.65	0.70
DTS	DTS_21	chr9_26895422	9	26895422	0.33	5.06E-04	3.30	0.62
DTS	DTS_21	chr9_26895450	9	26895450	0.33	3.22E-04	3.49	0.67
DTS	DTS_21	chr9_26942084	9	26942084	0.33	2.28E-04	3.64	0.70
DTS	DTS_21	chr9_27171435	9	27171435	0.41	3.90E-04	3.41	0.65
DTS	DTS_21	chr9_27222938	9	27222938	0.43	1.00E-03	3.00	0.56
DTS	DTS_21	chr9_27229780	9	27229780	0.43	1.69E-04	3.77	0.73
DTS	DTS_21	chr9_27229781	9	27229781	0.40	5.67E-06	5.25	1.07
DTS	DTS_22	chr9_31209295	9	31209295	0.42	5.70E-04	3.24	0.61
DTS	DTS_22	chr9_31290915	9	31290915	0.42	1.71E-04	3.77	0.73
DTS	DTS_22	chr9_31384764	9	31384764	0.43	3.05E-05	4.52	0.90

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTS	DTS_22	chr9_31384808	9	31384808	0.43	2.82E-05	4.55	0.91
DTS	DTS_22	chr9_31384821	9	31384821	0.43	1.80E-05	4.74	0.95
DTS	DTS_22	chr9_31386162	9	31386162	0.44	1.74E-04	3.76	0.73
DTS	DTS_22	chr9_31386167	9	31386167	0.44	2.12E-04	3.67	0.71
DTS	DTS_22	chr9_31386190	9	31386190	0.44	1.97E-04	3.71	0.71
DTS	DTS_22	chr9_31386218	9	31386218	0.44	1.97E-04	3.71	0.71
DTS	DTS_22	chr9_31386231	9	31386231	0.44	2.46E-04	3.61	0.69
DTS	DTS_22	chr9_31386233	9	31386233	0.44	2.46E-04	3.61	0.69
DTS	DTS_22	chr9_32251801	9	32251801	0.40	5.83E-04	3.23	0.61
DTS	DTS_22	chr9_32335308	9	32335308	0.43	2.84E-04	3.55	0.68
DTS	DTS_23	chr9_33714704	9	33714704	0.32	2.21E-04	3.65	0.70
DTS	DTS_23	chr9_33800482	9	33800482	0.47	9.05E-04	3.04	0.57
DTS	DTS_23	chr9_34242075	9	34242075	0.43	8.99E-04	3.05	0.57
DTS	DTS_23	chr9_34242135	9	34242135	0.43	8.99E-04	3.05	0.57
DTS	DTS_24	chr9_35969543	9	35969543	0.43	2.95E-04	3.53	0.68
DTS	DTS_25	chr9_37405983	9	37405983	0.43	3.86E-04	3.41	0.65
DTS	DTS_25	chr9_37405996	9	37405996	0.43	3.86E-04	3.41	0.65
DTS	DTS_25	chr9_37406005	9	37406005	0.43	9.32E-04	3.03	0.56
DTS	DTS_25	chr9_37406020	9	37406020	0.43	2.92E-04	3.53	0.68
DTS	DTS_25	chr9_37520724	9	37520724	0.40	5.37E-04	3.27	0.62
DTS	DTS_25	chr9_37700056	9	37700056	0.42	6.49E-04	3.19	0.60
DTS	DTS_26	chr9_39393365	9	39393365	0.43	2.00E-04	3.70	0.71
DTS	DTS_27	chr9_40600623	9	40600623	0.33	4.58E-04	3.34	0.63
DTS	DTS_27	chr9_40600728	9	40600728	0.42	3.89E-04	3.41	0.65
DTS	DTS_27	chr9_40772377	9	40772377	0.30	6.53E-04	3.19	0.60
DTS	DTS_27	chr9_40772401	9	40772401	0.30	6.53E-04	3.19	0.60
DTS	DTS_27	chr9_40773772	9	40773772	0.41	8.57E-04	3.07	0.57
DTS	DTS_27	chr9_40773820	9	40773820	0.40	6.20E-04	3.21	0.60
DTS	DTS_27	chr9_41050223	9	41050223	0.43	9.90E-04	3.00	0.56
DTS	DTS_28	chr9_42840883	9	42840883	0.43	3.56E-05	4.45	0.88
DTS	DTS_28	chr9_42840886	9	42840886	0.43	4.26E-05	4.37	0.86
DTS	DTS_28	chr9_42840888	9	42840888	0.43	4.26E-05	4.37	0.86
DTS	DTS_28	chr9_43274338	9	43274338	0.33	8.33E-04	3.08	0.58
DTS	DTS_28	chr9_43274375	9	43274375	0.33	4.56E-04	3.34	0.63
DTS	DTS_28	chr9_43680157	9	43680157	0.42	6.31E-04	3.20	0.60
DTS	DTS_29	chr9_45640324	9	45640324	0.43	4.92E-04	3.31	0.63
DTS	DTS_30	chr9_61340315	9	61340315	0.42	8.65E-04	3.06	0.57
DTS	DTS_31	chr9_63969437	9	63969437	0.43	8.79E-04	3.06	0.57

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTS	DTS_32	chr9_69176207	9	69176207	0.42	9.35E-04	3.03	0.56
DTS	DTS_33	chr9_73245840	9	73245840	0.42	4.41E-04	3.36	0.64
DTS	DTS_34	chr9_74531283	9	74531283	0.43	7.34E-04	3.13	0.59
DTS	DTS_35	chr9_106626910	9	106626910	0.37	4.19E-04	3.38	0.64
DTS	DTS_36	chr9_131520078	9	131520078	0.22	6.55E-04	3.18	0.60
DTS	DTS_36	chr9_131669536	9	131669536	0.23	1.66E-04	3.78	0.73
DTS	DTS_36	chr9_131669703	9	131669703	0.23	1.90E-04	3.72	0.72
DTS	DTS_36	chr9_131671104	9	131671104	0.24	8.51E-04	3.07	0.57
DTS	DTS_36	chr9_131721502	9	131721502	0.23	6.65E-04	3.18	0.60
DTS	DTS_36	chr9_131721506	9	131721506	0.23	6.65E-04	3.18	0.60
DTS	DTS_37	chr9_133587476	9	133587476	0.22	5.46E-04	3.26	0.62
DTS	DTS_38	chr9_143952985	9	143952985	0.25	5.21E-04	3.28	0.62
DTS	DTS_38	chr9_143952997	9	143952997	0.25	5.21E-04	3.28	0.62
DTS	DTS_38	chr9_144525073	9	144525073	0.27	4.93E-04	3.31	0.63
DTS	DTS_38	chr9_144525127	9	144525127	0.27	3.65E-04	3.44	0.65
DTS	DTS_38	chr9_144525131	9	144525131	0.27	6.16E-04	3.21	0.60
DTS	DTS_38	chr9_144882687	9	144882687	0.27	5.88E-04	3.23	0.61

B5. SNPs above 3 LOD for B73olc1 x Tx903 subpopulation using the 12,740 marker subset for plant height (PH), ear height (EH), days to anthesis (DTA) and days to silking (DTS). QTL were classified by group adjacent SNP that differ by less than 1 Mbps.

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
PH	PH_1	chr1_275693848	1	275693848	0.49	1.91E-02	1.72	3.03
PH	PH_1	chr1_275766083	1	275766083	0.48	9.11E-03	2.04	3.77
PH	PH_1	chr1_276323701	1	276323701	0.50	9.21E-03	2.04	3.76
PH	PH_2	chr2_10789995	2	10789995	0.50	9.72E-04	3.01	6.14
PH	PH_3	chr2_186789026	2	186789026	0.50	1.34E-02	1.87	3.38
PH	PH_4	chr2_194119308	2	194119308	0.50	8.76E-03	2.06	3.81
PH	PH_5	chr2_195286651	2	195286651	0.41	1.77E-02	1.75	3.11
PH	PH_6	chr3_156796659	3	156796659	0.36	1.37E-02	1.86	3.36
PH	PH_6	chr3_156796666	3	156796666	0.36	1.37E-02	1.86	3.36
PH	PH_6	chr3_157572126	3	157572126	0.31	4.51E-03	2.35	4.50
PH	PH_6	chr3_157572131	3	157572131	0.31	4.51E-03	2.35	4.50
PH	PH_6	chr3_157572136	3	157572136	0.31	4.51E-03	2.35	4.50
PH	PH_6	chr3_157572152	3	157572152	0.31	4.51E-03	2.35	4.50
PH	PH_6	chr3_157572182	3	157572182	0.31	4.51E-03	2.35	4.50
PH	PH_6	chr3_157761578	3	157761578	0.33	7.56E-05	4.12	9.02
PH	PH_6	chr3_157761602	3	157761602	0.35	6.75E-04	3.17	6.54
PH	PH_6	chr3_157761610	3	157761610	0.33	4.37E-05	4.36	9.66
PH	PH_6	chr3_157773525	3	157773525	0.31	9.29E-05	4.03	8.78
PH	PH_6	chr3_158348209	3	158348209	0.32	3.81E-03	2.42	4.67
PH	PH_6	chr3_158650511	3	158650511	0.29	6.77E-04	3.17	6.54
PH	PH_6	chr3_158890884	3	158890884	0.29	1.73E-03	2.76	5.51
PH	PH_6	chr3_159380134	3	159380134	0.29	1.46E-05	4.84	10.96
PH	PH_6	chr3_159380154	3	159380154	0.29	1.46E-05	4.84	10.96
PH	PH_6	chr3_159380194	3	159380194	0.38	4.96E-03	2.30	4.40
PH	PH_6	chr3_159380236	3	159380236	0.27	1.49E-04	3.83	8.23
PH	PH_6	chr3_159380239	3	159380239	0.27	1.49E-04	3.83	8.23
PH	PH_6	chr3_159380248	3	159380248	0.27	1.49E-04	3.83	8.23
PH	PH_6	chr3_159380250	3	159380250	0.27	1.49E-04	3.83	8.23
PH	PH_6	chr3_159380253	3	159380253	0.27	1.49E-04	3.83	8.23
PH	PH_6	chr3_159381121	3	159381121	0.29	3.34E-06	5.48	12.75
PH	PH_6	chr3_159381162	3	159381162	0.30	1.07E-06	5.97	14.17
PH	PH_6	chr3_159381256	3	159381256	0.29	1.35E-05	4.87	11.05
PH	PH_6	chr3_159385192	3	159385192	0.30	1.02E-03	2.99	6.08
PH	PH_6	chr3_159678385	3	159678385	0.28	1.30E-04	3.89	8.39

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
PH	PH_6	chr3_159801025	3	159801025	0.30	6.48E-04	3.19	6.58
PH	PH_6	chr3_159810124	3	159810124	0.29	1.77E-05	4.75	10.72
PH	PH_6	chr3_159818701	3	159818701	0.31	1.05E-04	3.98	8.64
PH	PH_6	chr3_159820547	3	159820547	0.31	5.80E-05	4.24	9.32
PH	PH_6	chr3_159870315	3	159870315	0.26	1.15E-02	1.94	3.54
PH	PH_6	chr3_159870409	3	159870409	0.35	7.31E-05	4.14	9.05
PH	PH_6	chr3_159870494	3	159870494	0.30	1.92E-03	2.72	5.40
PH	PH_7	chr3_161259884	3	161259884	0.29	9.00E-04	3.05	6.22
PH	PH_7	chr3_161259896	3	161259896	0.29	9.00E-04	3.05	6.22
PH	PH_7	chr3_161364532	3	161364532	0.27	3.26E-03	2.49	4.84
PH	PH_7	chr3_161364626	3	161364626	0.27	3.90E-03	2.41	4.65
PH	PH_7	chr3_161364643	3	161364643	0.27	3.90E-03	2.41	4.65
PH	PH_7	chr3_161563404	3	161563404	0.29	8.17E-05	4.09	8.93
PH	PH_7	chr3_161573899	3	161573899	0.29	1.21E-03	2.92	5.90
PH	PH_7	chr3_161574131	3	161574131	0.29	5.74E-04	3.24	6.72
PH	PH_7	chr3_161575030	3	161575030	0.30	5.17E-04	3.29	6.83
PH	PH_7	chr3_161575049	3	161575049	0.30	5.17E-04	3.29	6.83
PH	PH_7	chr3_161575068	3	161575068	0.30	5.17E-04	3.29	6.83
PH	PH_7	chr3_161575111	3	161575111	0.31	1.23E-04	3.91	8.46
PH	PH_7	chr3_161575140	3	161575140	0.31	1.23E-04	3.91	8.46
PH	PH_7	chr3_161971270	3	161971270	0.29	1.34E-03	2.87	5.79
PH	PH_7	chr3_162064220	3	162064220	0.32	2.11E-03	2.68	5.30
PH	PH_7	chr3_162096179	3	162096179	0.32	8.82E-05	4.05	8.84
PH	PH_7	chr3_162096214	3	162096214	0.32	8.82E-05	4.05	8.84
PH	PH_7	chr3_162097205	3	162097205	0.31	6.10E-04	3.21	6.65
PH	PH_7	chr3_162097279	3	162097279	0.32	1.52E-04	3.82	8.21
PH	PH_7	chr3_162179721	3	162179721	0.31	1.17E-04	3.93	8.51
PH	PH_7	chr3_162179722	3	162179722	0.31	1.17E-04	3.93	8.51
PH	PH_7	chr3_162318003	3	162318003	0.33	3.82E-05	4.42	9.81
PH	PH_7	chr3_162318161	3	162318161	0.32	9.01E-05	4.05	8.81
PH	PH_7	chr3_162318227	3	162318227	0.32	6.61E-05	4.18	9.17
PH	PH_7	chr3_162318357	3	162318357	0.32	1.97E-04	3.71	7.92
PH	PH_7	chr3_162318376	3	162318376	0.31	1.23E-04	3.91	8.46
PH	PH_7	chr3_162587602	3	162587602	0.31	1.07E-04	3.97	8.62
PH	PH_7	chr3_162587662	3	162587662	0.31	6.15E-04	3.21	6.64
PH	PH_7	chr3_162696410	3	162696410	0.31	1.67E-04	3.78	8.10
PH	PH_8	chr3_164155282	3	164155282	0.29	2.72E-04	3.57	7.55
PH	PH_8	chr3_164250193	3	164250193	0.36	1.13E-04	3.95	8.55

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
PH	PH_8	chr3_164524652	3	164524652	0.30	1.02E-04	3.99	8.67
PH	PH_8	chr3_164525227	3	164525227	0.29	2.83E-03	2.55	4.99
PH	PH_8	chr3_164587464	3	164587464	0.31	7.67E-05	4.11	9.00
PH	PH_8	chr3_164589024	3	164589024	0.33	2.53E-05	4.60	10.30
PH	PH_8	chr3_164884525	3	164884525	0.32	8.92E-04	3.05	6.23
PH	PH_8	chr3_164967251	3	164967251	0.33	2.51E-04	3.60	7.64
PH	PH_8	chr3_164976865	3	164976865	0.32	4.58E-04	3.34	6.97
PH	PH_8	chr3_164976883	3	164976883	0.32	4.58E-04	3.34	6.97
PH	PH_8	chr3_165017962	3	165017962	0.29	2.83E-04	3.55	7.51
PH	PH_8	chr3_165021955	3	165021955	0.29	1.47E-03	2.83	5.69
PH	PH_8	chr3_165021985	3	165021985	0.29	1.47E-03	2.83	5.69
PH	PH_8	chr3_165168084	3	165168084	0.31	8.66E-05	4.06	8.86
PH	PH_8	chr3_165412676	3	165412676	0.33	2.75E-04	3.56	7.54
PH	PH_8	chr3_165412700	3	165412700	0.32	3.12E-05	4.51	10.05
PH	PH_8	chr3_165412702	3	165412702	0.32	3.12E-05	4.51	10.05
PH	PH_8	chr3_165457973	3	165457973	0.35	1.21E-04	3.92	8.48
PH	PH_8	chr3_165457997	3	165457997	0.35	1.21E-04	3.92	8.48
PH	PH_8	chr3_165458043	3	165458043	0.30	5.73E-04	3.24	6.72
PH	PH_8	chr3_165458062	3	165458062	0.31	5.17E-04	3.29	6.83
PH	PH_8	chr3_165458089	3	165458089	0.30	5.73E-04	3.24	6.72
PH	PH_8	chr3_165458092	3	165458092	0.30	5.73E-04	3.24	6.72
PH	PH_8	chr3_165458515	3	165458515	0.31	4.65E-04	3.33	6.95
PH	PH_8	chr3_165458612	3	165458612	0.33	1.26E-04	3.90	8.43
PH	PH_8	chr3_165461844	3	165461844	0.31	5.33E-05	4.27	9.42
PH	PH_8	chr3_165722971	3	165722971	0.31	1.12E-04	3.95	8.56
PH	PH_8	chr3_165862848	3	165862848	0.32	8.41E-04	3.08	6.30
PH	PH_8	chr3_165862913	3	165862913	0.32	9.68E-04	3.01	6.14
PH	PH_8	chr3_166151687	3	166151687	0.33	1.00E-03	3.00	6.11
PH	PH_8	chr3_166152102	3	166152102	0.32	7.07E-04	3.15	6.49
PH	PH_8	chr3_166203067	3	166203067	0.31	9.58E-03	2.02	3.72
PH	PH_8	chr3_166203075	3	166203075	0.31	9.58E-03	2.02	3.72
PH	PH_8	chr3_166203095	3	166203095	0.31	9.58E-03	2.02	3.72
PH	PH_8	chr3_166203195	3	166203195	0.30	4.68E-03	2.33	4.46
PH	PH_8	chr3_166203740	3	166203740	0.31	5.19E-04	3.28	6.83
PH	PH_8	chr3_166397950	3	166397950	0.30	1.72E-02	1.76	3.13
PH	PH_9	chr3_179415178	3	179415178	0.45	1.94E-02	1.71	3.01
PH	PH_10	chr3_187474573	3	187474573	0.44	1.39E-02	1.86	3.34
PH	PH_11	chr4_20513785	4	20513785	0.32	1.46E-02	1.84	3.30

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
PH	PH_12	chr4_38021920	4	38021920	0.48	1.64E-02	1.78	3.18
PH	PH_13	chr4_183912882	4	183912882	0.44	1.83E-02	1.74	3.08
PH	PH_13	chr4_183912884	4	183912884	0.44	1.83E-02	1.74	3.08
PH	PH_13	chr4_183913059	4	183913059	0.43	1.84E-02	1.74	3.07
PH	PH_14	chr4_186658840	4	186658840	0.45	1.07E-02	1.97	3.61
PH	PH_14	chr4_186658864	4	186658864	0.45	1.07E-02	1.97	3.61
PH	PH_14	chr4_186710528	4	186710528	0.44	1.85E-02	1.73	3.06
PH	PH_14	chr4_186826235	4	186826235	0.44	1.32E-02	1.88	3.40
PH	PH_14	chr4_186838011	4	186838011	0.42	8.28E-03	2.08	3.87
PH	PH_14	chr4_187034124	4	187034124	0.42	1.19E-02	1.92	3.50
PH	PH_14	chr4_187273386	4	187273386	0.44	7.50E-03	2.12	3.97
PH	PH_14	chr4_187273397	4	187273397	0.44	7.50E-03	2.12	3.97
PH	PH_14	chr4_187289899	4	187289899	0.41	7.26E-03	2.14	4.00
PH	PH_14	chr4_187290014	4	187290014	0.37	1.96E-02	1.71	3.01
PH	PH_14	chr4_187290019	4	187290019	0.40	3.96E-03	2.40	4.63
PH	PH_14	chr4_187418583	4	187418583	0.41	9.68E-03	2.01	3.71
PH	PH_14	chr4_187465455	4	187465455	0.40	8.38E-03	2.08	3.86
PH	PH_14	chr4_187465767	4	187465767	0.43	1.95E-02	1.71	3.01
PH	PH_14	chr4_187465778	4	187465778	0.43	1.95E-02	1.71	3.01
PH	PH_14	chr4_188328465	4	188328465	0.40	8.26E-03	2.08	3.87
PH	PH_15	chr5_187003594	5	187003594	0.47	1.16E-02	1.94	3.53
PH	PH_16	chr5_214608613	5	214608613	0.38	1.86E-02	1.73	3.05
PH	PH_16	chr5_214608734	5	214608734	0.35	1.52E-02	1.82	3.26
PH	PH_17	chr7_5564712	7	5564712	0.48	1.23E-02	1.91	3.47
PH	PH_17	chr7_5874143	7	5874143	0.49	1.26E-02	1.90	3.44
PH	PH_17	chr7_5874244	7	5874244	0.47	9.24E-03	2.03	3.76
PH	PH_17	chr7_5897020	7	5897020	0.42	6.03E-03	2.22	4.20
PH	PH_17	chr7_5897097	7	5897097	0.42	9.21E-03	2.04	3.76
PH	PH_18	chr7_10047226	7	10047226	0.48	1.12E-02	1.95	3.56
PH	PH_19	chr8_95019937	8	95019937	0.21	8.64E-03	2.06	3.83
PH	PH_20	chr9_3312225	9	3312225	0.46	1.78E-02	1.75	3.10
PH	PH_20	chr9_3312233	9	3312233	0.46	1.78E-02	1.75	3.10
PH	PH_20	chr9_3312282	9	3312282	0.47	1.42E-02	1.85	3.32
PH	PH_21	chr9_10804699	9	10804699	0.49	3.47E-03	2.46	4.77
PH	PH_21	chr9_10963789	9	10963789	0.48	6.28E-03	2.20	4.15
PH	PH_21	chr9_11068485	9	11068485	0.47	1.57E-03	2.80	5.62
PH	PH_21	chr9_11078511	9	11078511	0.49	6.13E-03	2.21	4.18
PH	PH_21	chr9_11340767	9	11340767	0.50	3.84E-03	2.42	4.67

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
PH	PH_21	chr9_11340773	9	11340773	0.50	3.84E-03	2.42	4.67
PH	PH_21	chr9_11340805	9	11340805	0.50	8.15E-03	2.09	3.89
PH	PH_21	chr9_11398647	9	11398647	0.50	4.36E-03	2.36	4.53
PH	PH_21	chr9_11550432	9	11550432	0.48	2.44E-03	2.61	5.15
PH	PH_21	chr9_11560329	9	11560329	0.48	1.98E-03	2.70	5.37
PH	PH_21	chr9_11560338	9	11560338	0.48	1.98E-03	2.70	5.37
PH	PH_21	chr9_11560350	9	11560350	0.48	1.98E-03	2.70	5.37
PH	PH_21	chr9_11730268	9	11730268	0.47	7.01E-03	2.15	4.04
PH	PH_21	chr9_11732691	9	11732691	0.50	7.28E-03	2.14	4.00
PH	PH_21	chr9_11732697	9	11732697	0.50	1.64E-02	1.78	3.18
PH	PH_21	chr9_11733387	9	11733387	0.49	1.77E-02	1.75	3.11
PH	PH_21	chr9_11739408	9	11739408	0.49	4.48E-03	2.35	4.51
PH	PH_21	chr9_11741128	9	11741128	0.48	5.49E-03	2.26	4.29
PH	PH_22	chr9_16732176	9	16732176	0.48	1.60E-02	1.80	3.20
PH	PH_23	chr9_134044334	9	134044334	0.28	8.67E-03	2.06	3.82
PH	PH_24	chr9_135855399	9	135855399	0.47	1.87E-02	1.73	3.05
PH	PH_25	chr10_126703385	10	126703385	0.47	8.36E-03	2.08	3.86
PH	PH_25	chr10_126898390	10	126898390	0.47	8.67E-03	2.06	3.82
PH	PH_25	chr10_126899214	10	126899214	0.46	1.91E-02	1.72	3.03
PH	PH_25	chr10_126911579	10	126911579	0.48	1.07E-02	1.97	3.61
PH	PH_25	chr10_126911594	10	126911594	0.48	1.07E-02	1.97	3.61
PH	PH_25	chr10_127256813	10	127256813	0.48	7.81E-03	2.11	3.93
PH	PH_25	chr10_127258914	10	127258914	0.47	5.46E-03	2.26	4.30
PH	PH_25	chr10_127264386	10	127264386	0.48	5.95E-03	2.23	4.21
PH	PH_25	chr10_127264403	10	127264403	0.30	5.96E-04	3.22	6.68
PH	PH_25	chr10_127264439	10	127264439	0.48	5.95E-03	2.23	4.21
PH	PH_26	chr10_137901401	10	137901401	0.40	1.73E-02	1.76	3.13
PH	PH_26	chr10_137903207	10	137903207	0.40	1.12E-02	1.95	3.56
PH	PH_26	chr10_138028482	10	138028482	0.23	4.83E-03	2.32	4.43
PH	PH_26	chr10_138028587	10	138028587	0.40	1.81E-02	1.74	3.09
EH	EH_1	chr3_157572126	3	157572126	0.31	1.25E-04	3.90	7.28
EH	EH_1	chr3_157572131	3	157572131	0.31	1.25E-04	3.90	7.28
EH	EH_1	chr3_157572136	3	157572136	0.31	1.25E-04	3.90	7.28
EH	EH_1	chr3_157572152	3	157572152	0.31	1.25E-04	3.90	7.28
EH	EH_1	chr3_157572182	3	157572182	0.31	1.25E-04	3.90	7.28
EH	EH_1	chr3_157761578	3	157761578	0.33	3.55E-05	4.45	8.55
EH	EH_1	chr3_157761602	3	157761602	0.35	1.71E-04	3.77	6.98
EH	EH_1	chr3_157761610	3	157761610	0.33	1.24E-05	4.91	9.63

