DEVELOPING A NEW SNP CHIP FOR GENOMIC SELECTION IN THE NORTH DAKOTA STATE UNIVERSITY BARLEY-BREEDING PROGRAM

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The Supervisory Committee certifies that this ***disquisition*** complies with North Dakota State University's regulations and meets the accepted standards for the degree of

DOCTOR OF PHILOSOPHY

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ABSTRACT

The use of Genomic Selection has become popular due to its wide success in private and public breeding programs. The current dissertation aims to derive information that will be used to produce a single nucleotide polymorphisms (SNP) chip that can be used to successfully predict traits of economic importance for the North Dakota State University (NDSU) barley breeding program. Three training populations were tested to determine which should be used for predictive modeling. Multiple predictive models were employed to verify the most effective method for each individual trait. Through this research, four major findings were concluded: the successful identification of (i) the traits that are candidates for prediction, (ii) the most successful models for each trait, (iii) the minimum number of markers required to predict a trait, and (iv) the markers that should be included on NDSU barley breeding program's new SNP chip for genomic selection.

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DEDICATION

This thesis is dedicated to my parents whom always believed in me and always offered unconditional love and support. I would also like to dedicate this work to my wife, without her offering continuous support, help and an immense amount of needed motivation in this time as a graduate student, coop employee and full time employee this work would have never been possible. I would also like to dedicate this dissertation to my whole family, for always motivating me to continue and never give up and my two dogs, Kike and Nico, for always being present and bringing lots of fun to long days of quarantine.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

INTRODUCTION

Barley (*Hordeum vulgare* L.) malt is a raw material used for the production of one of the most popular drinks consumed worldwide, beer. The major challenges of breeding barley have consistently been the time and money required to release a cultivar and the space utilized while testing multiple genotypes across many environments. During the evolution of plant breeding as an art and a science, breeders have been able to incorporate technological advances into their practices. For example, a recent advancement in the selection of improved genotypes is the ability to select individuals based on probabilities and predictions obtained by genomic selection. Genomic selection is a marker-assisted approach in which high density markers covering the entire genome and phenotypic values are used to predict the genetic value of a trait or individual (Heffner et al., 2009). Different from phenotypic selection, the foundation of genotypic selection lies in calculating genomic estimated breeding values (GEBVs) using a training population (TP) that has been genotyped and phenotyped. The GEBVs are estimated by calculating values for the best linear unbiased predictions (BLUPs). As will be discussed in the *Literature Review*, studies have been conducted that estimate a very high level of accuracy using genomic selection with marker data alone. Use of this method could provide a potential solution to the aforementioned impairments as breeders could accelerate the program with better gains per unit of time (Desta and Ortiz, 2014).

The ultimate of goal of my research was to identify SNPs that should be included in the construction of the second-generation SNP chip to be used by the NDSU barley breeding program for genotyping F_4 and F_5 lines that are grown each year in the Yuma, AZ winter nursery. The current SNP chip used by the program consists of 462 markers and is used for calculating GEBVs for ß-glucan and marker assisted selection for resistance to net blotch and spot blotch. To accomplish this goal, I needed to determine the training population the NDSU barley breeding program should use for genomic selection, identify the traits that are candidates for predicting, and develop genomic selection models to use for calculating GEBVs.

In the current study, three TPs were compared to determine which of the populations would be better for predicting GEBVs. The first TP consisted of 81 two-rowed lines utilized by Jung (2015) that was representative of the germplasm utilized by the North Dakota State University (NDSU) Barley-Breeding Program at the time of her research. The second TP consisted of 137 two-rowed breeding lines and cultivars that were used as parents by the NDSU Barley-Breeding Program during the last nine years. The third TP combines lines from the first two TP's. The BLUPs for 24 traits in which data are regularly collected each year were calculated using the statistical software, JMP Pro 14. All data for the TPs were previously collected as part of the NDSU Barley-Breeding Program. Four models were tested to determine their utility for genomic selection using JMP Genomics 9. The models were ridge regression (RR), partial least squares (PLS), Bayes B (GBR), and the machine learning method XGBoost.

LITERATURE REVIEW

Barley

Since the inception of agricultural development, barley has been an important crop. Looking into the past, this crop was believed to play a vital role in humans' transition from a hunting and gathering lifestyle to an agrarian one (Ullrich, S.E., 2011). Present day, barley is used as animal and human feed, as well as for malt production.

Barley is in the genus *Hordeum* and consists of 32 species and 45 taxa. These include diploid (2n = 2x = 14), tetraploid (2n = 4x = 28), and hexaploid (2n = 6x = 42) cytotypes (Bothmer et al., 2003). All species in the genus *Hordeum* have three one-flowered spikelets at a rachis node. The two lateral spikelets are sterile in two-rowed types and fertile in six-rowed types. Bothmer et al. (2003) state that there is biological diversity among the species in the genus *Hordeum* in terms of growth habit (annual or perennials) and mode of reproduction (inbreeding or self-incompatible). Based on the gene pool concept, cultivated barley and *Hordeum spontaneum* are in the primary gene pool while *Hordeum bulbosum* is in the secondary gene pool. All remaining species that are in the genus *Hordeum* are in the tertiary gene pool (Bothmer et al., 2003).