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
EH	EH_1	chr3_157773525	3	157773525	0.31	3.04E-06	5.52	11.11
EH	EH_1	chr3_158348209	3	158348209	0.32	2.17E-04	3.66	6.74
EH	EH_1	chr3_158650511	3	158650511	0.29	2.49E-05	4.60	8.91
EH	EH_1	chr3_158890884	3	158890884	0.29	2.73E-05	4.56	8.82
EH	EH_1	chr3_159380134	3	159380134	0.29	7.81E-07	6.11	12.58
EH	EH_1	chr3_159380154	3	159380154	0.29	7.81E-07	6.11	12.58
EH	EH_1	chr3_159380194	3	159380194	0.38	3.83E-04	3.42	6.19
EH	EH_1	chr3_159380236	3	159380236	0.27	2.91E-06	5.54	11.16
EH	EH_1	chr3_159380239	3	159380239	0.27	2.91E-06	5.54	11.16
EH	EH_1	chr3_159380248	3	159380248	0.27	2.91E-06	5.54	11.16
EH	EH_1	chr3_159380250	3	159380250	0.27	2.91E-06	5.54	11.16
EH	EH_1	chr3_159380253	3	159380253	0.27	2.91E-06	5.54	11.16
EH	EH_1	chr3_159381121	3	159381121	0.29	8.96E-08	7.05	15.00
EH	EH_1	chr3_159381162	3	159381162	0.30	5.41E-08	7.27	15.58
EH	EH_1	chr3_159381256	3	159381256	0.29	1.24E-07	6.91	14.64
EH	EH_1	chr3_159385192	3	159385192	0.30	6.18E-06	5.21	10.36
EH	EH_1	chr3_159678385	3	159678385	0.28	9.21E-07	6.04	12.40
EH	EH_1	chr3_159801025	3	159801025	0.30	2.28E-05	4.64	9.00
EH	EH_1	chr3_159810124	3	159810124	0.29	4.28E-07	6.37	13.25
EH	EH_1	chr3_159818701	3	159818701	0.31	1.82E-05	4.74	9.23
EH	EH_1	chr3_159820547	3	159820547	0.31	1.91E-05	4.72	9.19
EH	EH_1	chr3_159870315	3	159870315	0.26	8.19E-05	4.09	7.71
EH	EH_1	chr3_159870409	3	159870409	0.35	1.57E-04	3.81	7.06
EH	EH_1	chr3_159870494	3	159870494	0.30	2.41E-04	3.62	6.64
EH	EH_2	chr3_161259884	3	161259884	0.29	3.57E-05	4.45	8.54
EH	EH_2	chr3_161259896	3	161259896	0.29	3.57E-05	4.45	8.54
EH	EH_2	chr3_161364532	3	161364532	0.27	5.00E-05	4.30	8.20
EH	EH_2	chr3_161364626	3	161364626	0.27	4.98E-05	4.30	8.21
EH	EH_2	chr3_161364643	3	161364643	0.27	4.98E-05	4.30	8.21
EH	EH_2	chr3_161563404	3	161563404	0.29	1.33E-06	5.88	12.00
EH	EH_2	chr3_161573899	3	161573899	0.29	1.18E-04	3.93	7.35
EH	EH_2	chr3_161574131	3	161574131	0.29	3.04E-05	4.52	8.71
EH	EH_2	chr3_161575030	3	161575030	0.30	3.96E-05	4.40	8.44
EH	EH_2	chr3_161575049	3	161575049	0.30	3.96E-05	4.40	8.44
EH	EH_2	chr3_161575068	3	161575068	0.30	3.96E-05	4.40	8.44
EH	EH_2	chr3_161575111	3	161575111	0.31	9.32E-06	5.03	9.93
EH	EH_2	chr3_161575140	3	161575140	0.31	9.32E-06	5.03	9.93
EH	EH_2	chr3_161971270	3	161971270	0.29	4.01E-05	4.40	8.43

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
EH	EH_2	chr3_162096179	3	162096179	0.32	5.79E-05	4.24	8.05
EH	EH_2	chr3_162096214	3	162096214	0.32	5.79E-05	4.24	8.05
EH	EH_2	chr3_162097205	3	162097205	0.31	2.28E-04	3.64	6.70
EH	EH_2	chr3_162097279	3	162097279	0.32	1.93E-04	3.72	6.86
EH	EH_2	chr3_162179721	3	162179721	0.31	2.59E-05	4.59	8.87
EH	EH_2	chr3_162179722	3	162179722	0.31	2.59E-05	4.59	8.87
EH	EH_2	chr3_162318003	3	162318003	0.33	4.54E-05	4.34	8.30
EH	EH_2	chr3_162318161	3	162318161	0.32	2.83E-05	4.55	8.78
EH	EH_2	chr3_162318227	3	162318227	0.32	3.18E-05	4.50	8.66
EH	EH_2	chr3_162318357	3	162318357	0.32	6.74E-05	4.17	7.90
EH	EH_2	chr3_162318376	3	162318376	0.31	4.33E-05	4.36	8.35
EH	EH_2	chr3_162587602	3	162587602	0.31	1.56E-05	4.81	9.39
EH	EH_2	chr3_162587662	3	162587662	0.31	5.49E-04	3.26	5.84
EH	EH_2	chr3_162696410	3	162696410	0.31	9.67E-05	4.01	7.54
EH	EH_3	chr3_164155282	3	164155282	0.29	7.64E-05	4.12	7.78
EH	EH_3	chr3_164250193	3	164250193	0.36	8.88E-04	3.05	5.39
EH	EH_3	chr3_164524652	3	164524652	0.30	4.24E-05	4.37	8.37
EH	EH_3	chr3_164525227	3	164525227	0.29	1.78E-04	3.75	6.94
EH	EH_3	chr3_164587464	3	164587464	0.31	4.50E-05	4.35	8.31
EH	EH_3	chr3_164589024	3	164589024	0.33	1.23E-04	3.91	7.30
EH	EH_3	chr3_164967251	3	164967251	0.33	8.39E-04	3.08	5.44
EH	EH_3	chr3_164976865	3	164976865	0.32	5.98E-04	3.22	5.76
EH	EH_3	chr3_164976883	3	164976883	0.32	5.98E-04	3.22	5.76
EH	EH_3	chr3_165017962	3	165017962	0.29	6.72E-05	4.17	7.90
EH	EH_3	chr3_165021955	3	165021955	0.29	4.12E-05	4.39	8.40
EH	EH_3	chr3_165021985	3	165021985	0.29	4.12E-05	4.39	8.40
EH	EH_3	chr3_165168084	3	165168084	0.31	4.26E-05	4.37	8.36
EH	EH_3	chr3_165412676	3	165412676	0.33	8.74E-05	4.06	7.64
EH	EH_3	chr3_165412700	3	165412700	0.32	3.53E-05	4.45	8.56
EH	EH_3	chr3_165412702	3	165412702	0.32	3.53E-05	4.45	8.56
EH	EH_3	chr3_165457973	3	165457973	0.35	8.20E-04	3.09	5.46
EH	EH_3	chr3_165457997	3	165457997	0.35	8.20E-04	3.09	5.46
EH	EH_3	chr3_165458043	3	165458043	0.30	1.07E-04	3.97	7.44
EH	EH_3	chr3_165458062	3	165458062	0.31	1.08E-04	3.97	7.43
EH	EH_3	chr3_165458089	3	165458089	0.30	1.07E-04	3.97	7.44
EH	EH_3	chr3_165458092	3	165458092	0.30	1.07E-04	3.97	7.44
EH	EH_3	chr3_165458515	3	165458515	0.31	1.03E-04	3.99	7.48
EH	EH_3	chr3_165458612	3	165458612	0.33	1.52E-04	3.82	7.09

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
EH	EH_3	chr3_165461844	3	165461844	0.31	8.68E-06	5.06	10.00
EH	EH_3	chr3_165722971	3	165722971	0.31	5.68E-05	4.25	8.07
EH	EH_3	chr3_165862848	3	165862848	0.32	4.23E-04	3.37	6.09
EH	EH_3	chr3_165862913	3	165862913	0.32	6.90E-04	3.16	5.63
EH	EH_3	chr3_166152102	3	166152102	0.32	8.04E-04	3.09	5.48
EH	EH_3	chr3_166203740	3	166203740	0.31	4.04E-04	3.39	6.14
EH	EH_3	chr5_214608734	5	214608734	0.35	9.32E-04	3.03	5.34
EH	EH_3	chr10_126898390	10	126898390	0.47	5.42E-04	3.27	5.86
DTA	DTA_1	chr3_154124966	3	154124966	0.38	6.02E-04	3.22	7.71
DTA	DTA_1	chr3_154125085	3	154125085	0.38	4.61E-04	3.34	8.05
DTA	DTA_1	chr3_154409040	3	154409040	0.36	4.55E-04	3.34	8.06
DTA	DTA_1	chr3_154627610	3	154627610	0.38	5.02E-04	3.30	7.94
DTA	DTA_1	chr3_154648244	3	154648244	0.38	6.31E-04	3.20	7.65
DTA	DTA_1	chr3_154648343	3	154648343	0.39	9.91E-04	3.00	7.07
DTA	DTA_1	chr3_154650655	3	154650655	0.38	3.34E-04	3.48	8.46
DTA	DTA_1	chr3_154732481	3	154732481	0.37	7.89E-04	3.10	7.36
DTA	DTA_1	chr3_154739840	3	154739840	0.36	7.80E-04	3.11	7.38
DTA	DTA_1	chr3_155317691	3	155317691	0.38	5.64E-04	3.25	7.79
DTA	DTA_2	chr3_157572126	3	157572126	0.31	4.06E-06	5.39	14.46
DTA	DTA_2	chr3_157572131	3	157572131	0.31	4.06E-06	5.39	14.46
DTA	DTA_2	chr3_157572136	3	157572136	0.31	4.06E-06	5.39	14.46
DTA	DTA_2	chr3_157572152	3	157572152	0.31	4.06E-06	5.39	14.46
DTA	DTA_2	chr3_157572182	3	157572182	0.31	4.06E-06	5.39	14.46
DTA	DTA_2	chr3_157761578	3	157761578	0.33	2.58E-05	4.59	11.88
DTA	DTA_2	chr3_157761602	3	157761602	0.35	2.10E-06	5.68	15.40
DTA	DTA_2	chr3_157761610	3	157761610	0.33	8.71E-06	5.06	13.38
DTA	DTA_2	chr3_157773525	3	157773525	0.31	2.75E-06	5.56	15.02
DTA	DTA_2	chr3_158650511	3	158650511	0.29	2.26E-06	5.65	15.30
DTA	DTA_2	chr3_158890884	3	158890884	0.29	2.50E-05	4.60	11.92
DTA	DTA_2	chr3_159380134	3	159380134	0.29	1.72E-06	5.76	15.69
DTA	DTA_2	chr3_159380154	3	159380154	0.29	1.72E-06	5.76	15.69
DTA	DTA_2	chr3_159380194	3	159380194	0.38	1.31E-05	4.88	12.82
DTA	DTA_2	chr3_159380236	3	159380236	0.27	3.54E-07	6.45	18.01
DTA	DTA_2	chr3_159380239	3	159380239	0.27	3.54E-07	6.45	18.01
DTA	DTA_2	chr3_159380248	3	159380248	0.27	3.54E-07	6.45	18.01
DTA	DTA_2	chr3_159380250	3	159380250	0.27	3.54E-07	6.45	18.01
DTA	DTA_2	chr3_159380253	3	159380253	0.27	3.54E-07	6.45	18.01
DTA	DTA_2	chr3_159381121	3	159381121	0.29	2.42E-07	6.62	18.57

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTA	DTA_2	chr3_159381162	3	159381162	0.30	2.86E-07	6.54	18.32
DTA	DTA_2	chr3_159381231	3	159381231	0.40	9.32E-04	3.03	7.15
DTA	DTA_2	chr3_159381240	3	159381240	0.40	9.32E-04	3.03	7.15
DTA	DTA_2	chr3_159381256	3	159381256	0.29	4.92E-07	6.31	17.52
DTA	DTA_2	chr3_159385192	3	159385192	0.30	9.51E-07	6.02	16.55
DTA	DTA_2	chr3_159675502	3	159675502	0.40	3.23E-04	3.49	8.51
DTA	DTA_2	chr3_159678385	3	159678385	0.28	2.21E-07	6.66	18.71
DTA	DTA_2	chr3_159801025	3	159801025	0.30	2.72E-04	3.56	8.73
DTA	DTA_2	chr3_159810124	3	159810124	0.29	1.58E-06	5.80	15.82
DTA	DTA_2	chr3_159818701	3	159818701	0.31	2.75E-06	5.56	15.01
DTA	DTA_2	chr3_159820547	3	159820547	0.31	8.37E-06	5.08	13.44
DTA	DTA_2	chr3_159870315	3	159870315	0.26	3.90E-06	5.41	14.52
DTA	DTA_2	chr3_159870409	3	159870409	0.35	5.83E-04	3.23	7.75
DTA	DTA_2	chr3_159870494	3	159870494	0.30	1.15E-04	3.94	9.86
DTA	DTA_3	chr3_161259884	3	161259884	0.29	9.94E-07	6.00	16.48
DTA	DTA_3	chr3_161259896	3	161259896	0.29	9.94E-07	6.00	16.48
DTA	DTA_3	chr3_161364532	3	161364532	0.27	2.14E-06	5.67	15.38
DTA	DTA_3	chr3_161364626	3	161364626	0.27	9.56E-07	6.02	16.54
DTA	DTA_3	chr3_161364643	3	161364643	0.27	9.56E-07	6.02	16.54
DTA	DTA_3	chr3_161563404	3	161563404	0.29	9.12E-08	7.04	20.04
DTA	DTA_3	chr3_161573899	3	161573899	0.29	3.41E-06	5.47	14.71
DTA	DTA_3	chr3_161574131	3	161574131	0.29	1.21E-07	6.92	19.61
DTA	DTA_3	chr3_161575030	3	161575030	0.30	3.52E-06	5.45	14.66
DTA	DTA_3	chr3_161575049	3	161575049	0.30	3.52E-06	5.45	14.66
DTA	DTA_3	chr3_161575068	3	161575068	0.30	3.52E-06	5.45	14.66
DTA	DTA_3	chr3_161575111	3	161575111	0.31	3.19E-06	5.50	14.80
DTA	DTA_3	chr3_161575140	3	161575140	0.31	3.19E-06	5.50	14.80
DTA	DTA_3	chr3_161971270	3	161971270	0.29	1.78E-06	5.75	15.64
DTA	DTA_3	chr3_162064220	3	162064220	0.32	6.80E-04	3.17	7.55
DTA	DTA_3	chr3_162096179	3	162096179	0.32	1.80E-05	4.75	12.38
DTA	DTA_3	chr3_162096214	3	162096214	0.32	1.80E-05	4.75	12.38
DTA	DTA_3	chr3_162097205	3	162097205	0.31	3.16E-05	4.50	11.60
DTA	DTA_3	chr3_162097279	3	162097279	0.32	6.39E-04	3.19	7.63
DTA	DTA_3	chr3_162179721	3	162179721	0.31	1.92E-05	4.72	12.28
DTA	DTA_3	chr3_162179722	3	162179722	0.31	1.92E-05	4.72	12.28
DTA	DTA_3	chr3_162318003	3	162318003	0.33	2.84E-05	4.55	11.75
DTA	DTA_3	chr3_162318161	3	162318161	0.32	8.95E-06	5.05	13.34
DTA	DTA_3	chr3_162318227	3	162318227	0.32	3.32E-05	4.48	11.54

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTA	DTA_3	chr3_162318357	3	162318357	0.32	2.83E-05	4.55	11.75
DTA	DTA_3	chr3_162318376	3	162318376	0.31	7.62E-06	5.12	13.57
DTA	DTA_3	chr3_162587602	3	162587602	0.31	3.32E-05	4.48	11.54
DTA	DTA_3	chr3_162587662	3	162587662	0.31	2.93E-04	3.53	8.64
DTA	DTA_3	chr3_162696410	3	162696410	0.31	1.38E-05	4.86	12.74
DTA	DTA_4	chr3_164155282	3	164155282	0.29	4.95E-06	5.31	14.18
DTA	DTA_4	chr3_164524652	3	164524652	0.30	1.80E-06	5.75	15.63
DTA	DTA_4	chr3_164525227	3	164525227	0.29	7.94E-05	4.10	10.36
DTA	DTA_4	chr3_164587464	3	164587464	0.31	4.31E-06	5.37	14.38
DTA	DTA_4	chr3_164589024	3	164589024	0.33	1.13E-05	4.95	13.01
DTA	DTA_4	chr3_164884525	3	164884525	0.32	5.20E-04	3.28	7.89
DTA	DTA_4	chr3_164976865	3	164976865	0.32	5.03E-04	3.30	7.94
DTA	DTA_4	chr3_164976883	3	164976883	0.32	5.03E-04	3.30	7.94
DTA	DTA_4	chr3_165017962	3	165017962	0.29	5.32E-06	5.27	14.08
DTA	DTA_4	chr3_165021955	3	165021955	0.29	4.18E-06	5.38	14.42
DTA	DTA_4	chr3_165021985	3	165021985	0.29	4.18E-06	5.38	14.42
DTA	DTA_4	chr3_165168084	3	165168084	0.31	1.07E-05	4.97	13.10
DTA	DTA_4	chr3_165412676	3	165412676	0.33	2.02E-05	4.69	12.22
DTA	DTA_4	chr3_165412700	3	165412700	0.32	8.87E-06	5.05	13.36
DTA	DTA_4	chr3_165412702	3	165412702	0.32	8.87E-06	5.05	13.36
DTA	DTA_4	chr3_165457973	3	165457973	0.35	2.48E-04	3.61	8.85
DTA	DTA_4	chr3_165457997	3	165457997	0.35	2.48E-04	3.61	8.85
DTA	DTA_4	chr3_165458043	3	165458043	0.30	1.65E-05	4.78	12.49
DTA	DTA_4	chr3_165458062	3	165458062	0.31	1.69E-05	4.77	12.46
DTA	DTA_4	chr3_165458089	3	165458089	0.30	1.65E-05	4.78	12.49
DTA	DTA_4	chr3_165458092	3	165458092	0.30	1.65E-05	4.78	12.49
DTA	DTA_4	chr3_165458515	3	165458515	0.31	5.90E-05	4.23	10.76
DTA	DTA_4	chr3_165458612	3	165458612	0.33	1.83E-04	3.74	9.25
DTA	DTA_4	chr3_165461844	3	165461844	0.31	6.03E-06	5.22	13.90
DTA	DTA_4	chr3_165722971	3	165722971	0.31	8.62E-05	4.06	10.25
DTA	DTA_4	chr3_165862848	3	165862848	0.32	4.32E-05	4.36	11.18
DTA	DTA_4	chr3_165862913	3	165862913	0.32	3.22E-05	4.49	11.58
DTA	DTA_4	chr3_166151687	3	166151687	0.33	3.69E-04	3.43	8.34
DTA	DTA_4	chr3_166152102	3	166152102	0.32	2.64E-04	3.58	8.77
DTA	DTA_4	chr3_166203067	3	166203067	0.31	4.14E-04	3.38	8.19
DTA	DTA_4	chr3_166203075	3	166203075	0.31	4.14E-04	3.38	8.19
DTA	DTA_4	chr3_166203095	3	166203095	0.31	4.14E-04	3.38	8.19
DTA	DTA_4	chr3_166203195	3	166203195	0.30	1.34E-04	3.87	9.66

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTA	DTA_4	chr3_166203740	3	166203740	0.31	1.29E-05	4.89	12.84
DTA	DTA_4	chr3_166397950	3	166397950	0.30	2.29E-04	3.64	8.96
DTA	DTA_4	chr3_166670576	3	166670576	0.29	4.70E-06	5.33	14.25
DTA	DTA_4	chr3_166691288	3	166691288	0.31	3.65E-05	4.44	11.41
DTA	DTA_4	chr3_166691294	3	166691294	0.31	5.65E-05	4.25	10.81
DTA	DTA_4	chr3_166691308	3	166691308	0.31	3.65E-05	4.44	11.41
DTA	DTA_4	chr3_166692423	3	166692423	0.28	1.79E-06	5.75	15.63
DTA	DTA_4	chr3_166799729	3	166799729	0.28	1.56E-04	3.81	9.46
DTA	DTA_4	chr3_166997981	3	166997981	0.29	2.04E-05	4.69	12.20
DTA	DTA_4	chr3_166998038	3	166998038	0.29	2.04E-05	4.69	12.20
DTA	DTA_4	chr3_167002310	3	167002310	0.30	3.84E-05	4.42	11.34
DTA	DTA_4	chr3_167002340	3	167002340	0.29	3.16E-04	3.50	8.54
DTA	DTA_4	chr3_167002342	3	167002342	0.29	3.16E-04	3.50	8.54
DTA	DTA_4	chr3_167004269	3	167004269	0.31	8.30E-05	4.08	10.30
DTA	DTA_4	chr3_167008553	3	167008553	0.33	6.17E-04	3.21	7.68
DTA	DTA_4	chr3_167072658	3	167072658	0.31	1.18E-04	3.93	9.83
DTA	DTA_4	chr3_167072800	3	167072800	0.31	2.72E-04	3.57	8.73
DTA	DTA_4	chr3_167072834	3	167072834	0.31	2.72E-04	3.57	8.73
DTA	DTA_4	chr3_167076052	3	167076052	0.32	2.30E-04	3.64	8.95
DTA	DTA_4	chr3_167076517	3	167076517	0.39	2.53E-04	3.60	8.82
DTA	DTA_4	chr3_167076559	3	167076559	0.32	7.90E-05	4.10	10.36
DTA	DTA_4	chr3_167488123	3	167488123	0.32	1.71E-04	3.77	9.34
DTA	DTA_4	chr3_167488179	3	167488179	0.31	2.19E-04	3.66	9.01
DTA	DTA_4	chr3_167488190	3	167488190	0.31	2.19E-04	3.66	9.01
DTA	DTA_4	chr3_167488232	3	167488232	0.31	2.19E-04	3.66	9.01
DTA	DTA_4	chr3_167488263	3	167488263	0.30	4.72E-05	4.33	11.06
DTA	DTA_5	chr3_168492759	3	168492759	0.31	1.46E-04	3.84	9.55
DTA	DTA_5	chr3_168697270	3	168697270	0.30	5.34E-05	4.27	10.89
DTA	DTA_5	chr3_168697617	3	168697617	0.31	1.31E-05	4.88	12.81
DTA	DTA_5	chr3_168697908	3	168697908	0.31	2.11E-05	4.68	12.16
DTA	DTA_5	chr3_168921952	3	168921952	0.31	8.91E-04	3.05	7.21
DTA	DTA_5	chr3_168921974	3	168921974	0.31	8.91E-04	3.05	7.21
DTA	DTA_5	chr3_168921987	3	168921987	0.31	8.91E-04	3.05	7.21
DTA	DTA_5	chr3_168922578	3	168922578	0.31	9.18E-05	4.04	10.16
DTA	DTA_5	chr3_168923050	3	168923050	0.30	8.57E-05	4.07	10.26
DTA	DTA_5	chr3_169078650	3	169078650	0.31	8.78E-06	5.06	13.37
DTA	DTA_5	chr3_169078733	3	169078733	0.31	1.24E-05	4.91	12.90
DTS	DTS_1	chr3_153764074	3	153764074	0.38	3.27E-04	3.48	9.65

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTS	DTS_1	chr3_154124966	3	154124966	0.38	1.55E-04	3.81	10.76
DTS	DTS_1	chr3_154125085	3	154125085	0.38	5.34E-05	4.27	12.37
DTS	DTS_1	chr3_154409040	3	154409040	0.36	1.86E-04	3.73	10.49
DTS	DTS_1	chr3_154561392	3	154561392	0.38	3.58E-04	3.45	9.51
DTS	DTS_1	chr3_154627512	3	154627512	0.38	8.82E-05	4.05	11.61
DTS	DTS_1	chr3_154627610	3	154627610	0.38	1.02E-04	3.99	11.38
DTS	DTS_1	chr3_154648244	3	154648244	0.38	8.32E-05	4.08	11.70
DTS	DTS_1	chr3_154648343	3	154648343	0.39	2.19E-04	3.66	10.24
DTS	DTS_1	chr3_154649914	3	154649914	0.38	1.62E-04	3.79	10.69
DTS	DTS_1	chr3_154650533	3	154650533	0.38	1.62E-04	3.79	10.69
DTS	DTS_1	chr3_154650548	3	154650548	0.38	1.62E-04	3.79	10.69
DTS	DTS_1	chr3_154650599	3	154650599	0.38	1.62E-04	3.79	10.69
DTS	DTS_1	chr3_154650655	3	154650655	0.38	5.83E-05	4.23	12.24
DTS	DTS_1	chr3_154661620	3	154661620	0.39	2.66E-04	3.58	9.95
DTS	DTS_1	chr3_154732481	3	154732481	0.37	1.44E-04	3.84	10.86
DTS	DTS_1	chr3_154739840	3	154739840	0.36	2.83E-04	3.55	9.86
DTS	DTS_1	chr3_154883258	3	154883258	0.36	7.04E-04	3.15	8.53
DTS	DTS_1	chr3_154883269	3	154883269	0.37	9.23E-04	3.03	8.14
DTS	DTS_1	chr3_155054222	3	155054222	0.38	6.86E-04	3.16	8.57
DTS	DTS_1	chr3_155054256	3	155054256	0.38	6.86E-04	3.16	8.57
DTS	DTS_1	chr3_155317687	3	155317687	0.33	8.97E-04	3.05	8.18
DTS	DTS_1	chr3_155317691	3	155317691	0.38	9.16E-05	4.04	11.55
DTS	DTS_1	chr3_155318033	3	155318033	0.38	2.42E-04	3.62	10.09
DTS	DTS_1	chr3_155318070	3	155318070	0.38	3.80E-04	3.42	9.43
DTS	DTS_1	chr3_155318124	3	155318124	0.38	3.80E-04	3.42	9.43
DTS	DTS_1	chr3_155318145	3	155318145	0.38	3.80E-04	3.42	9.43
DTS	DTS_1	chr3_155318148	3	155318148	0.38	4.82E-04	3.32	9.08
DTS	DTS_1	chr3_155688738	3	155688738	0.38	5.08E-04	3.29	9.00
DTS	DTS_1	chr3_155803339	3	155803339	0.35	5.42E-04	3.27	8.91
DTS	DTS_1	chr3_156287758	3	156287758	0.35	7.88E-04	3.10	8.37
DTS	DTS_1	chr3_156799630	3	156799630	0.35	6.41E-04	3.19	8.66
DTS	DTS_1	chr3_156799845	3	156799845	0.36	5.95E-04	3.23	8.77
DTS	DTS_1	chr3_156969980	3	156969980	0.37	4.76E-04	3.32	9.10
DTS	DTS_1	chr3_156969997	3	156969997	0.37	4.76E-04	3.32	9.10
DTS	DTS_1	chr3_157572126	3	157572126	0.31	2.31E-05	4.64	13.67
DTS	DTS_1	chr3_157572131	3	157572131	0.31	2.31E-05	4.64	13.67
DTS	DTS_1	chr3_157572136	3	157572136	0.31	2.31E-05	4.64	13.67
DTS	DTS_1	chr3_157572152	3	157572152	0.31	2.31E-05	4.64	13.67

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTS	DTS_1	chr3_157572182	3	157572182	0.31	2.31E-05	4.64	13.67
DTS	DTS_1	chr3_157761578	3	157761578	0.33	6.02E-05	4.22	12.19
DTS	DTS_1	chr3_157761602	3	157761602	0.35	3.05E-05	4.52	13.24
DTS	DTS_1	chr3_157761610	3	157761610	0.33	2.78E-05	4.56	13.38
DTS	DTS_1	chr3_157773525	3	157773525	0.31	9.65E-06	5.02	15.04
DTS	DTS_1	chr3_158650511	3	158650511	0.29	1.69E-05	4.77	14.15
DTS	DTS_1	chr3_158890884	3	158890884	0.29	1.87E-04	3.73	10.47
DTS	DTS_1	chr3_159380134	3	159380134	0.29	6.60E-07	6.18	19.41
DTS	DTS_1	chr3_159380154	3	159380154	0.29	6.60E-07	6.18	19.41
DTS	DTS_1	chr3_159380194	3	159380194	0.38	1.07E-04	3.97	11.31
DTS	DTS_1	chr3_159380236	3	159380236	0.27	1.73E-06	5.76	17.81
DTS	DTS_1	chr3_159380239	3	159380239	0.27	1.73E-06	5.76	17.81
DTS	DTS_1	chr3_159380248	3	159380248	0.27	1.73E-06	5.76	17.81
DTS	DTS_1	chr3_159380250	3	159380250	0.27	1.73E-06	5.76	17.81
DTS	DTS_1	chr3_159380253	3	159380253	0.27	1.73E-06	5.76	17.81
DTS	DTS_1	chr3_159381121	3	159381121	0.29	2.44E-07	6.61	21.08
DTS	DTS_1	chr3_159381162	3	159381162	0.30	1.97E-07	6.71	21.45
DTS	DTS_1	chr3_159381256	3	159381256	0.29	7.16E-07	6.15	19.27
DTS	DTS_1	chr3_159385192	3	159385192	0.30	6.34E-07	6.20	19.48
DTS	DTS_1	chr3_159678385	3	159678385	0.28	4.66E-07	6.33	19.99
DTS	DTS_1	chr3_159801025	3	159801025	0.30	2.12E-04	3.67	10.29
DTS	DTS_1	chr3_159810124	3	159810124	0.29	2.56E-06	5.59	17.18
DTS	DTS_1	chr3_159818701	3	159818701	0.31	1.08E-05	4.96	14.86
DTS	DTS_1	chr3_159820547	3	159820547	0.31	7.56E-06	5.12	15.43
DTS	DTS_1	chr3_159870315	3	159870315	0.26	6.67E-05	4.18	12.03
DTS	DTS_1	chr3_159870409	3	159870409	0.35	8.90E-05	4.05	11.59
DTS	DTS_1	chr3_159870494	3	159870494	0.30	3.41E-04	3.47	9.59
DTS	DTS_2	chr3_161259884	3	161259884	0.29	6.28E-06	5.20	15.73
DTS	DTS_2	chr3_161259896	3	161259896	0.29	6.28E-06	5.20	15.73
DTS	DTS_2	chr3_161364532	3	161364532	0.27	2.82E-05	4.55	13.36
DTS	DTS_2	chr3_161364626	3	161364626	0.27	2.47E-05	4.61	13.57
DTS	DTS_2	chr3_161364643	3	161364643	0.27	2.47E-05	4.61	13.57
DTS	DTS_2	chr3_161563404	3	161563404	0.29	6.03E-07	6.22	19.56
DTS	DTS_2	chr3_161573899	3	161573899	0.29	9.04E-06	5.04	15.14
DTS	DTS_2	chr3_161574131	3	161574131	0.29	1.00E-06	6.00	18.72
DTS	DTS_2	chr3_161575030	3	161575030	0.30	7.52E-06	5.12	15.44
DTS	DTS_2	chr3_161575049	3	161575049	0.30	7.52E-06	5.12	15.44
DTS	DTS_2	chr3_161575068	3	161575068	0.30	7.52E-06	5.12	15.44

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTS	DTS_2	chr3_161575111	3	161575111	0.31	3.22E-06	5.49	16.80
DTS	DTS_2	chr3_161575140	3	161575140	0.31	3.22E-06	5.49	16.80
DTS	DTS_2	chr3_161971270	3	161971270	0.29	1.44E-05	4.84	14.41
DTS	DTS_2	chr3_162064220	3	162064220	0.32	9.12E-04	3.04	8.16
DTS	DTS_2	chr3_162096179	3	162096179	0.32	4.50E-05	4.35	12.63
DTS	DTS_2	chr3_162096214	3	162096214	0.32	4.50E-05	4.35	12.63
DTS	DTS_2	chr3_162097205	3	162097205	0.31	2.01E-04	3.70	10.37
DTS	DTS_2	chr3_162179721	3	162179721	0.31	1.12E-04	3.95	11.24
DTS	DTS_2	chr3_162179722	3	162179722	0.31	1.12E-04	3.95	11.24
DTS	DTS_2	chr3_162318003	3	162318003	0.33	4.09E-05	4.39	12.78
DTS	DTS_2	chr3_162318161	3	162318161	0.32	2.85E-05	4.55	13.34
DTS	DTS_2	chr3_162318227	3	162318227	0.32	6.03E-05	4.22	12.19
DTS	DTS_2	chr3_162318357	3	162318357	0.32	3.82E-05	4.42	12.89
DTS	DTS_2	chr3_162318376	3	162318376	0.31	2.13E-05	4.67	13.79
DTS	DTS_2	chr3_162587602	3	162587602	0.31	5.01E-05	4.30	12.47
DTS	DTS_2	chr3_162696410	3	162696410	0.31	1.95E-05	4.71	13.93
DTS	DTS_3	chr3_164155282	3	164155282	0.29	3.60E-05	4.44	12.98
DTS	DTS_3	chr3_164524652	3	164524652	0.30	8.22E-06	5.09	15.30
DTS	DTS_3	chr3_164525227	3	164525227	0.29	1.58E-04	3.80	10.73
DTS	DTS_3	chr3_164587464	3	164587464	0.31	4.63E-06	5.33	16.22
DTS	DTS_3	chr3_164589024	3	164589024	0.33	2.34E-05	4.63	13.65
DTS	DTS_3	chr3_164976865	3	164976865	0.32	7.36E-04	3.13	8.46
DTS	DTS_3	chr3_164976883	3	164976883	0.32	7.36E-04	3.13	8.46
DTS	DTS_3	chr3_165017962	3	165017962	0.29	4.76E-05	4.32	12.55
DTS	DTS_3	chr3_165021955	3	165021955	0.29	2.80E-05	4.55	13.37
DTS	DTS_3	chr3_165021985	3	165021985	0.29	2.80E-05	4.55	13.37
DTS	DTS_3	chr3_165168084	3	165168084	0.31	1.69E-05	4.77	14.16
DTS	DTS_3	chr3_165412676	3	165412676	0.33	5.80E-05	4.24	12.24
DTS	DTS_3	chr3_165412700	3	165412700	0.32	9.75E-06	5.01	15.02
DTS	DTS_3	chr3_165412702	3	165412702	0.32	9.75E-06	5.01	15.02
DTS	DTS_3	chr3_165457973	3	165457973	0.35	1.09E-04	3.96	11.28
DTS	DTS_3	chr3_165457997	3	165457997	0.35	1.09E-04	3.96	11.28
DTS	DTS_3	chr3_165458043	3	165458043	0.30	8.32E-05	4.08	11.69
DTS	DTS_3	chr3_165458062	3	165458062	0.31	7.29E-05	4.14	11.90
DTS	DTS_3	chr3_165458089	3	165458089	0.30	8.32E-05	4.08	11.69
DTS	DTS_3	chr3_165458092	3	165458092	0.30	8.32E-05	4.08	11.69
DTS	DTS_3	chr3_165458515	3	165458515	0.31	9.71E-05	4.01	11.46
DTS	DTS_3	chr3_165458612	3	165458612	0.33	2.02E-04	3.69	10.36

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTS	DTS_3	chr3_165461844	3	165461844	0.31	1.11E-05	4.96	14.82
DTS	DTS_3	chr3_165722971	3	165722971	0.31	1.80E-04	3.75	10.54
DTS	DTS_3	chr3_165862848	3	165862848	0.32	1.37E-04	3.86	10.94
DTS	DTS_3	chr3_165862913	3	165862913	0.32	1.12E-04	3.95	11.24
DTS	DTS_3	chr3_166151687	3	166151687	0.33	2.59E-04	3.59	9.99
DTS	DTS_3	chr3_166152102	3	166152102	0.32	6.14E-04	3.21	8.73
DTS	DTS_3	chr3_166203067	3	166203067	0.31	6.35E-04	3.20	8.68
DTS	DTS_3	chr3_166203075	3	166203075	0.31	6.35E-04	3.20	8.68
DTS	DTS_3	chr3_166203095	3	166203095	0.31	6.35E-04	3.20	8.68
DTS	DTS_3	chr3_166203195	3	166203195	0.30	2.20E-04	3.66	10.24
DTS	DTS_3	chr3_166203740	3	166203740	0.31	5.58E-06	5.25	15.91
DTS	DTS_3	chr3_166670576	3	166670576	0.29	7.65E-05	4.12	11.82
DTS	DTS_3	chr3_166691288	3	166691288	0.31	3.67E-04	3.44	9.48
DTS	DTS_3	chr3_166691294	3	166691294	0.31	4.70E-04	3.33	9.12
DTS	DTS_3	chr3_166691308	3	166691308	0.31	3.67E-04	3.44	9.48
DTS	DTS_3	chr3_166692423	3	166692423	0.28	5.93E-05	4.23	12.21
DTS	DTS_3	chr3_166997981	3	166997981	0.29	2.80E-04	3.55	9.88
DTS	DTS_3	chr3_166998038	3	166998038	0.29	2.80E-04	3.55	9.88
DTS	DTS_3	chr3_167002310	3	167002310	0.30	4.06E-04	3.39	9.33
DTS	DTS_3	chr3_167002340	3	167002340	0.29	7.50E-04	3.12	8.44
DTS	DTS_3	chr3_167002342	3	167002342	0.29	7.50E-04	3.12	8.44
DTS	DTS_3	chr3_167004269	3	167004269	0.31	7.83E-04	3.11	8.37
DTS	DTS_3	chr3_167488263	3	167488263	0.30	6.82E-04	3.17	8.57
DTS	DTS_4	chr3_168697270	3	168697270	0.30	7.70E-04	3.11	8.40
DTS	DTS_4	chr3_168697617	3	168697617	0.31	1.51E-04	3.82	10.79
DTS	DTS_4	chr3_168697908	3	168697908	0.31	5.70E-04	3.24	8.84
DTS	DTS_4	chr3_168922578	3	168922578	0.31	8.58E-04	3.07	8.24
DTS	DTS_4	chr3_169078650	3	169078650	0.31	4.03E-04	3.39	9.34
DTS	DTS_4	chr3_169078733	3	169078733	0.31	3.54E-04	3.45	9.53
DTS	DTS_5	chr7_152805686	7	152805686	0.42	4.61E-04	3.34	9.14
DTS	DTS_5	chr7_152805691	7	152805691	0.42	4.61E-04	3.34	9.14

B6. SNPs above 3 LOD in Tx772 x Tx906 subpopulation using the 12,740 marker subset for plant height (PH), ear height (EH), days to anthesis (DTA) and days to silking (DTS). QTL were classified by group adjacent SNP that differ by less than 1 Mbps.

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
PH	PH_1	chr9_136829657	9	136829657	0.42	7.63E-04	3.12	9.29
PH	PH_2	chr9_138309892	9	138309892	0.41	5.24E-04	3.28	9.90
PH	PH_2	chr9_138424244	9	138424244	0.18	9.31E-04	3.03	8.98
PH	PH_3	chr9_153610437	9	153610437	0.22	5.05E-04	3.30	9.96
PH	PH_3	chr9_153616129	9	153616129	0.44	4.08E-04	3.39	10.31
PH	PH_3	chr9_153616259	9	153616259	0.46	3.22E-04	3.49	10.69
PH	PH_3	chr9_153616303	9	153616303	0.46	6.01E-04	3.22	9.68
PH	PH_3	chr9_153674989	9	153674989	0.45	5.69E-04	3.24	9.77
PH	PH_3	chr9_153689037	9	153689037	0.45	6.26E-04	3.20	9.61
PH	PH_3	chr9_154016983	9	154016983	0.46	5.40E-04	3.27	9.85
PH	PH_3	chr9_154030951	9	154030951	0.42	3.65E-04	3.44	10.49
EH	EH_1	chr7_9326665	7	9326665	0.48	9.08E-04	3.04	9.61
EH	EH_2	chr7_95538266	7	95538266	0.36	3.47E-04	3.46	11.26
EH	EH_3	chr8_124839484	8	124839484	0.41	3.41E-04	3.47	11.30
EH	EH_3	chr8_124839520	8	124839520	0.41	3.41E-04	3.47	11.30
EH	EH_3	chr8_124839600	8	124839600	0.40	2.90E-04	3.54	11.58
EH	EH_3	chr8_124840214	8	124840214	0.37	6.03E-05	4.22	14.38
EH	EH_3	chr8_124848847	8	124848847	0.45	4.50E-04	3.35	10.81
EH	EH_3	chr8_124951504	8	124951504	0.41	5.28E-04	3.28	10.53
EH	EH_3	chr8_124951555	8	124951555	0.41	9.74E-04	3.01	9.49
EH	EH_3	chr8_124951903	8	124951903	0.42	5.92E-04	3.23	10.34
EH	EH_3	chr8_125181978	8	125181978	0.42	4.01E-04	3.40	11.01
EH	EH_3	chr8_125196506	8	125196506	0.42	2.48E-04	3.61	11.85
EH	EH_4	chr8_132876605	8	132876605	0.41	2.64E-04	3.58	11.74
EH	EH_4	chr8_133179114	8	133179114	0.39	3.02E-04	3.52	11.51
EH	EH_4	chr8_133260870	8	133260870	0.39	1.23E-04	3.91	13.10
EH	EH_4	chr8_133276224	8	133276224	0.41	2.61E-04	3.58	11.77
EH	EH_4	chr8_133440329	8	133440329	0.38	5.81E-04	3.24	10.37
EH	EH_4	chr8_133933401	8	133933401	0.40	3.59E-05	4.44	15.33
EH	EH_4	chr8_133934205	8	133934205	0.39	8.36E-05	4.08	13.79
EH	EH_4	chr8_133934223	8	133934223	0.19	1.00E-04	4.00	13.47
EH	EH_4	chr8_134005735	8	134005735	0.41	1.15E-04	3.94	13.22
EH	EH_4	chr8_134005737	8	134005737	0.41	1.15E-04	3.94	13.22
EH	EH_5	chr8_136040830	8	136040830	0.40	6.08E-05	4.22	14.37

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
EH	EH_5	chr8_136040997	8	136040997	0.38	8.37E-05	4.08	13.79
EH	EH_5	chr8_136041103	8	136041103	0.39	6.58E-05	4.18	14.22
EH	EH_5	chr8_136285390	8	136285390	0.38	7.54E-04	3.12	9.92
EH	EH_5	chr8_136381106	8	136381106	0.40	3.12E-04	3.51	11.45
EH	EH_5	chr8_136911788	8	136911788	0.41	1.29E-04	3.89	13.01
EH	EH_5	chr8_136912371	8	136912371	0.39	7.49E-05	4.13	13.99
EH	EH_5	chr8_136912486	8	136912486	0.38	4.11E-04	3.39	10.97
EH	EH_5	chr8_137047139	8	137047139	0.39	8.09E-05	4.09	13.85
EH	EH_5	chr8_137047258	8	137047258	0.39	7.18E-05	4.14	14.07
EH	EH_5	chr8_137752464	8	137752464	0.42	3.17E-04	3.50	11.42
EH	EH_5	chr8_137766743	8	137766743	0.38	1.14E-04	3.94	13.24
EH	EH_5	chr8_138226369	8	138226369	0.40	1.32E-04	3.88	12.97
EH	EH_5	chr8_138226387	8	138226387	0.40	1.32E-04	3.88	12.97
EH	EH_5	chr8_138657123	8	138657123	0.44	2.12E-04	3.67	12.13
EH	EH_5	chr8_139106730	8	139106730	0.24	6.62E-04	3.18	10.15
EH	EH_6	chr8_149611603	8	149611603	0.36	9.76E-04	3.01	9.48
EH	EH_6	chr8_149613506	8	149613506	0.39	7.79E-04	3.11	9.87
EH	EH_6	chr8_149891434	8	149891434	0.39	3.64E-04	3.44	11.18
EH	EH_6	chr8_149892532	8	149892532	0.38	7.06E-04	3.15	10.04
EH	EH_6	chr8_150013729	8	150013729	0.38	7.43E-04	3.13	9.95
DTA	DTA_1	chr3_148974648	3	148974648	0.49	9.92E-04	3.00	9.70
DTA	DTA_2	chr3_156287758	3	156287758	0.49	8.20E-05	4.09	14.18
DTA	DTA_3	chr3_156799630	3	156799630	0.50	7.64E-04	3.12	10.16
DTA	DTA_3	chr3_156799845	3	156799845	0.50	4.50E-04	3.35	11.09
DTA	DTA_3	chr3_156799962	3	156799962	0.46	7.72E-04	3.11	10.14
DTA	DTA_3	chr3_156969980	3	156969980	0.50	7.16E-04	3.15	10.27
DTA	DTA_3	chr3_156969997	3	156969997	0.50	7.16E-04	3.15	10.27
DTA	DTA_3	chr3_157761578	3	157761578	0.49	6.40E-04	3.19	10.47
DTA	DTA_3	chr3_157761610	3	157761610	0.49	6.40E-04	3.19	10.47
DTA	DTA_3	chr3_158348267	3	158348267	0.27	2.58E-04	3.59	12.09
DTA	DTA_3	chr3_158890884	3	158890884	0.50	1.41E-04	3.85	13.18
DTA	DTA_4	chr8_134630371	8	134630371	0.39	6.91E-04	3.16	10.33
DTA	DTA_5	chr8_136912371	8	136912371	0.39	3.30E-04	3.48	11.64
DTA	DTA_6	chr9_143906355	9	143906355	0.44	6.83E-06	5.17	18.92
DTA	DTA_6	chr9_143906439	9	143906439	0.26	6.40E-05	4.19	14.64
DTA	DTA_6	chr9_143906444	9	143906444	0.46	2.22E-05	4.65	16.64
DTA	DTA_6	chr9_144443067	9	144443067	0.45	1.69E-05	4.77	17.17
DTA	DTA_6	chr9_144597858	9	144597858	0.45	5.26E-04	3.28	10.81

Trait	QTL	SNP	Chr	Position	maf	P-value	LOD	Var explained
DTA	DTA_6	chr9_144597868	9	144597868	0.45	5.26E-04	3.28	10.81
DTA	DTA_6	chr9_144597872	9	144597872	0.45	5.26E-04	3.28	10.81
DTA	DTA_6	chr9_144597890	9	144597890	0.45	5.26E-04	3.28	10.81
DTA	DTA_6	chr9_144762792	9	144762792	0.45	3.63E-04	3.44	11.47
DTA	DTA_6	chr9_144993089	9	144993089	0.50	2.86E-04	3.54	11.90
DTA	DTA_7	chr9_146470991	9	146470991	0.47	1.92E-04	3.72	12.62
DTA	DTA_8	chr10_133673779	10	133673779	0.27	9.70E-04	3.01	9.74
DTS	DTS_1	chr3_142733931	3	142733931	0.50	6.69E-04	3.17	10.67
DTS	DTS_2	chr3_146607404	3	146607404	0.27	3.01E-04	3.52	12.13
DTS	DTS_2	chr3_147328706	3	147328706	0.49	5.50E-04	3.26	11.03
DTS	DTS_3	chr3_148974530	3	148974530	0.48	5.60E-04	3.25	10.99
DTS	DTS_3	chr3_148974537	3	148974537	0.48	5.60E-04	3.25	10.99
DTS	DTS_3	chr3_148974648	3	148974648	0.49	1.61E-04	3.79	13.30
DTS	DTS_3	chr3_148975376	3	148975376	0.48	3.25E-04	3.49	11.99
DTS	DTS_3	chr3_148975403	3	148975403	0.49	3.33E-04	3.48	11.94
DTS	DTS_3	chr3_148975409	3	148975409	0.49	3.33E-04	3.48	11.94
DTS	DTS_3	chr3_148975431	3	148975431	0.49	3.33E-04	3.48	11.94
DTS	DTS_3	chr3_148975438	3	148975438	0.49	3.33E-04	3.48	11.94
DTS	DTS_3	chr3_149242369	3	149242369	0.50	5.47E-04	3.26	11.04
DTS	DTS_3	chr3_149250047	3	149250047	0.49	9.76E-04	3.01	9.99
DTS	DTS_3	chr3_149250050	3	149250050	0.49	9.76E-04	3.01	9.99
DTS	DTS_4	chr3_156287758	3	156287758	0.49	1.94E-04	3.71	12.95
DTS	DTS_5	chr3_158348267	3	158348267	0.27	2.34E-04	3.63	12.59
DTS	DTS_5	chr3_158890884	3	158890884	0.50	4.13E-04	3.38	11.55
DTS	DTS_6	chr9_143906355	9	143906355	0.44	1.13E-05	4.95	18.43
DTS	DTS_6	chr9_143906439	9	143906439	0.26	3.22E-04	3.49	12.01
DTS	DTS_6	chr9_143906444	9	143906444	0.46	2.53E-05	4.60	16.84
DTS	DTS_6	chr9_144443067	9	144443067	0.45	1.60E-05	4.79	17.73
DTS	DTS_6	chr9_144597858	9	144597858	0.45	6.16E-04	3.21	10.82
DTS	DTS_6	chr9_144597868	9	144597868	0.45	6.16E-04	3.21	10.82
DTS	DTS_6	chr9_144597872	9	144597872	0.45	6.16E-04	3.21	10.82
DTS	DTS_6	chr9_144597890	9	144597890	0.45	6.16E-04	3.21	10.82
DTS	DTS_6	chr9_144762792	9	144762792	0.45	4.57E-04	3.34	11.37
DTS	DTS_6	chr9_144993089	9	144993089	0.50	1.67E-04	3.78	13.23
DTS	DTS_7	chr9_146470991	9	146470991	0.47	4.97E-04	3.30	11.21
DTS	DTS_8	chr10_133673779	10	133673779	0.27	4.90E-04	3.31	11.24

B7. SNPs above 3-LOD in multi-environment trial (MET) analysis and individual environment GWAS of leaf rolling (CS13N, CS14D, CS14I, CS15T, CS15TP). QTL were classified by group adjacent SNP that differ by less than 1 Mbps.

Env	QTL	SNP	Chr	Position	maf	P-value	LOD	Var Exp
MET	MET_LR_1	chr1_6569757	1	6569757	0.00	3.26E-04	3.49	0.94
MET	MET_LR_1	chr1_7489979	1	7489979	0.01	6.28E-04	3.20	0.85
MET	MET_LR_2	chr1_14036950	1	14036950	0.21	8.84E-04	3.05	0.80
MET	MET_LR_3	chr1_29037161	1	29037161	0.31	1.72E-04	3.76	1.03
MET	MET_LR_3	chr1_29037181	1	29037181	0.30	6.31E-04	3.20	0.85
MET	MET_LR_3	chr1_29082661	1	29082661	0.32	9.88E-04	3.01	0.79
MET	MET_LR_3	chr1_29082673	1	29082673	0.32	9.88E-04	3.01	0.79
MET	MET_LR_3	chr1_29190704	1	29190704	0.33	1.03E-04	3.99	1.10
MET	MET_LR_3	chr1_29543112	1	29543112	0.37	2.27E-04	3.64	0.99
MET	MET_LR_4	chr1_33162621	1	33162621	0.43	4.65E-04	3.33	0.89
MET	MET_LR_5	chr1_82633119	1	82633119	0.13	8.65E-04	3.06	0.81
MET	MET_LR_6	chr1_86497558	1	86497558	0.22	3.42E-04	3.47	0.93
MET	MET_LR_6	chr1_86585557	1	86585557	0.21	8.49E-04	3.07	0.81
MET	MET_LR_6	chr1_86613161	1	86613161	0.22	7.72E-04	3.11	0.82
MET	MET_LR_6	chr1_86613197	1	86613197	0.22	8.28E-04	3.08	0.81
MET	MET_LR_6	chr1_86613223	1	86613223	0.22	2.11E-04	3.67	1.00
MET	MET_LR_6	chr1_86613285	1	86613285	0.22	9.18E-04	3.04	0.80
MET	MET_LR_6	chr1_87299271	1	87299271	0.21	4.53E-04	3.34	0.90
MET	MET_LR_6	chr1_87602191	1	87602191	0.21	6.70E-04	3.17	0.84
MET	MET_LR_6	chr1_87602202	1	87602202	0.21	7.22E-04	3.14	0.83
MET	MET_LR_6	chr1_87602213	1	87602213	0.21	6.70E-04	3.17	0.84
MET	MET_LR_6	chr1_87602307	1	87602307	0.21	5.42E-04	3.27	0.87
MET	MET_LR_6	chr1_87766396	1	87766396	0.22	5.58E-04	3.25	0.87
MET	MET_LR_6	chr1_87766419	1	87766419	0.22	5.58E-04	3.25	0.87
MET	MET_LR_6	chr1_87766763	1	87766763	0.21	6.92E-04	3.16	0.84
MET	MET_LR_6	chr1_87766772	1	87766772	0.22	4.22E-04	3.37	0.90
MET	MET_LR_6	chr1_87876991	1	87876991	0.23	5.04E-04	3.30	0.88
MET	MET_LR_6	chr1_87979897	1	87979897	0.24	8.65E-04	3.06	0.81
MET	MET_LR_6	chr1_87983098	1	87983098	0.25	3.20E-04	3.50	0.94
MET	MET_LR_6	chr1_87983100	1	87983100	0.25	3.37E-04	3.47	0.94
MET	MET_LR_6	chr1_87983106	1	87983106	0.24	6.16E-04	3.21	0.85
MET	MET_LR_6	chr1_87983162	1	87983162	0.24	5.06E-04	3.30	0.88
MET	MET_LR_7	chr1_296175139	1	296175139	0.36	6.75E-04	3.17	0.84
MET	MET_LR_8	chr2_6972968	2	6972968	0.24	9.28E-04	3.03	0.80

Env	QTL	SNP	Chr	Position	maf	P-value	LOD	Var Exp
MET	MET_LR_8	chr2_6973279	2	6973279	0.25	8.63E-04	3.06	0.81
MET	MET_LR_9	chr2_13850814	2	13850814	0.50	7.14E-05	4.15	1.15
MET	MET_LR_10	chr2_17220051	2	17220051	0.31	9.22E-04	3.04	0.80
MET	MET_LR_11	chr2_18249561	2	18249561	0.30	6.73E-04	3.17	0.84
MET	MET_LR_11	chr2_18417962	2	18417962	0.32	2.09E-04	3.68	1.00
MET	MET_LR_11	chr2_18626749	2	18626749	0.31	6.72E-04	3.17	0.84
MET	MET_LR_11	chr2_18712957	2	18712957	0.31	9.20E-04	3.04	0.80
MET	MET_LR_11	chr2_19266680	2	19266680	0.45	8.86E-04	3.05	0.80
MET	MET_LR_11	chr2_19319964	2	19319964	0.46	2.76E-04	3.56	0.96
MET	MET_LR_11	chr2_19320067	2	19320067	0.48	2.89E-04	3.54	0.96
MET	MET_LR_11	chr2_20110029	2	20110029	0.44	6.30E-04	3.20	0.85
MET	MET_LR_12	chr2_184754512	2	184754512	0.50	1.01E-03	3.00	0.79
MET	MET_LR_12	chr2_185023662	2	185023662	0.23	4.11E-05	4.39	1.23
MET	MET_LR_12	chr2_185221168	2	185221168	0.26	1.01E-03	3.00	0.79
MET	MET_LR_13	chr3_156434758	3	156434758	0.14	2.29E-04	3.64	0.99
MET	MET_LR_14	chr3_170778982	3	170778982	0.48	6.39E-04	3.19	0.85
MET	MET_LR_15	chr3_188555184	3	188555184	0.30	7.35E-04	3.13	0.83
MET	MET_LR_15	chr3_188555222	3	188555222	0.30	7.30E-04	3.14	0.83
MET	MET_LR_16	chr3_210508085	3	210508085	0.19	8.14E-04	3.09	0.82
MET	MET_LR_16	chr3_210523454	3	210523454	0.22	4.02E-04	3.40	0.91
MET	MET_LR_17	chr3_211718651	3	211718651	0.24	3.47E-04	3.46	0.93
MET	MET_LR_17	chr3_211718660	3	211718660	0.24	6.71E-04	3.17	0.84
MET	MET_LR_17	chr3_211718735	3	211718735	0.23	7.85E-04	3.11	0.82
MET	MET_LR_17	chr3_212431627	3	212431627	0.23	4.08E-04	3.39	0.91
MET	MET_LR_17	chr3_212431666	3	212431666	0.23	3.37E-04	3.47	0.94
MET	MET_LR_17	chr3_212431673	3	212431673	0.23	3.37E-04	3.47	0.94
MET	MET_LR_17	chr3_212503505	3	212503505	0.22	6.01E-04	3.22	0.86
MET	MET_LR_17	chr3_212544357	3	212544357	0.20	2.38E-04	3.62	0.98
MET	MET_LR_17	chr3_212544386	3	212544386	0.19	2.78E-04	3.56	0.96
MET	MET_LR_17	chr3_212544402	3	212544402	0.18	2.12E-04	3.67	1.00
MET	MET_LR_17	chr3_212544407	3	212544407	0.18	3.18E-04	3.50	0.94
MET	MET_LR_17	chr3_212544446	3	212544446	0.18	2.30E-04	3.64	0.99
MET	MET_LR_17	chr3_212548086	3	212548086	0.34	4.16E-05	4.38	1.22
MET	MET_LR_18	chr3_214477068	3	214477068	0.14	7.31E-04	3.14	0.83
MET	MET_LR_19	chr3_216007444	3	216007444	0.22	8.79E-04	3.06	0.81
MET	MET_LR_19	chr3_216469326	3	216469326	0.23	6.21E-05	4.21	1.17
MET	MET_LR_19	chr3_216471587	3	216471587	0.22	2.29E-04	3.64	0.99
MET	MET_LR_19	chr3_216473159	3	216473159	0.23	3.49E-04	3.46	0.93

Env	QTL	SNP	Chr	Position	maf	P-value	LOD	Var Exp
MET	MET_LR_19	chr3_216473192	3	216473192	0.23	3.49E-04	3.46	0.93
MET	MET_LR_19	chr3_216883752	3	216883752	0.25	6.32E-04	3.20	0.85
MET	MET_LR_19	chr3_216883757	3	216883757	0.25	1.99E-04	3.70	1.01
MET	MET_LR_19	chr3_216883831	3	216883831	0.25	7.09E-05	4.15	1.15
MET	MET_LR_19	chr3_216986453	3	216986453	0.22	3.62E-05	4.44	1.24
MET	MET_LR_19	chr3_216986511	3	216986511	0.21	2.36E-04	3.63	0.98
MET	MET_LR_19	chr3_216987644	3	216987644	0.22	4.28E-05	4.37	1.22
MET	MET_LR_19	chr3_216987686	3	216987686	0.22	4.48E-05	4.35	1.21
MET	MET_LR_19	chr3_216988574	3	216988574	0.22	9.38E-04	3.03	0.80
MET	MET_LR_19	chr3_217007695	3	217007695	0.22	9.23E-05	4.03	1.11
MET	MET_LR_19	chr3_217008553	3	217008553	0.23	2.68E-04	3.57	0.97
MET	MET_LR_19	chr3_217008607	3	217008607	0.23	2.68E-04	3.57	0.97
MET	MET_LR_19	chr3_217008706	3	217008706	0.22	8.61E-04	3.07	0.81
MET	MET_LR_19	chr3_217008748	3	217008748	0.23	5.37E-05	4.27	1.19
MET	MET_LR_19	chr3_217096387	3	217096387	0.23	3.66E-04	3.44	0.92
MET	MET_LR_19	chr3_217096642	3	217096642	0.21	2.12E-04	3.67	1.00
MET	MET_LR_19	chr3_217096655	3	217096655	0.21	1.69E-04	3.77	1.03
MET	MET_LR_19	chr3_217213085	3	217213085	0.23	8.63E-06	5.06	1.45
MET	MET_LR_19	chr3_217213193	3	217213193	0.24	5.71E-05	4.24	1.18
MET	MET_LR_19	chr3_217292671	3	217292671	0.23	7.33E-05	4.14	1.15
MET	MET_LR_19	chr3_217292677	3	217292677	0.24	4.70E-05	4.33	1.21
MET	MET_LR_19	chr3_217293516	3	217293516	0.24	1.56E-05	4.81	1.36
MET	MET_LR_19	chr3_217293519	3	217293519	0.24	1.56E-05	4.81	1.36
MET	MET_LR_19	chr3_217294002	3	217294002	0.24	4.92E-05	4.31	1.20
MET	MET_LR_19	chr3_217358505	3	217358505	0.25	1.24E-04	3.91	1.07
MET	MET_LR_19	chr3_217358612	3	217358612	0.25	8.85E-05	4.05	1.12
MET	MET_LR_19	chr3_217358652	3	217358652	0.26	2.15E-04	3.67	1.00
MET	MET_LR_19	chr3_217358657	3	217358657	0.23	2.02E-04	3.70	1.01
MET	MET_LR_19	chr3_217358660	3	217358660	0.23	1.17E-04	3.93	1.08
MET	MET_LR_19	chr3_217358974	3	217358974	0.22	3.15E-04	3.50	0.94
MET	MET_LR_19	chr3_217359376	3	217359376	0.22	5.70E-04	3.24	0.86
MET	MET_LR_19	chr3_217461401	3	217461401	0.24	8.01E-04	3.10	0.82
MET	MET_LR_19	chr3_217463033	3	217463033	0.48	1.80E-04	3.75	1.02
MET	MET_LR_19	chr3_217463044	3	217463044	0.47	1.47E-04	3.83	1.05
MET	MET_LR_19	chr3_217463072	3	217463072	0.47	1.46E-04	3.83	1.05
MET	MET_LR_19	chr3_217573081	3	217573081	0.25	1.90E-04	3.72	1.01
MET	MET_LR_19	chr3_217576592	3	217576592	0.25	2.56E-04	3.59	0.97
MET	MET_LR_19	chr3_217576603	3	217576603	0.25	2.32E-04	3.63	0.99

Env	QTL	SNP	Chr	Position	maf	P-value	LOD	Var Exp
MET	MET_LR_19	chr3_217576622	3	217576622	0.23	4.81E-04	3.32	0.89
MET	MET_LR_19	chr3_217576652	3	217576652	0.26	8.54E-04	3.07	0.81
MET	MET_LR_19	chr3_217576679	3	217576679	0.23	6.26E-04	3.20	0.85
MET	MET_LR_19	chr3_217633065	3	217633065	0.26	2.29E-04	3.64	0.99
MET	MET_LR_19	chr3_217633111	3	217633111	0.26	6.25E-04	3.20	0.85
MET	MET_LR_19	chr3_217633164	3	217633164	0.26	4.02E-04	3.40	0.91
MET	MET_LR_19	chr3_217637708	3	217637708	0.46	1.34E-04	3.87	1.06
MET	MET_LR_19	chr3_217637712	3	217637712	0.24	9.03E-04	3.04	0.80
MET	MET_LR_19	chr3_217651336	3	217651336	0.25	1.13E-04	3.95	1.09
MET	MET_LR_19	chr3_217651338	3	217651338	0.24	1.33E-04	3.88	1.06
MET	MET_LR_19	chr3_217651342	3	217651342	0.47	2.64E-04	3.58	0.97
MET	MET_LR_19	chr3_217651494	3	217651494	0.27	5.81E-04	3.24	0.86
MET	MET_LR_19	chr3_217651500	3	217651500	0.43	8.98E-04	3.05	0.80
MET	MET_LR_19	chr3_217656898	3	217656898	0.26	7.27E-04	3.14	0.83
MET	MET_LR_19	chr3_217659852	3	217659852	0.25	1.50E-04	3.82	1.05
MET	MET_LR_19	chr3_217659912	3	217659912	0.25	2.90E-04	3.54	0.96
MET	MET_LR_19	chr3_217664640	3	217664640	0.26	6.03E-04	3.22	0.86
MET	MET_LR_19	chr3_217664643	3	217664643	0.23	7.54E-04	3.12	0.83
MET	MET_LR_19	chr3_217664657	3	217664657	0.26	3.45E-04	3.46	0.93
MET	MET_LR_19	chr3_217664779	3	217664779	0.47	2.10E-04	3.68	1.00
MET	MET_LR_19	chr3_217664830	3	217664830	0.47	7.77E-04	3.11	0.82
MET	MET_LR_19	chr3_217670323	3	217670323	0.26	3.87E-04	3.41	0.92
MET	MET_LR_19	chr3_217670855	3	217670855	0.25	5.41E-04	3.27	0.87
MET	MET_LR_19	chr3_217670991	3	217670991	0.26	5.53E-04	3.26	0.87
MET	MET_LR_19	chr3_217704895	3	217704895	0.46	9.34E-04	3.03	0.80
MET	MET_LR_19	chr3_217704943	3	217704943	0.46	9.45E-04	3.02	0.80
MET	MET_LR_19	chr3_217877595	3	217877595	0.26	6.12E-04	3.21	0.85
MET	MET_LR_19	chr3_217893690	3	217893690	0.46	9.59E-04	3.02	0.79
MET	MET_LR_19	chr3_217893698	3	217893698	0.46	9.79E-04	3.01	0.79
MET	MET_LR_19	chr3_217936114	3	217936114	0.44	2.70E-05	4.57	1.29
MET	MET_LR_19	chr3_217936224	3	217936224	0.47	8.77E-05	4.06	1.12
MET	MET_LR_19	chr3_217936234	3	217936234	0.46	8.36E-05	4.08	1.13
MET	MET_LR_19	chr3_217936427	3	217936427	0.28	8.41E-04	3.08	0.81
MET	MET_LR_19	chr3_217939593	3	217939593	0.25	6.50E-04	3.19	0.85
MET	MET_LR_19	chr3_218176291	3	218176291	0.23	9.05E-05	4.04	1.12
MET	MET_LR_19	chr3_218184190	3	218184190	0.22	2.82E-04	3.55	0.96
MET	MET_LR_19	chr3_218184213	3	218184213	0.26	4.79E-04	3.32	0.89
MET	MET_LR_19	chr3_218184307	3	218184307	0.27	7.68E-04	3.11	0.82

Env	QTL	SNP	Chr	Position	maf	P-value	LOD	Var Exp
MET	MET_LR_19	chr3_218184327	3	218184327	0.27	7.68E-04	3.11	0.82
MET	MET_LR_19	chr3_218264905	3	218264905	0.24	7.58E-04	3.12	0.83
MET	MET_LR_19	chr3_218323511	3	218323511	0.44	7.54E-04	3.12	0.83
MET	MET_LR_19	chr3_218323603	3	218323603	0.46	7.51E-04	3.12	0.83
MET	MET_LR_19	chr3_218323831	3	218323831	0.45	6.74E-04	3.17	0.84
MET	MET_LR_19	chr3_218362523	3	218362523	0.22	8.23E-04	3.08	0.81
MET	MET_LR_19	chr3_218362541	3	218362541	0.22	8.23E-04	3.08	0.81
MET	MET_LR_19	chr3_218835686	3	218835686	0.26	7.59E-04	3.12	0.82
MET	MET_LR_20	chr5_190238327	5	190238327	0.05	7.54E-04	3.12	0.83
MET	MET_LR_21	chr5_210557993	5	210557993	0.30	4.68E-04	3.33	0.89
MET	MET_LR_21	chr5_210589747	5	210589747	0.30	3.91E-04	3.41	0.92
MET	MET_LR_21	chr5_210598205	5	210598205	0.30	6.91E-04	3.16	0.84
MET	MET_LR_21	chr5_210769955	5	210769955	0.31	7.45E-04	3.13	0.83
MET	MET_LR_21	chr5_210870003	5	210870003	0.48	8.99E-04	3.05	0.80
MET	MET_LR_21	chr5_211184051	5	211184051	0.13	5.98E-04	3.22	0.86
MET	MET_LR_22	chr6_15585446	6	15585446	0.27	6.82E-04	3.17	0.84
MET	MET_LR_23	chr6_16798376	6	16798376	0.27	1.24E-04	3.91	1.07
MET	MET_LR_24	chr6_18596628	6	18596628	0.49	2.08E-04	3.68	1.00
MET	MET_LR_24	chr6_18845753	6	18845753	0.28	3.75E-04	3.43	0.92
MET	MET_LR_24	chr6_18845787	6	18845787	0.29	1.37E-04	3.86	1.06
MET	MET_LR_24	chr6_18845793	6	18845793	0.29	2.99E-04	3.52	0.95
MET	MET_LR_24	chr6_18845871	6	18845871	0.28	4.07E-04	3.39	0.91
MET	MET_LR_24	chr6_18846033	6	18846033	0.29	3.00E-04	3.52	0.95
MET	MET_LR_24	chr6_18924417	6	18924417	0.28	5.25E-04	3.28	0.88
MET	MET_LR_25	chr6_22003178	6	22003178	0.26	7.80E-04	3.11	0.82
MET	MET_LR_25	chr6_22267127	6	22267127	0.26	2.18E-04	3.66	1.00
MET	MET_LR_25	chr6_22267155	6	22267155	0.26	2.34E-04	3.63	0.99
MET	MET_LR_25	chr6_22267162	6	22267162	0.26	1.77E-04	3.75	1.02
MET	MET_LR_25	chr6_22267185	6	22267185	0.26	1.77E-04	3.75	1.02
MET	MET_LR_25	chr6_23251762	6	23251762	0.27	7.90E-04	3.10	0.82
MET	MET_LR_25	chr6_23827975	6	23827975	0.27	2.68E-04	3.57	0.97
MET	MET_LR_25	chr6_23828062	6	23828062	0.18	8.97E-04	3.05	0.80
MET	MET_LR_26	chr6_25291474	6	25291474	0.27	2.85E-04	3.55	0.96
MET	MET_LR_26	chr6_25337116	6	25337116	0.27	2.34E-04	3.63	0.99
MET	MET_LR_27	chr6_26965917	6	26965917	0.27	6.34E-04	3.20	0.85
MET	MET_LR_27	chr6_27120382	6	27120382	0.27	8.84E-04	3.05	0.80
MET	MET_LR_28	chr6_29640871	6	29640871	0.28	7.20E-04	3.14	0.83
MET	MET_LR_28	chr6_30107699	6	30107699	0.27	2.80E-04	3.55	0.96

Env	QTL	SNP	Chr	Position	maf	P-value	LOD	Var Exp
MET	MET_LR_28	chr6_30107846	6	30107846	0.27	6.47E-04	3.19	0.85
MET	MET_LR_28	chr6_31013853	6	31013853	0.29	8.43E-04	3.07	0.81
MET	MET_LR_29	chr6_150778426	6	150778426	0.28	3.74E-04	3.43	0.92
MET	MET_LR_29	chr6_151463038	6	151463038	0.27	8.94E-04	3.05	0.80
MET	MET_LR_30	chr7_5036761	7	5036761	0.01	7.74E-04	3.11	0.82
MET	MET_LR_31	chr7_118528185	7	118528185	0.28	2.90E-04	3.54	0.96
MET	MET_LR_31	chr7_118532679	7	118532679	0.19	3.96E-04	3.40	0.91
MET	MET_LR_32	chr8_12717725	8	12717725	0.00	8.35E-04	3.08	0.81
MET	MET_LR_33	chr8_22027341	8	22027341	0.01	9.15E-04	3.04	0.80
MET	MET_LR_34	chr8_139346153	8	139346153	0.28	3.60E-04	3.44	0.93
MET	MET_LR_34	chr8_139346155	8	139346155	0.28	3.38E-04	3.47	0.94
MET	MET_LR_35	chr8_140467785	8	140467785	0.01	5.62E-04	3.25	0.87
MET	MET_LR_36	chr9_1331695	9	1331695	0.36	9.27E-04	3.03	0.80
MET	MET_LR_37	chr9_13149694	9	13149694	0.17	2.45E-04	3.61	0.98
MET	MET_LR_38	chr9_16733642	9	16733642	0.31	5.06E-04	3.30	0.88
MET	MET_LR_39	chr10_137161901	10	137161901	0.24	5.27E-04	3.28	0.87
MET	MET_LR_39	chr10_137161960	10	137161960	0.24	9.64E-04	3.02	0.79
CS13N	CS13N_LR_1	chr1_28609035	1	28609035	0.32	6.39E-04	3.19	0.94
CS13N	CS13N_LR_1	chr1_28609081	1	28609081	0.32	7.37E-04	3.13	0.92
CS13N	CS13N_LR_1	chr1_29033984	1	29033984	0.32	2.09E-04	3.68	1.11
CS13N	CS13N_LR_1	chr1_29036741	1	29036741	0.30	5.78E-04	3.24	0.95
CS13N	CS13N_LR_1	chr1_29082661	1	29082661	0.32	1.75E-04	3.76	1.13
CS13N	CS13N_LR_1	chr1_29082673	1	29082673	0.32	1.75E-04	3.76	1.13
CS13N	CS13N_LR_1	chr1_29190704	1	29190704	0.33	6.22E-05	4.21	1.29
CS13N	CS13N_LR_1	chr1_29232447	1	29232447	0.32	5.00E-04	3.30	0.97
CS13N	CS13N_LR_1	chr1_29543112	1	29543112	0.37	1.74E-04	3.76	1.13
CS13N	CS13N_LR_1	chr1_30278884	1	30278884	0.31	9.37E-04	3.03	0.88
CS13N	CS13N_LR_2	chr1_34205794	1	34205794	0.32	1.00E-03	3.00	0.87
CS13N	CS13N_LR_3	chr1_84346366	1	84346366	0.20	7.70E-04	3.11	0.91
CS13N	CS13N_LR_4	chr1_86613223	1	86613223	0.22	9.40E-04	3.03	0.88
CS13N	CS13N_LR_4	chr1_87299271	1	87299271	0.21	8.65E-04	3.06	0.89
CS13N	CS13N_LR_4	chr1_87602191	1	87602191	0.21	6.11E-04	3.21	0.94
CS13N	CS13N_LR_4	chr1_87602202	1	87602202	0.21	5.25E-04	3.28	0.97
CS13N	CS13N_LR_4	chr1_87602213	1	87602213	0.21	6.11E-04	3.21	0.94
CS13N	CS13N_LR_4	chr1_87602307	1	87602307	0.21	7.83E-04	3.11	0.91
CS13N	CS13N_LR_4	chr1_87766396	1	87766396	0.22	5.08E-04	3.29	0.97
CS13N	CS13N_LR_4	chr1_87766419	1	87766419	0.22	5.08E-04	3.29	0.97
CS13N	CS13N_LR_4	chr1_87766763	1	87766763	0.21	5.72E-04	3.24	0.95

Env	QTL	SNP	Chr	Position	maf	P-value	LOD	Var Exp
CS13N	CS13N_LR_4	chr1_87766772	1	87766772	0.22	4.31E-04	3.37	1.00
CS13N	CS13N_LR_4	chr1_87983098	1	87983098	0.25	6.93E-04	3.16	0.93
CS13N	CS13N_LR_4	chr1_87983100	1	87983100	0.25	6.79E-04	3.17	0.93
CS13N	CS13N_LR_5	chr2_17476080	2	17476080	0.31	6.44E-04	3.19	0.94
CS13N	CS13N_LR_5	chr2_18249561	2	18249561	0.30	6.98E-04	3.16	0.92
CS13N	CS13N_LR_5	chr2_18464148	2	18464148	0.19	7.54E-04	3.12	0.91
CS13N	CS13N_LR_5	chr2_18626749	2	18626749	0.31	4.20E-04	3.38	1.00
CS13N	CS13N_LR_5	chr2_18712957	2	18712957	0.31	6.97E-04	3.16	0.92
CS13N	CS13N_LR_6	chr2_185023662	2	185023662	0.23	3.99E-05	4.40	1.36
CS13N	CS13N_LR_6	chr2_185111923	2	185111923	0.26	5.72E-04	3.24	0.95
CS13N	CS13N_LR_6	chr2_185221061	2	185221061	0.26	5.52E-04	3.26	0.96
CS13N	CS13N_LR_6	chr2_185221168	2	185221168	0.26	4.38E-04	3.36	0.99
CS13N	CS13N_LR_6	chr2_185439664	2	185439664	0.26	3.53E-04	3.45	1.03
CS13N	CS13N_LR_7	chr2_203516404	2	203516404	0.12	7.17E-04	3.14	0.92
CS13N	CS13N_LR_8	chr3_209843961	3	209843961	0.22	7.18E-04	3.14	0.92
CS13N	CS13N_LR_8	chr3_210523454	3	210523454	0.22	2.62E-04	3.58	1.07
CS13N	CS13N_LR_8	chr3_210944934	3	210944934	0.23	5.64E-04	3.25	0.96
CS13N	CS13N_LR_8	chr3_210945766	3	210945766	0.24	9.79E-04	3.01	0.87
CS13N	CS13N_LR_8	chr3_211685092	3	211685092	0.23	3.42E-04	3.47	1.03
CS13N	CS13N_LR_8	chr3_211685137	3	211685137	0.23	3.97E-04	3.40	1.01
CS13N	CS13N_LR_8	chr3_211718651	3	211718651	0.24	1.60E-04	3.80	1.15
CS13N	CS13N_LR_8	chr3_211718660	3	211718660	0.24	3.16E-04	3.50	1.04
CS13N	CS13N_LR_8	chr3_211718735	3	211718735	0.23	3.99E-04	3.40	1.01
CS13N	CS13N_LR_8	chr3_211719003	3	211719003	0.24	2.32E-04	3.63	1.09
CS13N	CS13N_LR_8	chr3_211719019	3	211719019	0.24	2.47E-04	3.61	1.08
CS13N	CS13N_LR_8	chr3_211719109	3	211719109	0.23	5.91E-04	3.23	0.95
CS13N	CS13N_LR_9	chr3_216986453	3	216986453	0.22	6.59E-04	3.18	0.93
CS13N	CS13N_LR_9	chr3_216987644	3	216987644	0.22	4.33E-04	3.36	1.00
CS13N	CS13N_LR_9	chr3_216987686	3	216987686	0.22	5.08E-04	3.29	0.97
CS13N	CS13N_LR_9	chr3_217213085	3	217213085	0.23	1.27E-04	3.90	1.18
CS13N	CS13N_LR_9	chr3_217213193	3	217213193	0.23	1.58E-04	3.80	1.15
CS13N	CS13N_LR_9	chr3_217292671	3	217292671	0.23	8.29E-04	3.08	0.90
CS13N	CS13N_LR_9	chr3_217293516	3	217293516	0.24	4.29E-04	3.37	1.00
CS13N	CS13N_LR_9	chr3_217293519	3	217293519	0.24	4.29E-04	3.37	1.00
CS13N	CS13N_LR_9	chr3_217573081	3	217573081	0.25	8.87E-04	3.05	0.89
CS13N	CS13N_LR_10	chr4_181895953	4	181895953	0.40	4.97E-04	3.30	0.98
CS13N	CS13N_LR_11	chr4_187045699	4	187045699	0.39	8.94E-04	3.05	0.89
CS13N	CS13N_LR_12	chr6_150661227	6	150661227	0.27	9.01E-04	3.05	0.89

Env	QTL	SNP	Chr	Position	maf	P-value	LOD	Var Exp
CS13N	CS13N_LR_12	chr6_150675114	6	150675114	0.27	8.17E-04	3.09	0.90
CS13N	CS13N_LR_12	chr6_150737470	6	150737470	0.27	3.06E-04	3.51	1.05
CS13N	CS13N_LR_12	chr6_150778426	6	150778426	0.27	5.22E-05	4.28	1.32
CS13N	CS13N_LR_12	chr6_150845713	6	150845713	0.28	4.06E-04	3.39	1.01
CS13N	CS13N_LR_12	chr6_150845716	6	150845716	0.28	4.06E-04	3.39	1.01
CS13N	CS13N_LR_12	chr6_150845718	6	150845718	0.28	4.56E-04	3.34	0.99
CS13N	CS13N_LR_12	chr6_151463038	6	151463038	0.27	1.35E-04	3.87	1.17
CS13N	CS13N_LR_12	chr6_151544772	6	151544772	0.27	9.93E-04	3.00	0.87
CS13N	CS13N_LR_13	chr7_100565386	7	100565386	0.23	6.20E-04	3.21	0.94
CS13N	CS13N_LR_13	chr7_100565390	7	100565390	0.23	6.20E-04	3.21	0.94
CS13N	CS13N_LR_14	chr7_118532591	7	118532591	0.29	4.70E-04	3.33	0.98
CS13N	CS13N_LR_15	chr8_139346153	8	139346153	0.28	2.63E-04	3.58	1.07
CS13N	CS13N_LR_15	chr8_139346155	8	139346155	0.28	2.53E-04	3.60	1.08
CS13N	CS13N_LR_16	chr9_1331369	9	1331369	0.37	4.88E-04	3.31	0.98
CS13N	CS13N_LR_16	chr9_1331695	9	1331695	0.36	1.70E-04	3.77	1.14
CS13N	CS13N_LR_17	chr10_77335329	10	77335329	0.23	8.01E-04	3.10	0.90
CS13N	CS13N_LR_18	chr10_80042833	10	80042833	0.24	7.75E-04	3.11	0.91
CS14D	CS14D_LR_1	chr1_3710572	1	3710572	0.24	9.88E-04	3.01	0.86
CS14D	CS14D_LR_2	chr1_82633119	1	82633119	0.13	8.34E-04	3.08	0.88
CS14D	CS14D_LR_2	chr1_82911291	1	82911291	0.13	4.35E-04	3.36	0.98
CS14D	CS14D_LR_3	chr1_84346366	1	84346366	0.20	8.38E-04	3.08	0.88
CS14D	CS14D_LR_4	chr1_86613223	1	86613223	0.22	4.01E-04	3.40	0.99
CS14D	CS14D_LR_4	chr1_87299271	1	87299271	0.21	3.29E-04	3.48	1.02
CS14D	CS14D_LR_4	chr1_87602191	1	87602191	0.21	8.33E-04	3.08	0.88
CS14D	CS14D_LR_4	chr1_87602202	1	87602202	0.21	9.49E-04	3.02	0.86
CS14D	CS14D_LR_4	chr1_87602213	1	87602213	0.21	8.33E-04	3.08	0.88
CS14D	CS14D_LR_4	chr1_87602307	1	87602307	0.21	7.91E-04	3.10	0.89
CS14D	CS14D_LR_4	chr1_87876991	1	87876991	0.23	4.43E-04	3.35	0.98
CS14D	CS14D_LR_4	chr1_87979897	1	87979897	0.24	3.61E-04	3.44	1.01
CS14D	CS14D_LR_4	chr1_87983039	1	87983039	0.24	4.50E-04	3.35	0.97
CS14D	CS14D_LR_4	chr1_87983062	1	87983062	0.24	4.50E-04	3.35	0.97
CS14D	CS14D_LR_4	chr1_87983098	1	87983098	0.25	1.35E-04	3.87	1.15
CS14D	CS14D_LR_4	chr1_87983100	1	87983100	0.25	1.41E-04	3.85	1.15
CS14D	CS14D_LR_4	chr1_87983106	1	87983106	0.24	5.76E-04	3.24	0.94
CS14D	CS14D_LR_4	chr1_87983162	1	87983162	0.24	6.07E-04	3.22	0.93
CS14D	CS14D_LR_4	chr1_88324570	1	88324570	0.24	9.46E-04	3.02	0.86
CS14D	CS14D_LR_5	chr1_91187634	1	91187634	0.21	4.40E-04	3.36	0.98
CS14D	CS14D_LR_5	chr1_91191720	1	91191720	0.20	2.14E-04	3.67	1.08

Env	QTL	SNP	Chr	Position	maf	P-value	LOD	Var Exp
CS14D	CS14D_LR_5	chr1_91247642	1	91247642	0.20	6.48E-04	3.19	0.92
CS14D	CS14D_LR_6	chr1_92349421	1	92349421	0.21	6.17E-04	3.21	0.93
CS14D	CS14D_LR_6	chr1_92785328	1	92785328	0.23	4.59E-04	3.34	0.97
CS14D	CS14D_LR_6	chr1_93073473	1	93073473	0.21	7.20E-04	3.14	0.90
CS14D	CS14D_LR_7	chr1_96623403	1	96623403	0.20	6.73E-04	3.17	0.91
CS14D	CS14D_LR_7	chr1_96688529	1	96688529	0.21	7.79E-04	3.11	0.89
CS14D	CS14D_LR_8	chr1_105471983	1	105471983	0.13	2.66E-04	3.57	1.05
CS14D	CS14D_LR_9	chr2_184537657	2	184537657	0.26	4.85E-04	3.31	0.96
CS14D	CS14D_LR_9	chr2_184646488	2	184646488	0.24	2.47E-04	3.61	1.06
CS14D	CS14D_LR_9	chr2_184966064	2	184966064	0.27	2.20E-04	3.66	1.08
CS14D	CS14D_LR_9	chr2_185023662	2	185023662	0.23	6.98E-06	5.16	1.60
CS14D	CS14D_LR_9	chr2_185023797	2	185023797	0.26	1.95E-04	3.71	1.10
CS14D	CS14D_LR_9	chr2_185023805	2	185023805	0.26	2.70E-04	3.57	1.05
CS14D	CS14D_LR_9	chr2_185025124	2	185025124	0.27	6.35E-04	3.20	0.92
CS14D	CS14D_LR_9	chr2_185025130	2	185025130	0.27	9.27E-04	3.03	0.87
CS14D	CS14D_LR_9	chr2_185111923	2	185111923	0.26	5.77E-04	3.24	0.94
CS14D	CS14D_LR_9	chr2_185112031	2	185112031	0.26	8.16E-04	3.09	0.89
CS14D	CS14D_LR_9	chr2_185221061	2	185221061	0.26	2.58E-04	3.59	1.06
CS14D	CS14D_LR_9	chr2_185221168	2	185221168	0.26	6.47E-05	4.19	1.26
CS14D	CS14D_LR_9	chr2_185439664	2	185439664	0.26	8.20E-05	4.09	1.23
CS14D	CS14D_LR_9	chr2_185608017	2	185608017	0.23	8.57E-04	3.07	0.88
CS14D	CS14D_LR_9	chr2_185646260	2	185646260	0.26	7.90E-04	3.10	0.89
CS14D	CS14D_LR_9	chr2_185842064	2	185842064	0.48	9.81E-04	3.01	0.86
CS14D	CS14D_LR_9	chr2_185842066	2	185842066	0.48	9.81E-04	3.01	0.86
CS14D	CS14D_LR_9	chr2_186164948	2	186164948	0.25	6.21E-04	3.21	0.93
CS14D	CS14D_LR_9	chr2_186186936	2	186186936	0.27	5.58E-04	3.25	0.94
CS14D	CS14D_LR_9	chr2_186642120	2	186642120	0.25	3.98E-05	4.40	1.34
CS14D	CS14D_LR_9	chr2_186788971	2	186788971	0.26	9.30E-04	3.03	0.87
CS14D	CS14D_LR_9	chr2_186789591	2	186789591	0.26	9.14E-04	3.04	0.87
CS14D	CS14D_LR_10	chr3_22385441	3	22385441	0.19	1.09E-04	3.96	1.18
CS14D	CS14D_LR_10	chr3_22385460	3	22385460	0.20	2.01E-04	3.70	1.09
CS14D	CS14D_LR_11	chr3_212740323	3	212740323	0.48	3.13E-04	3.50	1.03
CS14D	CS14D_LR_11	chr3_212740367	3	212740367	0.48	3.13E-04	3.50	1.03
CS14D	CS14D_LR_12	chr3_213797602	3	213797602	0.50	5.74E-04	3.24	0.94
CS14D	CS14D_LR_13	chr3_216469326	3	216469326	0.23	2.43E-04	3.61	1.06
CS14D	CS14D_LR_13	chr3_216473159	3	216473159	0.23	6.46E-04	3.19	0.92
CS14D	CS14D_LR_13	chr3_216473192	3	216473192	0.23	6.46E-04	3.19	0.92
CS14D	CS14D_LR_13	chr3_216883757	3	216883757	0.25	5.24E-04	3.28	0.95

Env	QTL	SNP	Chr	Position	maf	P-value	LOD	Var Exp
CS14D	CS14D_LR_13	chr3_216883831	3	216883831	0.25	2.77E-04	3.56	1.05
CS14D	CS14D_LR_13	chr3_216986453	3	216986453	0.22	3.25E-04	3.49	1.02
CS14D	CS14D_LR_13	chr3_216986511	3	216986511	0.21	4.17E-04	3.38	0.98
CS14D	CS14D_LR_13	chr3_216987644	3	216987644	0.22	1.71E-04	3.77	1.12
CS14D	CS14D_LR_13	chr3_216987686	3	216987686	0.22	1.74E-04	3.76	1.12
CS14D	CS14D_LR_13	chr3_217007695	3	217007695	0.22	2.28E-04	3.64	1.07
CS14D	CS14D_LR_13	chr3_217008553	3	217008553	0.23	7.64E-04	3.12	0.89
CS14D	CS14D_LR_13	chr3_217008607	3	217008607	0.23	7.64E-04	3.12	0.89
CS14D	CS14D_LR_13	chr3_217008748	3	217008748	0.23	2.56E-04	3.59	1.06
CS14D	CS14D_LR_13	chr3_217096387	3	217096387	0.23	7.59E-04	3.12	0.90
CS14D	CS14D_LR_13	chr3_217213085	3	217213085	0.23	7.21E-04	3.14	0.90
CS14D	CS14D_LR_13	chr3_217213193	3	217213193	0.23	7.36E-04	3.13	0.90
CS14D	CS14D_LR_13	chr3_217292677	3	217292677	0.24	1.38E-04	3.86	1.15
CS14D	CS14D_LR_13	chr3_217293516	3	217293516	0.24	1.07E-04	3.97	1.19
CS14D	CS14D_LR_13	chr3_217293519	3	217293519	0.24	1.07E-04	3.97	1.19
CS14D	CS14D_LR_13	chr3_217358505	3	217358505	0.25	1.85E-04	3.73	1.11
CS14D	CS14D_LR_13	chr3_217358612	3	217358612	0.25	1.63E-04	3.79	1.12
CS14D	CS14D_LR_13	chr3_217358652	3	217358652	0.26	4.74E-04	3.32	0.97
CS14D	CS14D_LR_13	chr3_217358657	3	217358657	0.23	1.10E-04	3.96	1.18
CS14D	CS14D_LR_13	chr3_217358660	3	217358660	0.23	2.64E-05	4.58	1.40
CS14D	CS14D_LR_13	chr3_217573081	3	217573081	0.25	2.48E-04	3.61	1.06
CS14D	CS14D_LR_13	chr3_217576592	3	217576592	0.25	9.21E-04	3.04	0.87
CS14D	CS14D_LR_13	chr3_217576652	3	217576652	0.26	1.01E-03	3.00	0.85
CS14D	CS14D_LR_13	chr3_217651336	3	217651336	0.25	1.52E-04	3.82	1.14
CS14D	CS14D_LR_13	chr3_217651338	3	217651338	0.25	1.63E-04	3.79	1.12
CS14D	CS14D_LR_13	chr3_217651342	3	217651342	0.47	8.82E-04	3.05	0.87
CS14D	CS14D_LR_13	chr3_217656898	3	217656898	0.26	6.20E-04	3.21	0.93
CS14D	CS14D_LR_13	chr3_217659852	3	217659852	0.25	2.70E-04	3.57	1.05
CS14D	CS14D_LR_13	chr3_217659912	3	217659912	0.25	3.68E-04	3.43	1.00
CS14D	CS14D_LR_13	chr3_217664640	3	217664640	0.26	4.05E-04	3.39	0.99
CS14D	CS14D_LR_13	chr3_217664657	3	217664657	0.26	2.67E-04	3.57	1.05
CS14D	CS14D_LR_14	chr5_152878478	5	152878478	0.14	9.07E-04	3.04	0.87
CS14D	CS14D_LR_15	chr5_168890531	5	168890531	0.19	7.07E-04	3.15	0.91
CS14D	CS14D_LR_15	chr5_169456606	5	169456606	0.20	7.85E-04	3.11	0.89
CS14D	CS14D_LR_16	chr5_209723088	5	209723088	0.29	1.96E-04	3.71	1.10
CS14D	CS14D_LR_16	chr5_209726342	5	209726342	0.29	6.91E-04	3.16	0.91
CS14D	CS14D_LR_17	chr5_211184051	5	211184051	0.14	2.32E-04	3.64	1.07
CS14D	CS14D_LR_18	chr6_30107699	6	30107699	0.27	3.08E-04	3.51	1.03

Env	QTL	SNP	Chr	Position	maf	P-value	LOD	Var Exp
CS14D	CS14D_LR_19	chr7_135832861	7	135832861	0.41	9.69E-04	3.01	0.86
CS14D	CS14D_LR_20	chr7_137521281	7	137521281	0.27	6.97E-04	3.16	0.91
CS14D	CS14D_LR_20	chr7_137522937	7	137522937	0.26	8.58E-04	3.07	0.88
CS14D	CS14D_LR_21	chr9_11155017	9	11155017	0.29	8.68E-04	3.06	0.88
CS14D	CS14D_LR_21	chr9_11340871	9	11340871	0.29	5.14E-04	3.29	0.95
CS14D	CS14D_LR_21	chr9_11340876	9	11340876	0.29	6.52E-04	3.19	0.92
CS14D	CS14D_LR_21	chr9_11436718	9	11436718	0.30	7.46E-04	3.13	0.90
CS14D	CS14D_LR_21	chr9_11779542	9	11779542	0.29	1.89E-04	3.72	1.10
CS14D	CS14D_LR_22	chr9_13149694	9	13149694	0.17	6.52E-06	5.19	1.61
CS14D	CS14D_LR_22	chr9_13161718	9	13161718	0.29	6.53E-04	3.19	0.92
CS14D	CS14D_LR_22	chr9_13162274	9	13162274	0.27	9.55E-04	3.02	0.86
CS14D	CS14D_LR_22	chr9_13930399	9	13930399	0.29	8.81E-04	3.06	0.87
CS14D	CS14D_LR_22	chr9_13930412	9	13930412	0.29	4.32E-04	3.37	0.98
CS14D	CS14D_LR_22	chr9_13930439	9	13930439	0.30	4.96E-04	3.30	0.96
CS14D	CS14D_LR_23	chr10_136616827	10	136616827	0.25	8.09E-04	3.09	0.89
CS14D	CS14D_LR_23	chr10_136616849	10	136616849	0.25	8.09E-04	3.09	0.89
CS14D	CS14D_LR_23	chr10_136616868	10	136616868	0.25	8.09E-04	3.09	0.89
CS14I	CS14I_LR_1	chr1_29190704	1	29190704	0.33	5.03E-04	3.30	0.91
CS14I	CS14I_LR_2	chr1_112889268	1	112889268	0.16	5.16E-04	3.29	0.91
CS14I	CS14I_LR_3	chr1_279911730	1	279911730	0.42	5.96E-04	3.23	0.89
CS14I	CS14I_LR_3	chr1_279911736	1	279911736	0.42	9.35E-04	3.03	0.83
CS14I	CS14I_LR_4	chr2_232986664	2	232986664	0.12	3.51E-04	3.45	0.96
CS14I	CS14I_LR_5	chr3_151334181	3	151334181	0.04	3.73E-04	3.43	0.96
CS14I	CS14I_LR_6	chr3_188555184	3	188555184	0.30	7.29E-04	3.14	0.86
CS14I	CS14I_LR_6	chr3_188555222	3	188555222	0.30	7.62E-04	3.12	0.85
CS14I	CS14I_LR_7	chr3_210508085	3	210508085	0.19	3.18E-04	3.50	0.98
CS14I	CS14I_LR_7	chr3_210508115	3	210508115	0.19	3.66E-04	3.44	0.96
CS14I	CS14I_LR_7	chr3_210523454	3	210523454	0.22	9.45E-04	3.02	0.82
CS14I	CS14I_LR_8	chr3_212431627	3	212431627	0.23	1.47E-04	3.83	1.09
CS14I	CS14I_LR_8	chr3_212431666	3	212431666	0.23	1.50E-04	3.82	1.08
CS14I	CS14I_LR_8	chr3_212431673	3	212431673	0.23	1.50E-04	3.82	1.08
CS14I	CS14I_LR_8	chr3_212500655	3	212500655	0.43	2.12E-04	3.67	1.04
CS14I	CS14I_LR_8	chr3_212500668	3	212500668	0.44	2.12E-04	3.67	1.04
CS14I	CS14I_LR_8	chr3_212500798	3	212500798	0.23	4.92E-04	3.31	0.92
CS14I	CS14I_LR_8	chr3_212503505	3	212503505	0.22	3.13E-04	3.50	0.98
CS14I	CS14I_LR_8	chr3_212503565	3	212503565	0.23	8.55E-04	3.07	0.84
CS14I	CS14I_LR_8	chr3_212503603	3	212503603	0.22	3.08E-04	3.51	0.98
CS14I	CS14I_LR_8	chr3_212503618	3	212503618	0.22	4.41E-04	3.36	0.93

Env	QTL	SNP	Chr	Position	maf	P-value	LOD	Var Exp
CS14I	CS14I_LR_8	chr3_212503621	3	212503621	0.22	4.41E-04	3.36	0.93
CS14I	CS14I_LR_8	chr3_212544357	3	212544357	0.20	9.56E-05	4.02	1.15
CS14I	CS14I_LR_8	chr3_212544386	3	212544386	0.19	7.47E-05	4.13	1.19
CS14I	CS14I_LR_8	chr3_212544402	3	212544402	0.18	3.02E-05	4.52	1.32
CS14I	CS14I_LR_8	chr3_212544407	3	212544407	0.18	8.24E-05	4.08	1.17
CS14I	CS14I_LR_8	chr3_212544446	3	212544446	0.19	7.19E-05	4.14	1.19
CS14I	CS14I_LR_8	chr3_212544490	3	212544490	0.23	4.14E-04	3.38	0.94
CS14I	CS14I_LR_8	chr3_212544517	3	212544517	0.23	4.86E-04	3.31	0.92
CS14I	CS14I_LR_8	chr3_212552797	3	212552797	0.22	9.98E-04	3.00	0.82
CS14I	CS14I_LR_8	chr3_212775559	3	212775559	0.22	4.72E-04	3.33	0.92
CS14I	CS14I_LR_8	chr3_213261438	3	213261438	0.24	2.82E-04	3.55	1.00
CS14I	CS14I_LR_8	chr3_214175963	3	214175963	0.23	3.02E-04	3.52	0.99
CS14I	CS14I_LR_9	chr3_216007444	3	216007444	0.22	9.48E-04	3.02	0.82
CS14I	CS14I_LR_9	chr3_216469079	3	216469079	0.14	3.30E-04	3.48	0.97
CS14I	CS14I_LR_9	chr3_216469326	3	216469326	0.23	3.08E-05	4.51	1.31
CS14I	CS14I_LR_9	chr3_216471587	3	216471587	0.22	4.03E-05	4.39	1.27
CS14I	CS14I_LR_9	chr3_216473159	3	216473159	0.23	7.68E-05	4.11	1.18
CS14I	CS14I_LR_9	chr3_216473192	3	216473192	0.23	7.68E-05	4.11	1.18
CS14I	CS14I_LR_9	chr3_216523181	3	216523181	0.22	5.49E-04	3.26	0.90
CS14I	CS14I_LR_9	chr3_216523205	3	216523205	0.22	5.41E-04	3.27	0.90
CS14I	CS14I_LR_9	chr3_216528320	3	216528320	0.23	9.89E-04	3.00	0.82
CS14I	CS14I_LR_9	chr3_216883752	3	216883752	0.24	7.84E-04	3.11	0.85
CS14I	CS14I_LR_9	chr3_216883757	3	216883757	0.25	3.26E-04	3.49	0.97
CS14I	CS14I_LR_9	chr3_216883831	3	216883831	0.25	4.11E-05	4.39	1.27
CS14I	CS14I_LR_9	chr3_216986453	3	216986453	0.22	1.02E-04	3.99	1.14
CS14I	CS14I_LR_9	chr3_216987644	3	216987644	0.22	1.07E-04	3.97	1.13
CS14I	CS14I_LR_9	chr3_216987686	3	216987686	0.22	1.06E-04	3.97	1.13
CS14I	CS14I_LR_9	chr3_217007695	3	217007695	0.22	1.07E-04	3.97	1.13
CS14I	CS14I_LR_9	chr3_217008553	3	217008553	0.23	3.50E-04	3.46	0.96
CS14I	CS14I_LR_9	chr3_217008607	3	217008607	0.23	3.50E-04	3.46	0.96
CS14I	CS14I_LR_9	chr3_217008706	3	217008706	0.22	7.29E-04	3.14	0.86
CS14I	CS14I_LR_9	chr3_217008748	3	217008748	0.23	5.24E-05	4.28	1.24
CS14I	CS14I_LR_9	chr3_217096387	3	217096387	0.23	8.56E-04	3.07	0.84
CS14I	CS14I_LR_9	chr3_217096655	3	217096655	0.21	8.31E-04	3.08	0.84
CS14I	CS14I_LR_9	chr3_217213085	3	217213085	0.23	6.35E-05	4.20	1.21
CS14I	CS14I_LR_9	chr3_217213193	3	217213193	0.23	8.48E-04	3.07	0.84
CS14I	CS14I_LR_9	chr3_217292671	3	217292671	0.23	3.52E-04	3.45	0.96
CS14I	CS14I_LR_9	chr3_217292677	3	217292677	0.24	6.25E-04	3.20	0.88

Env	QTL	SNP	Chr	Position	maf	P-value	LOD	Var Exp
CS14I	CS14I_LR_9	chr3_217293516	3	217293516	0.24	2.31E-04	3.64	1.02
CS14I	CS14I_LR_9	chr3_217293519	3	217293519	0.24	2.31E-04	3.64	1.02
CS14I	CS14I_LR_9	chr3_217294002	3	217294002	0.24	1.35E-04	3.87	1.10
CS14I	CS14I_LR_9	chr3_217461401	3	217461401	0.24	6.59E-04	3.18	0.87
CS14I	CS14I_LR_9	chr3_217651336	3	217651336	0.25	9.08E-04	3.04	0.83
CS14I	CS14I_LR_9	chr3_217651342	3	217651342	0.47	7.99E-04	3.10	0.85
CS14I	CS14I_LR_9	chr3_217936114	3	217936114	0.44	2.16E-04	3.67	1.03
CS14I	CS14I_LR_9	chr3_217936224	3	217936224	0.47	3.14E-04	3.50	0.98
CS14I	CS14I_LR_9	chr3_217936234	3	217936234	0.46	2.78E-04	3.56	1.00
CS14I	CS14I_LR_9	chr3_218176291	3	218176291	0.23	2.73E-04	3.56	1.00
CS14I	CS14I_LR_9	chr3_218184190	3	218184190	0.22	3.78E-04	3.42	0.95
CS14I	CS14I_LR_9	chr3_218184213	3	218184213	0.27	9.58E-04	3.02	0.82
CS14I	CS14I_LR_9	chr3_218264905	3	218264905	0.24	8.79E-04	3.06	0.83
CS14I	CS14I_LR_9	chr3_218362523	3	218362523	0.22	9.53E-04	3.02	0.82
CS14I	CS14I_LR_9	chr3_218362541	3	218362541	0.22	9.53E-04	3.02	0.82
CS14I	CS14I_LR_9	chr3_218835686	3	218835686	0.26	7.24E-04	3.14	0.86
CS14I	CS14I_LR_9	chr3_218836461	3	218836461	0.21	9.00E-04	3.05	0.83
CS14I	CS14I_LR_10	chr5_210058373	5	210058373	0.32	5.87E-04	3.23	0.89
CS14I	CS14I_LR_10	chr5_210475872	5	210475872	0.29	5.85E-04	3.23	0.89
CS14I	CS14I_LR_10	chr5_210557993	5	210557993	0.30	1.21E-04	3.92	1.12
CS14I	CS14I_LR_10	chr5_210589634	5	210589634	0.29	3.34E-04	3.48	0.97
CS14I	CS14I_LR_10	chr5_210589747	5	210589747	0.30	6.35E-05	4.20	1.21
CS14I	CS14I_LR_10	chr5_210598205	5	210598205	0.30	1.69E-04	3.77	1.07
CS14I	CS14I_LR_10	chr5_210769806	5	210769806	0.30	2.25E-04	3.65	1.03
CS14I	CS14I_LR_10	chr5_210769828	5	210769828	0.29	5.44E-04	3.26	0.90
CS14I	CS14I_LR_10	chr5_210769863	5	210769863	0.30	1.93E-04	3.71	1.05
CS14I	CS14I_LR_10	chr5_210769955	5	210769955	0.31	1.92E-04	3.72	1.05
CS14I	CS14I_LR_10	chr5_210772379	5	210772379	0.30	5.13E-04	3.29	0.91
CS14I	CS14I_LR_11	chr6_15585446	6	15585446	0.27	8.53E-04	3.07	0.84
CS14I	CS14I_LR_12	chr6_16798376	6	16798376	0.28	2.87E-05	4.54	1.32
CS14I	CS14I_LR_13	chr6_18845753	6	18845753	0.29	1.55E-04	3.81	1.08
CS14I	CS14I_LR_13	chr6_18845787	6	18845787	0.29	6.55E-05	4.18	1.20
CS14I	CS14I_LR_13	chr6_18845793	6	18845793	0.29	2.57E-04	3.59	1.01
CS14I	CS14I_LR_13	chr6_18845871	6	18845871	0.28	1.57E-04	3.80	1.08
CS14I	CS14I_LR_13	chr6_18845949	6	18845949	0.27	2.92E-04	3.53	0.99
CS14I	CS14I_LR_13	chr6_18846033	6	18846033	0.29	2.37E-04	3.62	1.02
CS14I	CS14I_LR_13	chr6_18924417	6	18924417	0.28	1.08E-04	3.97	1.13
CS14I	CS14I_LR_14	chr6_22003178	6	22003178	0.26	3.41E-04	3.47	0.97

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CS14I	CS14I_LR_14	chr6_22267127	6	22267127	0.26	1.42E-04	3.85	1.09
CS14I	CS14I_LR_14	chr6_22267155	6	22267155	0.26	2.28E-04	3.64	1.03
CS14I	CS14I_LR_14	chr6_22267162	6	22267162	0.26	1.86E-04	3.73	1.05
CS14I	CS14I_LR_14	chr6_22267185	6	22267185	0.26	1.86E-04	3.73	1.05
CS14I	CS14I_LR_14	chr6_23251762	6	23251762	0.27	9.89E-05	4.00	1.14
CS14I	CS14I_LR_14	chr6_23827975	6	23827975	0.27	4.79E-05	4.32	1.25
CS14I	CS14I_LR_14	chr6_24317651	6	24317651	0.26	8.37E-04	3.08	0.84
CS14I	CS14I_LR_14	chr6_25291474	6	25291474	0.27	4.17E-04	3.38	0.94
CS14I	CS14I_LR_14	chr6_25337116	6	25337116	0.27	3.29E-04	3.48	0.97
CS14I	CS14I_LR_14	chr6_25545255	6	25545255	0.27	8.42E-04	3.07	0.84
CS14I	CS14I_LR_15	chr6_26709927	6	26709927	0.29	9.93E-04	3.00	0.82
CS14I	CS14I_LR_15	chr6_26709942	6	26709942	0.29	9.93E-04	3.00	0.82
CS14I	CS14I_LR_15	chr6_26709979	6	26709979	0.29	9.93E-04	3.00	0.82
CS14I	CS14I_LR_15	chr6_26709986	6	26709986	0.29	9.93E-04	3.00	0.82
CS14I	CS14I_LR_15	chr6_26709996	6	26709996	0.29	9.93E-04	3.00	0.82
CS14I	CS14I_LR_16	chr6_150778426	6	150778426	0.27	5.24E-04	3.28	0.91
CS15T	CS15T_LR_1	chr1_12871691	1	12871691	0.22	6.37E-04	3.20	0.87
CS15T	CS15T_LR_1	chr1_12871707	1	12871707	0.22	4.90E-04	3.31	0.91
CS15T	CS15T_LR_2	chr1_14036950	1	14036950	0.21	9.68E-04	3.01	0.82
CS15T	CS15T_LR_2	chr1_14037142	1	14037142	0.22	4.61E-04	3.34	0.92
CS15T	CS15T_LR_2	chr1_14103610	1	14103610	0.46	1.00E-03	3.00	0.81
CS15T	CS15T_LR_3	chr1_29543112	1	29543112	0.37	5.16E-04	3.29	0.90
CS15T	CS15T_LR_4	chr1_33162621	1	33162621	0.43	2.15E-04	3.67	1.03
CS15T	CS15T_LR_5	chr1_191369247	1	191369247	0.25	9.87E-04	3.01	0.81
CS15T	CS15T_LR_5	chr1_191369813	1	191369813	0.26	8.73E-04	3.06	0.83
CS15T	CS15T_LR_5	chr1_191862495	1	191862495	0.30	1.68E-04	3.77	1.06
CS15T	CS15T_LR_5	chr1_191895505	1	191895505	0.24	9.40E-04	3.03	0.82
CS15T	CS15T_LR_6	chr2_17611727	2	17611727	0.31	7.05E-04	3.15	0.86
CS15T	CS15T_LR_6	chr2_17862992	2	17862992	0.30	6.73E-04	3.17	0.87
CS15T	CS15T_LR_6	chr2_18133200	2	18133200	0.30	8.02E-04	3.10	0.84
CS15T	CS15T_LR_6	chr2_18238652	2	18238652	0.29	6.61E-04	3.18	0.87
CS15T	CS15T_LR_6	chr2_18238654	2	18238654	0.30	4.68E-04	3.33	0.92
CS15T	CS15T_LR_6	chr2_18249561	2	18249561	0.30	4.07E-04	3.39	0.94
CS15T	CS15T_LR_6	chr2_18417962	2	18417962	0.32	1.70E-05	4.77	1.39
CS15T	CS15T_LR_6	chr2_18418080	2	18418080	0.32	6.28E-04	3.20	0.88
CS15T	CS15T_LR_6	chr2_18626749	2	18626749	0.31	2.48E-04	3.60	1.01
CS15T	CS15T_LR_6	chr2_18712957	2	18712957	0.31	8.17E-04	3.09	0.84
CS15T	CS15T_LR_6	chr2_19143945	2	19143945	0.30	8.49E-04	3.07	0.83

Env	QTL	SNP	Chr	Position	maf	P-value	LOD	Var Exp
CS15T	CS15T_LR_6	chr2_19257420	2	19257420	0.30	6.88E-04	3.16	0.86
CS15T	CS15T_LR_6	chr2_19265231	2	19265231	0.31	8.84E-04	3.05	0.83
CS15T	CS15T_LR_6	chr2_19265289	2	19265289	0.31	7.35E-04	3.13	0.85
CS15T	CS15T_LR_6	chr2_19266169	2	19266169	0.43	8.46E-06	5.07	1.49
CS15T	CS15T_LR_6	chr2_19319964	2	19319964	0.46	1.33E-06	5.88	1.76
CS15T	CS15T_LR_6	chr2_19320066	2	19320066	0.29	7.45E-04	3.13	0.85
CS15T	CS15T_LR_6	chr2_19320067	2	19320067	0.48	1.46E-06	5.84	1.75
CS15T	CS15T_LR_6	chr2_19359455	2	19359455	0.30	8.80E-04	3.06	0.83
CS15T	CS15T_LR_6	chr2_19439245	2	19439245	0.44	2.00E-05	4.70	1.37
CS15T	CS15T_LR_6	chr2_19440190	2	19440190	0.44	1.02E-04	3.99	1.13
CS15T	CS15T_LR_6	chr2_19440207	2	19440207	0.44	1.02E-04	3.99	1.13
CS15T	CS15T_LR_6	chr2_19440431	2	19440431	0.32	3.69E-04	3.43	0.95
CS15T	CS15T_LR_6	chr2_19460480	2	19460480	0.42	2.04E-04	3.69	1.03
CS15T	CS15T_LR_6	chr2_19460481	2	19460481	0.42	1.91E-04	3.72	1.04
CS15T	CS15T_LR_6	chr2_19829207	2	19829207	0.45	1.50E-04	3.82	1.08
CS15T	CS15T_LR_6	chr2_19921646	2	19921646	0.44	1.05E-04	3.98	1.13
CS15T	CS15T_LR_6	chr2_19921664	2	19921664	0.44	1.05E-04	3.98	1.13
CS15T	CS15T_LR_6	chr2_20003159	2	20003159	0.43	1.02E-04	3.99	1.13
CS15T	CS15T_LR_6	chr2_20003167	2	20003167	0.43	1.02E-04	3.99	1.13
CS15T	CS15T_LR_6	chr2_20003181	2	20003181	0.43	1.02E-04	3.99	1.13
CS15T	CS15T_LR_6	chr2_20033092	2	20033092	0.43	6.16E-05	4.21	1.21
CS15T	CS15T_LR_6	chr2_20109780	2	20109780	0.16	5.45E-04	3.26	0.90
CS15T	CS15T_LR_6	chr2_20109986	2	20109986	0.44	1.70E-05	4.77	1.39
CS15T	CS15T_LR_6	chr2_20110027	2	20110027	0.44	1.34E-05	4.87	1.43
CS15T	CS15T_LR_6	chr2_20110029	2	20110029	0.44	9.70E-06	5.01	1.47
CS15T	CS15T_LR_6	chr2_20120085	2	20120085	0.44	7.04E-05	4.15	1.19
CS15T	CS15T_LR_6	chr2_20120123	2	20120123	0.44	8.11E-05	4.09	1.17
CS15T	CS15T_LR_6	chr2_20120142	2	20120142	0.44	5.92E-05	4.23	1.21
CS15T	CS15T_LR_6	chr2_20120193	2	20120193	0.44	5.72E-05	4.24	1.22
CS15T	CS15T_LR_6	chr2_20120214	2	20120214	0.44	9.52E-05	4.02	1.14
CS15T	CS15T_LR_6	chr2_20120216	2	20120216	0.44	7.89E-05	4.10	1.17
CS15T	CS15T_LR_6	chr2_20120218	2	20120218	0.44	1.09E-04	3.96	1.12
CS15T	CS15T_LR_6	chr2_20120373	2	20120373	0.45	1.77E-04	3.75	1.05
CS15T	CS15T_LR_6	chr2_20120413	2	20120413	0.45	4.71E-04	3.33	0.92
CS15T	CS15T_LR_6	chr2_20120457	2	20120457	0.44	9.73E-04	3.01	0.81
CS15T	CS15T_LR_6	chr2_20410450	2	20410450	0.44	7.14E-04	3.15	0.86
CS15T	CS15T_LR_6	chr2_20410474	2	20410474	0.44	7.61E-04	3.12	0.85
CS15T	CS15T_LR_6	chr2_20418120	2	20418120	0.16	3.36E-04	3.47	0.96

Env	QTL	SNP	Chr	Position	maf	P-value	LOD	Var Exp
CS15T	CS15T_LR_7	chr3_156434758	3	156434758	0.14	1.00E-04	4.00	1.14
CS15T	CS15T_LR_8	chr3_170778982	3	170778982	0.48	8.54E-04	3.07	0.83
CS15T	CS15T_LR_9	chr3_210523454	3	210523454	0.22	4.63E-04	3.33	0.92
CS15T	CS15T_LR_10	chr3_212503505	3	212503505	0.22	6.68E-04	3.18	0.87
CS15T	CS15T_LR_10	chr3_212544357	3	212544357	0.20	2.62E-04	3.58	1.00
CS15T	CS15T_LR_10	chr3_212544386	3	212544386	0.19	5.31E-04	3.28	0.90
CS15T	CS15T_LR_10	chr3_212544402	3	212544402	0.18	4.49E-04	3.35	0.92
CS15T	CS15T_LR_10	chr3_212544407	3	212544407	0.18	5.66E-04	3.25	0.89
CS15T	CS15T_LR_10	chr3_212544446	3	212544446	0.19	3.77E-04	3.42	0.95
CS15T	CS15T_LR_11	chr3_213778726	3	213778726	0.23	7.44E-04	3.13	0.85
CS15T	CS15T_LR_12	chr3_214858102	3	214858102	0.22	5.30E-04	3.28	0.90
CS15T	CS15T_LR_12	chr3_214858593	3	214858593	0.22	8.71E-04	3.06	0.83
CS15T	CS15T_LR_12	chr3_214858647	3	214858647	0.22	5.76E-04	3.24	0.89
CS15T	CS15T_LR_13	chr3_216469326	3	216469326	0.23	2.44E-04	3.61	1.01
CS15T	CS15T_LR_13	chr3_216471587	3	216471587	0.22	2.99E-04	3.52	0.98
CS15T	CS15T_LR_13	chr3_216473159	3	216473159	0.23	7.78E-04	3.11	0.85
CS15T	CS15T_LR_13	chr3_216473192	3	216473192	0.23	7.78E-04	3.11	0.85
CS15T	CS15T_LR_13	chr3_216523181	3	216523181	0.22	9.43E-04	3.03	0.82
CS15T	CS15T_LR_13	chr3_216883757	3	216883757	0.25	7.56E-04	3.12	0.85
CS15T	CS15T_LR_13	chr3_216883831	3	216883831	0.25	7.41E-04	3.13	0.85
CS15T	CS15T_LR_13	chr3_216986453	3	216986453	0.22	1.74E-04	3.76	1.06
CS15T	CS15T_LR_13	chr3_216986511	3	216986511	0.21	2.46E-04	3.61	1.01
CS15T	CS15T_LR_13	chr3_216987644	3	216987644	0.22	4.53E-04	3.34	0.92
CS15T	CS15T_LR_13	chr3_216987686	3	216987686	0.22	4.65E-04	3.33	0.92
CS15T	CS15T_LR_13	chr3_217007695	3	217007695	0.22	3.59E-04	3.45	0.95
CS15T	CS15T_LR_13	chr3_217008553	3	217008553	0.23	4.08E-04	3.39	0.94
CS15T	CS15T_LR_13	chr3_217008607	3	217008607	0.23	4.08E-04	3.39	0.94
CS15T	CS15T_LR_13	chr3_217008748	3	217008748	0.23	1.99E-04	3.70	1.04
CS15T	CS15T_LR_13	chr3_217096387	3	217096387	0.23	7.54E-04	3.12	0.85
CS15T	CS15T_LR_13	chr3_217096642	3	217096642	0.21	1.30E-04	3.89	1.10
CS15T	CS15T_LR_13	chr3_217096655	3	217096655	0.21	1.43E-04	3.84	1.08
CS15T	CS15T_LR_13	chr3_217096851	3	217096851	0.22	7.71E-04	3.11	0.85
CS15T	CS15T_LR_13	chr3_217213085	3	217213085	0.23	2.03E-05	4.69	1.36
CS15T	CS15T_LR_13	chr3_217213193	3	217213193	0.23	1.26E-04	3.90	1.10
CS15T	CS15T_LR_13	chr3_217292671	3	217292671	0.23	2.45E-05	4.61	1.34
CS15T	CS15T_LR_13	chr3_217292677	3	217292677	0.24	4.06E-05	4.39	1.27
CS15T	CS15T_LR_13	chr3_217293516	3	217293516	0.24	1.84E-05	4.74	1.38
CS15T	CS15T_LR_13	chr3_217293519	3	217293519	0.24	1.84E-05	4.74	1.38

Env	QTL	SNP	Chr	Position	maf	P-value	LOD	Var Exp
CS15T	CS15T_LR_13	chr3_217294002	3	217294002	0.24	3.78E-05	4.42	1.28
CS15T	CS15T_LR_13	chr3_217358505	3	217358505	0.25	1.72E-05	4.77	1.39
CS15T	CS15T_LR_13	chr3_217358612	3	217358612	0.25	1.55E-05	4.81	1.40
CS15T	CS15T_LR_13	chr3_217358652	3	217358652	0.26	4.94E-05	4.31	1.24
CS15T	CS15T_LR_13	chr3_217358657	3	217358657	0.23	7.41E-05	4.13	1.18
CS15T	CS15T_LR_13	chr3_217358660	3	217358660	0.23	1.07E-04	3.97	1.13
CS15T	CS15T_LR_13	chr3_217358898	3	217358898	0.22	3.51E-04	3.45	0.96
CS15T	CS15T_LR_13	chr3_217358974	3	217358974	0.22	3.17E-05	4.50	1.30
CS15T	CS15T_LR_13	chr3_217359376	3	217359376	0.22	4.97E-05	4.30	1.24
CS15T	CS15T_LR_13	chr3_217461401	3	217461401	0.24	2.71E-04	3.57	0.99
CS15T	CS15T_LR_13	chr3_217463033	3	217463033	0.48	3.27E-05	4.48	1.30
CS15T	CS15T_LR_13	chr3_217463044	3	217463044	0.47	3.02E-05	4.52	1.31
CS15T	CS15T_LR_13	chr3_217463072	3	217463072	0.47	3.10E-05	4.51	1.30
CS15T	CS15T_LR_13	chr3_217573062	3	217573062	0.23	3.43E-04	3.46	0.96
CS15T	CS15T_LR_13	chr3_217573081	3	217573081	0.25	6.38E-05	4.20	1.20
CS15T	CS15T_LR_13	chr3_217576592	3	217576592	0.25	1.02E-04	3.99	1.13
CS15T	CS15T_LR_13	chr3_217576603	3	217576603	0.25	7.54E-05	4.12	1.18
CS15T	CS15T_LR_13	chr3_217576622	3	217576622	0.23	3.95E-05	4.40	1.27
CS15T	CS15T_LR_13	chr3_217576652	3	217576652	0.26	1.41E-04	3.85	1.09
CS15T	CS15T_LR_13	chr3_217576679	3	217576679	0.23	1.04E-04	3.98	1.13
CS15T	CS15T_LR_13	chr3_217584263	3	217584263	0.27	5.14E-04	3.29	0.90
CS15T	CS15T_LR_13	chr3_217584373	3	217584373	0.27	2.11E-04	3.68	1.03
CS15T	CS15T_LR_13	chr3_217584382	3	217584382	0.27	1.76E-04	3.76	1.06
CS15T	CS15T_LR_13	chr3_217633065	3	217633065	0.26	3.83E-05	4.42	1.27
CS15T	CS15T_LR_13	chr3_217633111	3	217633111	0.26	8.33E-05	4.08	1.16
CS15T	CS15T_LR_13	chr3_217633164	3	217633164	0.26	3.77E-05	4.42	1.28
CS15T	CS15T_LR_13	chr3_217637698	3	217637698	0.23	3.33E-04	3.48	0.97
CS15T	CS15T_LR_13	chr3_217637708	3	217637708	0.46	2.28E-05	4.64	1.35
CS15T	CS15T_LR_13	chr3_217637712	3	217637712	0.24	5.25E-04	3.28	0.90
CS15T	CS15T_LR_13	chr3_217637717	3	217637717	0.32	6.16E-04	3.21	0.88
CS15T	CS15T_LR_13	chr3_217637726	3	217637726	0.23	4.22E-04	3.37	0.93
CS15T	CS15T_LR_13	chr3_217651324	3	217651324	0.31	1.31E-04	3.88	1.10
CS15T	CS15T_LR_13	chr3_217651336	3	217651336	0.25	6.53E-05	4.19	1.20
CS15T	CS15T_LR_13	chr3_217651338	3	217651338	0.25	6.07E-05	4.22	1.21
CS15T	CS15T_LR_13	chr3_217651342	3	217651342	0.47	1.06E-04	3.97	1.13
CS15T	CS15T_LR_13	chr3_217651356	3	217651356	0.31	1.35E-04	3.87	1.09
CS15T	CS15T_LR_13	chr3_217651494	3	217651494	0.27	1.45E-04	3.84	1.08
CS15T	CS15T_LR_13	chr3_217651500	3	217651500	0.43	1.27E-04	3.90	1.10

Env	QTL	SNP	Chr	Position	maf	P-value	LOD	Var Exp
CS15T	CS15T_LR_13	chr3_217656898	3	217656898	0.26	9.25E-05	4.03	1.15
CS15T	CS15T_LR_13	chr3_217657019	3	217657019	0.46	2.06E-04	3.69	1.03
CS15T	CS15T_LR_13	chr3_217657054	3	217657054	0.26	3.47E-04	3.46	0.96
CS15T	CS15T_LR_13	chr3_217657059	3	217657059	0.46	2.06E-04	3.69	1.03
CS15T	CS15T_LR_13	chr3_217659544	3	217659544	0.29	1.50E-04	3.82	1.08
CS15T	CS15T_LR_13	chr3_217659852	3	217659852	0.25	8.68E-05	4.06	1.16
CS15T	CS15T_LR_13	chr3_217659912	3	217659912	0.25	4.92E-05	4.31	1.24
CS15T	CS15T_LR_13	chr3_217664640	3	217664640	0.26	2.57E-04	3.59	1.00
CS15T	CS15T_LR_13	chr3_217664657	3	217664657	0.26	1.18E-04	3.93	1.11
CS15T	CS15T_LR_13	chr3_217664779	3	217664779	0.47	3.26E-05	4.49	1.30
CS15T	CS15T_LR_13	chr3_217664830	3	217664830	0.47	1.40E-04	3.85	1.09
CS15T	CS15T_LR_13	chr3_217666097	3	217666097	0.47	4.17E-04	3.38	0.93
CS15T	CS15T_LR_13	chr3_217666196	3	217666196	0.25	4.31E-04	3.37	0.93
CS15T	CS15T_LR_13	chr3_217670323	3	217670323	0.26	1.04E-04	3.98	1.13
CS15T	CS15T_LR_13	chr3_217670855	3	217670855	0.25	7.16E-05	4.14	1.18
CS15T	CS15T_LR_13	chr3_217670991	3	217670991	0.26	1.32E-04	3.88	1.10
CS15T	CS15T_LR_13	chr3_217704895	3	217704895	0.46	1.94E-04	3.71	1.04
CS15T	CS15T_LR_13	chr3_217704943	3	217704943	0.46	1.95E-04	3.71	1.04
CS15T	CS15T_LR_13	chr3_217821048	3	217821048	0.46	2.23E-04	3.65	1.02
CS15T	CS15T_LR_13	chr3_217877595	3	217877595	0.26	3.13E-04	3.50	0.97
CS15T	CS15T_LR_13	chr3_217877648	3	217877648	0.29	5.76E-05	4.24	1.21
CS15T	CS15T_LR_13	chr3_217877679	3	217877679	0.25	2.77E-04	3.56	0.99
CS15T	CS15T_LR_13	chr3_217936114	3	217936114	0.44	4.11E-06	5.39	1.60
CS15T	CS15T_LR_13	chr3_217936224	3	217936224	0.47	1.83E-05	4.74	1.38
CS15T	CS15T_LR_13	chr3_217936234	3	217936234	0.46	2.43E-05	4.61	1.34
CS15T	CS15T_LR_13	chr3_217936427	3	217936427	0.28	9.47E-05	4.02	1.14
CS15T	CS15T_LR_13	chr3_218176291	3	218176291	0.23	1.32E-04	3.88	1.10
CS15T	CS15T_LR_13	chr3_218184190	3	218184190	0.22	8.64E-04	3.06	0.83
CS15T	CS15T_LR_13	chr3_218184213	3	218184213	0.27	1.18E-04	3.93	1.11
CS15T	CS15T_LR_13	chr3_218184307	3	218184307	0.27	1.31E-04	3.88	1.10
CS15T	CS15T_LR_13	chr3_218184327	3	218184327	0.27	1.31E-04	3.88	1.10
CS15T	CS15T_LR_13	chr3_218323511	3	218323511	0.44	4.99E-05	4.30	1.24
CS15T	CS15T_LR_13	chr3_218323603	3	218323603	0.46	2.49E-04	3.60	1.01
CS15T	CS15T_LR_13	chr3_218323831	3	218323831	0.45	2.73E-04	3.56	0.99
CS15T	CS15T_LR_13	chr3_218323915	3	218323915	0.45	2.76E-04	3.56	0.99
CS15T	CS15T_LR_13	chr3_218362523	3	218362523	0.22	7.05E-04	3.15	0.86
CS15T	CS15T_LR_13	chr3_218362541	3	218362541	0.22	7.05E-04	3.15	0.86
CS15T	CS15T_LR_13	chr3_218782424	3	218782424	0.26	8.98E-04	3.05	0.83

Env	QTL	SNP	Chr	Position	maf	P-value	LOD	Var Exp
CS15T	CS15T_LR_13	chr3_218835611	3	218835611	0.30	3.73E-04	3.43	0.95
CS15T	CS15T_LR_13	chr3_219183310	3	219183310	0.26	6.89E-05	4.16	1.19
CS15T	CS15T_LR_13	chr3_219183317	3	219183317	0.26	1.45E-04	3.84	1.08
CS15T	CS15T_LR_13	chr3_219183329	3	219183329	0.25	6.88E-05	4.16	1.19
CS15T	CS15T_LR_13	chr3_219183330	3	219183330	0.25	6.88E-05	4.16	1.19
CS15T	CS15T_LR_13	chr3_219183339	3	219183339	0.25	6.18E-05	4.21	1.20
CS15T	CS15T_LR_13	chr3_219190502	3	219190502	0.14	4.52E-04	3.35	0.92
CS15T	CS15T_LR_13	chr3_219253658	3	219253658	0.28	7.81E-04	3.11	0.85
CS15T	CS15T_LR_13	chr3_219467330	3	219467330	0.25	5.96E-04	3.22	0.88
CS15T	CS15T_LR_13	chr3_219467464	3	219467464	0.26	4.74E-04	3.32	0.92
CS15T	CS15T_LR_13	chr3_219577381	3	219577381	0.14	2.61E-04	3.58	1.00
CS15T	CS15T_LR_14	chr4_32604570	4	32604570	0.46	9.06E-04	3.04	0.82
CS15T	CS15T_LR_15	chr5_84800434	5	84800434	0.25	5.75E-04	3.24	0.89
CS15T	CS15T_LR_16	chr6_15585446	6	15585446	0.27	3.53E-04	3.45	0.96
CS15T	CS15T_LR_17	chr6_16798376	6	16798376	0.28	2.46E-04	3.61	1.01
CS15T	CS15T_LR_18	chr6_18845753	6	18845753	0.29	7.43E-04	3.13	0.85
CS15T	CS15T_LR_18	chr6_18845787	6	18845787	0.29	4.01E-04	3.40	0.94
CS15T	CS15T_LR_18	chr6_18845793	6	18845793	0.29	6.07E-04	3.22	0.88
CS15T	CS15T_LR_18	chr6_18845871	6	18845871	0.28	7.04E-04	3.15	0.86
CS15T	CS15T_LR_18	chr6_18846033	6	18846033	0.29	1.62E-04	3.79	1.07
CS15T	CS15T_LR_18	chr6_18924417	6	18924417	0.28	5.99E-04	3.22	0.88
CS15T	CS15T_LR_19	chr6_22267127	6	22267127	0.26	5.20E-04	3.28	0.90
CS15T	CS15T_LR_19	chr6_22267155	6	22267155	0.26	4.71E-04	3.33	0.92
CS15T	CS15T_LR_19	chr6_22267162	6	22267162	0.26	3.97E-04	3.40	0.94
CS15T	CS15T_LR_19	chr6_22267185	6	22267185	0.26	3.97E-04	3.40	0.94
CS15T	CS15T_LR_20	chr6_23827975	6	23827975	0.27	7.06E-04	3.15	0.86
CS15T	CS15T_LR_21	chr6_25337116	6	25337116	0.27	2.73E-04	3.56	0.99
CS15T	CS15T_LR_22	chr6_26908759	6	26908759	0.27	9.67E-04	3.01	0.82
CS15T	CS15T_LR_22	chr6_26965917	6	26965917	0.27	9.91E-04	3.00	0.81
CS15T	CS15T_LR_22	chr6_27108514	6	27108514	0.28	3.15E-04	3.50	0.97
CS15T	CS15T_LR_23	chr6_28176551	6	28176551	0.29	8.02E-04	3.10	0.84
CS15T	CS15T_LR_23	chr6_28176556	6	28176556	0.29	6.68E-04	3.18	0.87
CS15T	CS15T_LR_23	chr6_28176569	6	28176569	0.29	9.69E-04	3.01	0.82
CS15T	CS15T_LR_24	chr6_29640871	6	29640871	0.28	4.92E-04	3.31	0.91
CS15T	CS15T_LR_24	chr6_30107699	6	30107699	0.27	4.27E-04	3.37	0.93
CS15T	CS15T_LR_24	chr6_30107846	6	30107846	0.27	1.71E-04	3.77	1.06
CS15T	CS15T_LR_25	chr6_31415881	6	31415881	0.27	1.01E-03	3.00	0.81
CS15T	CS15T_LR_26	chr6_150082817	6	150082817	0.39	3.73E-04	3.43	0.95

Env	QTL	SNP	Chr	Position	maf	P-value	LOD	Var Exp
CS15T	CS15T_LR_26	chr6_150103925	6	150103925	0.27	7.88E-04	3.10	0.84
CS15T	CS15T_LR_26	chr6_150103929	6	150103929	0.27	8.22E-04	3.08	0.84
CS15T	CS15T_LR_26	chr6_150341675	6	150341675	0.24	8.46E-04	3.07	0.83
CS15T	CS15T_LR_26	chr6_150664926	6	150664926	0.27	3.83E-04	3.42	0.95
CS15T	CS15T_LR_26	chr6_150664929	6	150664929	0.27	3.83E-04	3.42	0.95
CS15T	CS15T_LR_26	chr6_150749586	6	150749586	0.49	3.64E-04	3.44	0.95
CS15T	CS15T_LR_26	chr6_150752640	6	150752640	0.24	7.36E-04	3.13	0.85
CS15T	CS15T_LR_26	chr6_150796190	6	150796190	0.25	9.37E-04	3.03	0.82
CS15T	CS15T_LR_26	chr6_150845279	6	150845279	0.24	2.56E-04	3.59	1.00
CS15T	CS15T_LR_26	chr6_150845287	6	150845287	0.24	2.56E-04	3.59	1.00
CS15T	CS15T_LR_26	chr6_150845375	6	150845375	0.25	6.20E-04	3.21	0.88
CS15T	CS15T_LR_26	chr6_150845380	6	150845380	0.25	8.60E-04	3.07	0.83
CS15T	CS15T_LR_26	chr6_150892963	6	150892963	0.25	2.75E-04	3.56	0.99
CS15T	CS15T_LR_26	chr6_150920561	6	150920561	0.24	2.77E-04	3.56	0.99
CS15T	CS15T_LR_26	chr6_150923451	6	150923451	0.24	5.54E-04	3.26	0.89
CS15T	CS15T_LR_26	chr6_150941781	6	150941781	0.24	5.53E-04	3.26	0.89
CS15T	CS15T_LR_26	chr6_151135782	6	151135782	0.26	6.30E-04	3.20	0.88
CS15T	CS15T_LR_26	chr6_151135805	6	151135805	0.26	8.18E-04	3.09	0.84
CS15T	CS15T_LR_26	chr6_151543661	6	151543661	0.25	3.42E-04	3.47	0.96
CS15T	CS15T_LR_26	chr6_151543670	6	151543670	0.25	3.02E-04	3.52	0.98
CS15T	CS15T_LR_27	chr7_118528185	7	118528185	0.28	4.08E-05	4.39	1.26
CS15T	CS15T_LR_27	chr7_118532591	7	118532591	0.29	2.00E-04	3.70	1.04
CS15T	CS15T_LR_27	chr7_118532662	7	118532662	0.28	2.38E-04	3.62	1.01
CS15T	CS15T_LR_27	chr7_118532679	7	118532679	0.19	1.26E-04	3.90	1.10
CS15T	CS15T_LR_27	chr7_118532681	7	118532681	0.28	2.55E-04	3.59	1.00
CS15T	CS15T_LR_28	chr9_16733642	9	16733642	0.31	7.24E-04	3.14	0.86
CS15T	CS15T_LR_29	chr10_137161901	10	137161901	0.24	8.97E-04	3.05	0.83
CS15TP	CS15TP_LR_1	chr1_29190704	1	29190704	0.33	1.60E-04	3.80	1.09
CS15TP	CS15TP_LR_1	chr1_29197757	1	29197757	0.47	2.64E-04	3.58	1.02
CS15TP	CS15TP_LR_1	chr1_29543112	1	29543112	0.37	4.02E-04	3.40	0.96
CS15TP	CS15TP_LR_2	chr1_87602307	1	87602307	0.21	7.60E-04	3.12	0.86
CS15TP	CS15TP_LR_2	chr1_87766772	1	87766772	0.22	4.60E-04	3.34	0.94
CS15TP	CS15TP_LR_2	chr1_87983162	1	87983162	0.24	9.30E-04	3.03	0.84
CS15TP	CS15TP_LR_3	chr1_253280955	1	253280955	0.32	9.44E-04	3.02	0.83
CS15TP	CS15TP_LR_4	chr1_258657988	1	258657988	0.48	9.64E-04	3.02	0.83
CS15TP	CS15TP_LR_5	chr2_17220039	2	17220039	0.30	5.89E-04	3.23	0.90
CS15TP	CS15TP_LR_5	chr2_17220051	2	17220051	0.30	3.29E-04	3.48	0.98
CS15TP	CS15TP_LR_5	chr2_17611727	2	17611727	0.31	4.17E-04	3.38	0.95

Env	QTL	SNP	Chr	Position	maf	P-value	LOD	Var Exp
CS15TP	CS15TP_LR_5	chr2_18133200	2	18133200	0.30	4.11E-04	3.39	0.95
CS15TP	CS15TP_LR_5	chr2_18133274	2	18133274	0.30	5.63E-04	3.25	0.91
CS15TP	CS15TP_LR_5	chr2_18238652	2	18238652	0.29	7.15E-04	3.15	0.87
CS15TP	CS15TP_LR_5	chr2_18238654	2	18238654	0.30	6.56E-04	3.18	0.89
CS15TP	CS15TP_LR_5	chr2_18249561	2	18249561	0.30	4.46E-04	3.35	0.94
CS15TP	CS15TP_LR_5	chr2_18417962	2	18417962	0.32	2.90E-04	3.54	1.00
CS15TP	CS15TP_LR_6	chr2_182188997	2	182188997	0.24	3.95E-04	3.40	0.96
CS15TP	CS15TP_LR_6	chr2_182726955	2	182726955	0.24	1.62E-04	3.79	1.09
CS15TP	CS15TP_LR_6	chr2_184754512	2	184754512	0.50	1.03E-04	3.99	1.15
CS15TP	CS15TP_LR_6	chr2_184966064	2	184966064	0.27	7.21E-04	3.14	0.87
CS15TP	CS15TP_LR_6	chr2_185023662	2	185023662	0.23	5.33E-05	4.27	1.25
CS15TP	CS15TP_LR_6	chr2_185111923	2	185111923	0.26	7.27E-04	3.14	0.87
CS15TP	CS15TP_LR_6	chr2_185221168	2	185221168	0.26	9.64E-04	3.02	0.83
CS15TP	CS15TP_LR_6	chr2_185439625	2	185439625	0.49	6.66E-04	3.18	0.88
CS15TP	CS15TP_LR_6	chr2_185608017	2	185608017	0.23	6.32E-04	3.20	0.89
CS15TP	CS15TP_LR_6	chr2_185646260	2	185646260	0.26	9.71E-04	3.01	0.83
CS15TP	CS15TP_LR_7	chr3_156434758	3	156434758	0.14	2.04E-04	3.69	1.05
CS15TP	CS15TP_LR_8	chr3_170778982	3	170778982	0.48	6.38E-05	4.20	1.22
CS15TP	CS15TP_LR_9	chr3_209843961	3	209843961	0.22	8.44E-04	3.07	0.85
CS15TP	CS15TP_LR_9	chr3_210508085	3	210508085	0.19	8.27E-04	3.08	0.85
CS15TP	CS15TP_LR_9	chr3_210508115	3	210508115	0.19	9.19E-04	3.04	0.84
CS15TP	CS15TP_LR_9	chr3_210523454	3	210523454	0.22	3.47E-04	3.46	0.98
CS15TP	CS15TP_LR_10	chr3_211718651	3	211718651	0.24	4.41E-04	3.36	0.94
CS15TP	CS15TP_LR_10	chr3_212431627	3	212431627	0.23	9.86E-04	3.01	0.83
CS15TP	CS15TP_LR_10	chr3_212544357	3	212544357	0.20	3.80E-04	3.42	0.96
CS15TP	CS15TP_LR_10	chr3_212544386	3	212544386	0.19	4.74E-04	3.32	0.93
CS15TP	CS15TP_LR_10	chr3_212544402	3	212544402	0.18	2.06E-04	3.69	1.05
CS15TP	CS15TP_LR_10	chr3_212544407	3	212544407	0.18	2.97E-04	3.53	1.00
CS15TP	CS15TP_LR_10	chr3_212544446	3	212544446	0.19	2.22E-04	3.65	1.04
CS15TP	CS15TP_LR_11	chr3_214854424	3	214854424	0.22	5.14E-04	3.29	0.92
CS15TP	CS15TP_LR_11	chr3_214858102	3	214858102	0.22	5.75E-04	3.24	0.90
CS15TP	CS15TP_LR_12	chr3_216007444	3	216007444	0.22	6.18E-04	3.21	0.89
CS15TP	CS15TP_LR_12	chr3_216469326	3	216469326	0.23	2.24E-05	4.65	1.37
CS15TP	CS15TP_LR_12	chr3_216471587	3	216471587	0.22	5.25E-04	3.28	0.92
CS15TP	CS15TP_LR_12	chr3_216473159	3	216473159	0.23	9.43E-04	3.03	0.83
CS15TP	CS15TP_LR_12	chr3_216473192	3	216473192	0.23	9.43E-04	3.03	0.83
CS15TP	CS15TP_LR_12	chr3_216523205	3	216523205	0.22	8.54E-04	3.07	0.85
CS15TP	CS15TP_LR_12	chr3_216883752	3	216883752	0.24	4.50E-04	3.35	0.94

Env	QTL	SNP	Chr	Position	maf	P-value	LOD	Var Exp
CS15TP	CS15TP_LR_12	chr3_216883757	3	216883757	0.25	1.48E-04	3.83	1.10
CS15TP	CS15TP_LR_12	chr3_216883831	3	216883831	0.25	9.56E-05	4.02	1.16
CS15TP	CS15TP_LR_12	chr3_216986453	3	216986453	0.22	2.30E-05	4.64	1.37
CS15TP	CS15TP_LR_12	chr3_216986511	3	216986511	0.21	7.00E-05	4.16	1.21
CS15TP	CS15TP_LR_12	chr3_216987644	3	216987644	0.22	5.49E-05	4.26	1.24
CS15TP	CS15TP_LR_12	chr3_216987686	3	216987686	0.22	5.59E-05	4.25	1.24
CS15TP	CS15TP_LR_12	chr3_216988574	3	216988574	0.22	9.07E-04	3.04	0.84
CS15TP	CS15TP_LR_12	chr3_217007695	3	217007695	0.22	1.22E-04	3.91	1.13
CS15TP	CS15TP_LR_12	chr3_217008553	3	217008553	0.23	4.72E-04	3.33	0.93
CS15TP	CS15TP_LR_12	chr3_217008607	3	217008607	0.23	4.72E-04	3.33	0.93
CS15TP	CS15TP_LR_12	chr3_217008748	3	217008748	0.23	4.40E-05	4.36	1.28
CS15TP	CS15TP_LR_12	chr3_217096387	3	217096387	0.23	2.00E-04	3.70	1.06
CS15TP	CS15TP_LR_12	chr3_217096642	3	217096642	0.21	1.04E-04	3.98	1.15
CS15TP	CS15TP_LR_12	chr3_217096655	3	217096655	0.21	7.84E-05	4.11	1.19
CS15TP	CS15TP_LR_12	chr3_217213085	3	217213085	0.23	3.24E-06	5.49	1.66
CS15TP	CS15TP_LR_12	chr3_217213193	3	217213193	0.23	2.28E-05	4.64	1.37
CS15TP	CS15TP_LR_12	chr3_217292671	3	217292671	0.23	2.41E-05	4.62	1.36
CS15TP	CS15TP_LR_12	chr3_217292677	3	217292677	0.24	4.96E-05	4.30	1.26
CS15TP	CS15TP_LR_12	chr3_217293516	3	217293516	0.24	1.76E-05	4.75	1.41
CS15TP	CS15TP_LR_12	chr3_217293519	3	217293519	0.24	1.76E-05	4.75	1.41
CS15TP	CS15TP_LR_12	chr3_217294002	3	217294002	0.24	2.23E-05	4.65	1.37
CS15TP	CS15TP_LR_12	chr3_217358505	3	217358505	0.25	1.00E-04	4.00	1.16
CS15TP	CS15TP_LR_12	chr3_217358612	3	217358612	0.25	6.60E-05	4.18	1.22
CS15TP	CS15TP_LR_12	chr3_217358652	3	217358652	0.26	1.60E-04	3.80	1.09
CS15TP	CS15TP_LR_12	chr3_217358657	3	217358657	0.23	3.68E-04	3.43	0.97
CS15TP	CS15TP_LR_12	chr3_217358660	3	217358660	0.23	2.55E-04	3.59	1.02
CS15TP	CS15TP_LR_12	chr3_217358898	3	217358898	0.22	7.59E-04	3.12	0.86
CS15TP	CS15TP_LR_12	chr3_217358974	3	217358974	0.22	2.36E-04	3.63	1.03
CS15TP	CS15TP_LR_12	chr3_217359376	3	217359376	0.22	5.34E-04	3.27	0.91
CS15TP	CS15TP_LR_12	chr3_217463033	3	217463033	0.48	5.99E-04	3.22	0.90
CS15TP	CS15TP_LR_12	chr3_217463044	3	217463044	0.47	5.44E-04	3.26	0.91
CS15TP	CS15TP_LR_12	chr3_217463072	3	217463072	0.47	5.50E-04	3.26	0.91
CS15TP	CS15TP_LR_12	chr3_217573081	3	217573081	0.25	3.36E-04	3.47	0.98
CS15TP	CS15TP_LR_12	chr3_217576592	3	217576592	0.25	3.77E-04	3.42	0.96
CS15TP	CS15TP_LR_12	chr3_217576603	3	217576603	0.25	3.06E-04	3.51	0.99
CS15TP	CS15TP_LR_12	chr3_217576622	3	217576622	0.23	9.00E-04	3.05	0.84
CS15TP	CS15TP_LR_12	chr3_217576652	3	217576652	0.26	7.24E-04	3.14	0.87
CS15TP	CS15TP_LR_12	chr3_217576679	3	217576679	0.23	6.97E-04	3.16	0.88

Env	QTL	SNP	Chr	Position	maf	P-value	LOD	Var Exp
CS15TP	CS15TP_LR_12	chr3_217633065	3	217633065	0.26	2.59E-04	3.59	1.02
CS15TP	CS15TP_LR_12	chr3_217633111	3	217633111	0.26	4.26E-04	3.37	0.95
CS15TP	CS15TP_LR_12	chr3_217633164	3	217633164	0.26	2.97E-04	3.53	1.00
CS15TP	CS15TP_LR_12	chr3_217637708	3	217637708	0.46	9.43E-04	3.03	0.83
CS15TP	CS15TP_LR_12	chr3_217651336	3	217651336	0.25	1.83E-04	3.74	1.07
CS15TP	CS15TP_LR_12	chr3_217651338	3	217651338	0.25	2.52E-04	3.60	1.02
CS15TP	CS15TP_LR_12	chr3_217651494	3	217651494	0.27	6.75E-04	3.17	0.88
CS15TP	CS15TP_LR_12	chr3_217659852	3	217659852	0.25	2.96E-04	3.53	1.00
CS15TP	CS15TP_LR_12	chr3_217659912	3	217659912	0.25	4.07E-04	3.39	0.95
CS15TP	CS15TP_LR_12	chr3_217664643	3	217664643	0.23	4.20E-04	3.38	0.95
CS15TP	CS15TP_LR_12	chr3_217664657	3	217664657	0.26	6.12E-04	3.21	0.90
CS15TP	CS15TP_LR_12	chr3_217670323	3	217670323	0.26	1.98E-04	3.70	1.06
CS15TP	CS15TP_LR_12	chr3_217670855	3	217670855	0.25	4.90E-04	3.31	0.93
CS15TP	CS15TP_LR_12	chr3_217670991	3	217670991	0.26	6.42E-04	3.19	0.89
CS15TP	CS15TP_LR_12	chr3_217704895	3	217704895	0.46	1.01E-03	3.00	0.82
CS15TP	CS15TP_LR_12	chr3_217704943	3	217704943	0.46	9.37E-04	3.03	0.83
CS15TP	CS15TP_LR_12	chr3_217877595	3	217877595	0.26	4.23E-04	3.37	0.95
CS15TP	CS15TP_LR_12	chr3_217936114	3	217936114	0.44	3.58E-05	4.45	1.31
CS15TP	CS15TP_LR_12	chr3_217936224	3	217936224	0.47	1.68E-04	3.78	1.08
CS15TP	CS15TP_LR_12	chr3_217936234	3	217936234	0.46	1.43E-04	3.84	1.10
CS15TP	CS15TP_LR_12	chr3_217936427	3	217936427	0.28	7.28E-04	3.14	0.87
CS15TP	CS15TP_LR_12	chr3_217939593	3	217939593	0.25	2.50E-04	3.60	1.02
CS15TP	CS15TP_LR_12	chr3_218176291	3	218176291	0.23	1.94E-05	4.71	1.40
CS15TP	CS15TP_LR_12	chr3_218184190	3	218184190	0.22	5.18E-05	4.29	1.25
CS15TP	CS15TP_LR_12	chr3_218184213	3	218184213	0.27	4.76E-04	3.32	0.93
CS15TP	CS15TP_LR_12	chr3_218264905	3	218264905	0.24	5.49E-04	3.26	0.91
CS15TP	CS15TP_LR_12	chr3_218323511	3	218323511	0.44	8.37E-04	3.08	0.85
CS15TP	CS15TP_LR_12	chr3_218323603	3	218323603	0.46	7.45E-04	3.13	0.87
CS15TP	CS15TP_LR_12	chr3_218323831	3	218323831	0.45	3.41E-04	3.47	0.98
CS15TP	CS15TP_LR_12	chr3_218362523	3	218362523	0.22	8.35E-04	3.08	0.85
CS15TP	CS15TP_LR_12	chr3_218362541	3	218362541	0.22	8.35E-04	3.08	0.85
CS15TP	CS15TP_LR_12	chr3_218836461	3	218836461	0.21	8.77E-04	3.06	0.84
CS15TP	CS15TP_LR_12	chr3_219467464	3	219467464	0.26	7.57E-04	3.12	0.86
CS15TP	CS15TP_LR_13	chr5_63706634	5	63706634	0.16	5.78E-04	3.24	0.90
CS15TP	CS15TP_LR_14	chr5_210050738	5	210050738	0.35	6.49E-04	3.19	0.89
CS15TP	CS15TP_LR_14	chr5_210058373	5	210058373	0.32	8.58E-04	3.07	0.85
CS15TP	CS15TP_LR_14	chr5_210557993	5	210557993	0.30	3.17E-04	3.50	0.99
CS15TP	CS15TP_LR_14	chr5_210589634	5	210589634	0.29	7.96E-04	3.10	0.86

Env	QTL	SNP	Chr	Position	maf	P-value	LOD	Var Exp
CS15TP	CS15TP_LR_14	chr5_210589747	5	210589747	0.30	3.76E-04	3.42	0.96
CS15TP	CS15TP_LR_14	chr5_210598205	5	210598205	0.30	7.02E-04	3.15	0.88
CS15TP	CS15TP_LR_14	chr5_210870003	5	210870003	0.48	4.31E-04	3.37	0.95
CS15TP	CS15TP_LR_14	chr5_211184051	5	211184051	0.14	4.05E-04	3.39	0.95
CS15TP	CS15TP_LR_15	chr6_16798376	6	16798376	0.28	2.71E-04	3.57	1.01
CS15TP	CS15TP_LR_16	chr6_18845753	6	18845753	0.29	2.69E-04	3.57	1.01
CS15TP	CS15TP_LR_16	chr6_18845787	6	18845787	0.29	1.67E-04	3.78	1.08
CS15TP	CS15TP_LR_16	chr6_18845793	6	18845793	0.29	2.85E-04	3.54	1.00
CS15TP	CS15TP_LR_16	chr6_18845871	6	18845871	0.28	4.61E-04	3.34	0.94
CS15TP	CS15TP_LR_16	chr6_18846033	6	18846033	0.29	2.21E-04	3.66	1.04
CS15TP	CS15TP_LR_16	chr6_18924417	6	18924417	0.28	3.53E-04	3.45	0.97
CS15TP	CS15TP_LR_17	chr6_22267127	6	22267127	0.26	8.42E-04	3.07	0.85
CS15TP	CS15TP_LR_17	chr6_22267155	6	22267155	0.26	7.35E-04	3.13	0.87
CS15TP	CS15TP_LR_17	chr6_22267162	6	22267162	0.26	7.26E-04	3.14	0.87
CS15TP	CS15TP_LR_17	chr6_22267185	6	22267185	0.26	7.26E-04	3.14	0.87
CS15TP	CS15TP_LR_18	chr6_23827975	6	23827975	0.27	4.39E-04	3.36	0.94
CS15TP	CS15TP_LR_19	chr6_25291474	6	25291474	0.27	6.90E-04	3.16	0.88
CS15TP	CS15TP_LR_19	chr6_25337116	6	25337116	0.27	2.95E-04	3.53	1.00
CS15TP	CS15TP_LR_20	chr6_26965917	6	26965917	0.27	1.00E-03	3.00	0.83
CS15TP	CS15TP_LR_20	chr6_27120382	6	27120382	0.27	6.81E-04	3.17	0.88
CS15TP	CS15TP_LR_21	chr7_36726561	7	36726561	0.21	9.77E-04	3.01	0.83
CS15TP	CS15TP_LR_21	chr7_36726583	7	36726583	0.21	9.77E-04	3.01	0.83
CS15TP	CS15TP_LR_21	chr7_36866839	7	36866839	0.20	7.71E-04	3.11	0.86
CS15TP	CS15TP_LR_22	chr7_118528185	7	118528185	0.28	4.43E-04	3.35	0.94
CS15TP	CS15TP_LR_22	chr7_118532679	7	118532679	0.19	8.83E-04	3.05	0.84
CS15TP	CS15TP_LR_23	chr8_139346153	8	139346153	0.28	9.29E-04	3.03	0.84
CS15TP	CS15TP_LR_23	chr8_139346155	8	139346155	0.28	9.49E-04	3.02	0.83
CS15TP	CS15TP_LR_24	chr9_1328898	9	1328898	0.29	7.88E-04	3.10	0.86
CS15TP	CS15TP_LR_24	chr9_1329281	9	1329281	0.28	8.59E-04	3.07	0.85
CS15TP	CS15TP_LR_24	chr9_1329348	9	1329348	0.29	5.56E-04	3.25	0.91
CS15TP	CS15TP_LR_24	chr9_1331369	9	1331369	0.37	2.21E-04	3.66	1.04
CS15TP	CS15TP_LR_24	chr9_1331695	9	1331695	0.36	3.36E-05	4.47	1.31
CS15TP	CS15TP_LR_25	chr9_16733642	9	16733642	0.31	3.79E-04	3.42	0.96
CS15TP	CS15TP_LR_26	chr10_137161901	10	137161901	0.24	7.46E-04	3.13	0.87

APPENDIX C. PROTOCOLS

C1. Surface Sterilization of Carrot Seed

1. Put desired amount of seed into 1.5 mL Eppendorf centrifuge tube and label with the variety name.
2. Add 1.0 mL of 70% ethanol and shake for 20 seconds.
3. Remove ethanol and rinse with sterilized ddH_2O.
4. Add 1.0 mL of 5% sodium hypochlorite (Clorox bleach) and Tween 20 solution (1 drop per 50 mL).
5. Stir continuously at 40 rpm for 15 minutes.
6. Remove bleach solution and rinse with sterile water.
7. Repeat step six an additional five times.
8. Place two sterile filter papers within a sterile 90 mm Petri dish.
9. Spread seeds upon filter paper and allow to dry before plating.

Rathore (2015)

C2. Surface Sterilization of Tobacco Seed

1. Put desired amount of seed into 1.5 mL Eppendorf centrifuge tube and label with the variety name.
2. Add 2.0 mL of 70% ethanol and shake for 20 seconds.
3. Remove ethanol and rinse with sterilized ddH_2O.
4. Add 2.0 mL of 20% sodium hypochlorite (Clorox bleach) and Tween 20 solution.
5. Stir continuously at 40 rpm for 15 minutes.
6. Remove bleach solution and rinse with sterile water.
7. Repeat step six an additional five times.
8. Place two sterile filter papers within a sterile 90 mm Petri dish.
9. Spread seeds upon filter paper and allow to dry before plating.

Clemente (2006)

C3. Tobacco Callus Induction

1. Place two sterile filter papers within a sterile 90 mm Petri dish, and moisten with sterile water.
2. Using a flamed #11 scalpel, cut tobacco leaf into one centimeter by one centimeter square segments and place on damp filter paper until you are ready to plate.
3. Using flamed forceps, plate leaf segments adaxial side down upon tobacco callus induction medium at desired density.
4. Label plates and seal with parafilm.
5. Place plates within 25° C incubation chamber and allow calli to form.
6. Transfer growing calli to fresh medium every three weeks to avoid embryogenesis.

Clemente (2006)

C4. Carrot Callus Induction

1. Place two sterile filter papers within a sterile 90 mm Petri dish, and moisten with sterile water.
2. Using a flamed #11 scalpel, cut etiolated hypocotyls into one centimeter segments and place on damp filter paper until you are ready to plate.
3. Using flamed forceps, plate hypocotyl segments, at desired density, on carrot callus induction medium.
4. Label plates and seal with parafilm.
5. Place plates within 25° C incubation chamber and allow calli to form.
6. Transfer growing calli to fresh medium every three weeks to avoid embryogenesis.

Rathore (2015)

C5. Tobacco Protoplast Isolation

1. Filter sterilize protoplast isolation medium with enzymes into a 60x15 mm Petri dish, using 0.2 µm syringe filter.
2. Incorporate 2.0 mL PCV of desired suspension culture into the filtered tobacco protoplast isolation medium with enzymes.
3. Seal Petri dish with parafilm and cover with aluminum foil.
4. Gently agitate at 50 rpm for 24 hours using a rotary shaker.
5. Place connector ring upon 50 mL centrifuge tube, followed by 40 µm and 100 µm cell strainers.
6. Pass cell/enzyme solution through cell strainers to remove residual cell clusters and debris.
7. Wash 100 µm strainer with 10 mL of protoplast isolation medium.
8. Repeat step seven.
9. Remove 100 µm strainer and wash 40 µm strainer with 10 mL protoplast isolation medium.
10. Remove remaining strainer and centrifuge protoplast solution at 104xg for 8 minutes.
11. Remove supernatant and suspend pellet with 2 mL modified KOA (mKAO) medium.
12. Carefully layer mKAO protoplast solution upon 8 mL of sucrose solution within a 15 mL centrifuge tube.
13. Centrifuge at 40xg for 10 minutes and centrifuge break set to zero.

14. Remove band of protoplasts, visible at the interphase between the sucrose pad and W5 solution, using a Pasteur pipette and place into sterile 15 mL centrifuge tube.
15. Suspend protoplast within 5 mL of mKAO.
16. Centrifuge at 104xg for 8 minutes.
17. Discard supernatant and repeat steps 15 and 16.
18. Discard supernatant and suspend pellet in 5 mL of W5 wash.
19. Repeat step 16.
20. Discard supernatant and suspend pellet with 10 mL of filter sterilized KAO 8p medium.
21. Store isolated protoplast in a sealed 30 mm Petri dish under 25° C, dark conditions for 72 hours.

Based on protocols of Lee, et al. (1989) and Kirchhoff, et al. (2012).

C6. Carrot Protoplast Isolation

1. Filter sterilize protoplast isolation medium with enzymes into a 60x15 mm Petri dish, using 0.2 µm syringe filter.
2. Incorporate 2.0 mL PCV of desired suspension culture into the filtered carrot protoplast isolation medium with enzymes.
3. Seal Petri dish with parafilm and cover with aluminum foil.
4. Gently agitate at 50 rpm for 24 hours using a rotary shaker.
5. Place connector ring on 50 mL centrifuge tube, followed by 40 µm and 100 µm cell strainers.
6. Pass cell/enzyme solution through cell strainers to remove residual cell clusters and debris.
7. Wash 100 µm strainer with 10 mL of protoplast isolation medium.
8. Repeat step seven.
9. Remove 100 µm strainer and wash 40 µm strainer with 10 mL protoplast isolation medium.
10. Remove remaining strainer and centrifuge protoplast solution at 80xg for 15 minutes.
11. Remove supernatant and suspend pellet with 2 mL W5 wash.
12. Carefully layer W5 protoplast solution upon 8 mL of sucrose solution within a 15 mL centrifuge tube.
13. Centrifuge at 40xg for 10 minutes and centrifuge break set to zero.

14. Remove band of protoplasts, visible at the interphase between the sucrose pad and W5 solution, using a Pasteur pipette and place into sterile 15 mL centrifuge tube.
15. Suspend protoplast within 5 mL of W5 wash.
16. Centrifuge at 80xg for 15 minutes.
17. Discard supernatant and suspend pellet in 5 mL of filter sterilized carrot protoplast regeneration medium.
18. Centrifuge at 80xg for 15 minutes.
19. Discard supernatant and suspend pellet in 10 mL of filter sterilized carrot protoplast regeneration medium.
20. Store isolated protoplast in a sealed 30 mm Petri dish at 25° C, under dark conditions for 72 hours.

Based on protocols of Lee, et al. (1989) and Grzebelus, et al. (2012)

APPENDIX D. MEDIUM

D1. Tobacco Growth Medium

MS Salts (PhytoTechnology)	4.3 g
B_5 Vitamin Stock (Appendix E4)	10 mL
Myo-Inositol	100 mg
Sucrose	30 g
ddH2O	990 mL
Phytagel	8 g

Adjust pH to 5.6.

Autoclave on liquid 20 minute cycle.

Clemente (2006)

D2. Carrot Growth Medium

MS Salts (PhytoTechnology Labs)	4.3 g
B_5 Vitamin Stock (Appendix E4)	10 mL
Myo-Inositol	100 mg
Sucrose	30 g
ddH2O	1 L
Phytagel	2 g

Adjust pH to 5.8.

Autoclave on liquid 20 minute cycle.

D3. Tobacco Callus Induction Medium

MS Salts (PhytoTechnology Labs)	4.3 g
Thiamine HCl Stock (Appendix E5)	40 µL
2,4-D Stock (Appendix E6)	10 mL
Kinetin Stock (Appendix E7)	1 mL
Myo-Inositol	100 mg
Sucrose	30 g
ddH2O	1 L
Phytagel	8 g

Adjust pH to 5.6

Autoclave on liquid 20 minute cycle.

D4. Carrot Callus Induction Medium

MS Salts (PhytoTechnology)	4.3 g
B_5 Vitamin Stock (Appendix E4)	10 mL
2,4-D Stock (Appendix E6)	4 mL
Myo-Inositol	100 mg
Sucrose	30 g
ddH2O	1 L
Phytagel	2 g

Adjust pH to 5.8.

Autoclave on liquid cycle for 20 minutes.

D5. Protoplast Isolation Medium with Enzyme

Cellulase-R10 (Gold BioTechnology)	240 mg
Macerozyme (Gold BioTechnology)	160 mg
Carrot/Tobacco Protoplast Isolation Medium	8 mL

Filter sterilize with 0.2 µm filter.

D6. Tobacco Protoplast Isolation Medium

KAO modified salt (PhytoTechnology)	3.90 g
Glucose	18 g
2,4-D stock (Appendix E6)	2.5 mL
Kinetin Stock (Appendix E7)	250 µL
ddH_2O	247 µL

Adjust pH to 5.6.

Autoclave on liquid 20 minute cycle.

Formulated based on PNT medium (Schnorf, et al., 1991).

D7. KAO 8p Medium

KAO modified salt (PhytoTechnology)	3.90 g
Glucose	0.25 g
Sucrose	68.4 g
2,4-D stock (Appendix E6)	10 mL
Kinetin Stock (appendix E7)	1 mL
Coconut Water	20 mL
Casamino Acid	250 mg
ddH_2O	969 mL

Adjust pH to 5.6.

Filter sterilize with 0.2 µm filter.

Kao and Michayluk (1975)

D8. Carrot Protoplast Isolation Medium

MES Buffer	976 mg
Mannitol	27.33g
CaCl2	138.7 mg
MS Salts	1.075 g
ddH2O	250 mL

Adjust pH to 5.8.

Autoclave on liquid 20 minute cycle.

Grzebelus, et al. (2012)

D9. Carrot Protoplast Regeneration Medium

KAO Salts (PhytoTechnology)	975 mg
Glucose	18.5 g
Casein Enzymatic Hydrolysate	62.5 mg
2,4-D Stock (Appendix E6)	1 mL
B_5 Stock Solution (Appendix E4)	2.5 mL
Coconut Water	5 mL
Casamino Acid	75 mg
ddH2O	241 mL

Adjust pH to 5.8.

Filter sterilize with 0.2 µm filter.

Based on CPP medium (Dirks, et al., 1996).

APPENDIX E. STOCK SOLUTIONS

E1. Sucrose Solution 0.6 N

Sucrose	20.54 g
ddH2O	100 mL

Autoclave on liquid 20 minute cycle.

E2. W5 Wash

NaCl	2.25 g
$CaCl_2 \bullet H_2O$	4.59 g
KCl	93 mg
Glucose	225 mg
ddH2O	250 mL

Autoclave on liquid 20 minute cycle.

Menczel, et al. (1981)

E3. Fluorescein Diacetate Stock

Fluorescein Diacetate	25 mg

Dissolve in 1.0 mL of acetone under dark conditions.

Store in -25° C under dark conditions.

E4. B$_5$ Vitamin Stock (100x)

Nicotinic acid	20 mg
Pyridoxine	20 mg
Thiamine HCl	200 mg
ddH$_2$0	200 mL

Store at 4° C for up to 1 month.

Gamborg, et al. (1968)

E5. Thiamine HCl Stock (0.01 mg/µL)

Thiamine HCl	20 mg
ddH$_2$O	2 mL

Store at -25° C.

E6. 2,4-D Stock (0.1 mg/mL)

2,4-dichlorophenoxyacetic acid	25 mg
ddH2O	250 mL

Dissolve in 1 mL of ethanol and bring to 250 mL with ddH2O.

Store at 4° C for up to 1 month.

E7. Kinetin Stock (0.1 mg/mL)

Kinetin	10 mg
DDH$_2$O	100 mL

Dissolve in 4 drops of 5 M KOH and bring to 100 mL with ddH$_2$0.

Store at 4° C for up to 1 month.

APPENDIX F. REAGENTS

2,4-dichlorophenoxyacetic acid (Sigma-Aldrich, D7299)

Calcium chloride dihydrate (Sigma-Aldrich, C7902)

Casein enzymatic hydrolysate (PhytoTechnology Laboratories, C184)

Cellulase-R10 (Gold Biotechnology, C8001)

Coconut Water (PhytoTechnology Laboratories, C195)

D-Mannitol (Sigma-Aldrich, M4125)

D-Sorbitol (Sigma-Aldrich, S6021

Fluorescein diacetate (Sigma-Aldrich, F7378)

Glucose (Sigma-Aldrich, G7021)

Kao & Michayluk modified basal salt mixture (PhytoTechnology Laboratories, K427)

Potassium chloride (Sigma-Aldrich, P8041)

Kinetin (Sigma-Aldrich, K0753)

Macerozyme R-10 (Gold Biotechnology, M8002)

MES hydrate (Sigma-Aldrich, M2933)

Murashige & Skoog basal salt mixture (PhytoTechnology Laboratories, M524)

Myo-Inositol (Sigma-Aldrich, I7508)

Nicotinic acid (Sigma-Aldrich, N0765)

Pyridoxine (Sigma-Aldrich, P8666)

Phytagel (Sigma-Aldrich, P8169)

Sodium chloride (Sigma-Aldrich, S3014)

Sucrose (Sigma-Aldrich, S0389

Thiamine HCl (Sigma-Aldrich, T1270)