Barley Quality

When determining a barley cultivar's acceptability, there are multiple factors that are taken into account. Although such factors depend on the purpose for which the crop is being cultivated, these can include its agronomic performance, malt quality, and disease resistance. In the following sections, a variety of agronomic traits that are measured in the field will be described, including heading date (HDDT), stem breakage (STM_BRK), disease resistance, lodging, height (HT), and harvest moisture. It is important to mention that, for quality purposes, after the seed is cleaned it is necessary to measure kernel plumpness, 1000-kernel weight (KWT), test weight (TWT), and grain protein.

Agronomic Traits

For a barley cultivar to be acceptable to producers, it must be as easy to grow and manage, harvest, and market as compared to other crops. Meeting these demands is becoming increasingly more difficult with the rise in popularity of maize (*Zea mays* L.) and soybean (*Glycine max* L.) in North Dakota. The agronomic traits that impact a producer's general crop management include HDDT, disease resistance, STM_BRK, lodging, and HT. Heading date is important for cereal cultivars to adapt to their respective environments and in maximizing yield potential (Bezant *et al.*, 1996). Upon approaching harvest season, the uniformity of the crops maturity can have a substantial impact on the producer's timeline within their cropping system.

Disease resistance ensures the viability of high-quality seed and easier harvestability. For example, the fungus *Fusarium graminearum* Schwabe [telomorph *Gibberella zea* (Schwein)] causes Fusarium head blight (FHB) and produces a mycotoxin that can be harmful to humans and animals (Paulitz and Steffenson, 2011). Other diseases can weaken straw strength and cause a phenomenon called lodging, or when the plant is no longer able to maintain an upright position after being exposed to climate changes in its environment (Pinthus, 1973) or disease. This can negatively impact both seed quality and harvestability as the whole spike will be either on the ground or very close to it. Such positions expose the spike and seeds to more environmental threats, making it difficult to harvest. The degree of lodging is typically heterogeneous in the field. Although lodging close to maturity may not impact yield loss directly, it may impact the crop indirectly as it can interfere with the crop's harvestability. Finally, lodging can lead to higher grain protein content as the seeds have less carbohydrates when the plants are lodged (Schwarz and Li, 2011).

1000-Kernel Weight

1000-kernel weight is the exact weight of 1000-kernels after the removal of broken grains and foreign material (Schwarz and Li, 2011). Given that moisture will increase the value, the values obtained for this trait test should be calculated on a moisture-free basis (ASBC, 2009). Higher KWT is desired as this is indicative of healthy seed that has greater amounts of carbohydrates that can lead to better malt quality.

Kernel Plumpness

Kernel plumpness is assorted mechanically with different size sieves, where 100 g of seed are separated with 19.0 x 2.8, 19.0 x 2.4, and 19.0 x 2.0 mm rectangular openings (Schwarz and Li, 2011). The grains that that remain on top of the 19.0 x 2.4 mm sieves are considered plump, those that pass through the 19.0 x 2.0 mm sieve are considered thin (ASBC, 2009). As with KWT, higher levels of kernel plumpness are desired as this is indicative of grain that may have better malt quality. Kernel plumpness less than 80% in two-rowed barley may be discounted in price or rejected if the level is too low.

Test Weight

Test weight is a density measure expressed in kg hL^{-1} and is the specific amount of barley required to fill a Standard Winchester bushel (Bu) measure of 2150.42 in^3 (ASBC, 2009). Test weight is dependent on factors such as cultivar, environmental conditions during production, sample cleanliness, presence of awns, and grain drying (Schwarz and Li, 2011). The standard bushel weight of barley in the US is 61.8 kg hL^{-1}. As with the previous traits, higher test weights are desired.

Grain Protein

Grain protein is important to predict both barley and malting quality. It is represented by total nitrogen content by weight. Higher protein levels will yield lower levels of fermentable extract (Schwarz and Li, 2011). Methods commonly used to determine protein content include determination of nitrogen by combustion analysis or the determination of protein by near-infrared (NIR) spectroscopy (Schwarz and Li, 2011). In the United States (US), the ideal barley protein content for an adjunct brewer is ≤12.8%, whereas the ideal two-rowed barley protein content for an all malt brewer is ≤11.8% (https://ambainc.org/wp-content/uploads/2019/10/Malting_Barley_Breeding_Guidelines_June_2019.pdf; verified 10 March 2020).

Kernel Color

Acceptable kernel color is generally a light yellow-straw color that is also bright in appearance (Schwarz and Li, 2011). Although visual appearance has always been a way to screen for unwanted barley, it is not always correct. Green kernels indicate immature grain and discoloration may indicate weathering or disease infection. The ASBC approved measure of kernel color (ASBC, 2009) is a measure of brightness and is usually expressed as the *L*-value of the tristimulus color scale (Shellhammer, 2009; Schwarz and Li, 2011).

Quality Problems

As with any crop, a variety of problems can arise from improper seed handling and practices, unfavorable environmental conditions, disease, transport, and grain storage (Schwarz and Li, 2011). Damaged seed results in low germination, directly affecting the malt extract, flavor, and reduces processing performance in the malt house and brewery (ASBC, 2009).

Malt Quality

Genetic and environmental factors influence barley malt quality (Lewis, 2012). Some characteristics that are viewed as desirable in malt include plump kernels, moderate levels of protein, high enzymatic activity, and kernel uniformity. These, however, are dependent on the brewer and the type of beer they are producing. This can be observed by the increase in craft brewers using cultivars with a larger variation when it comes to malt quality. Plump kernels are related to higher malt extract and the uniformity in size ensures uniform water uptake and germination during malting. The desired levels of enzymatic activity in the malt is dependent on the brewing processes used by the brewer. Brewers producing all malt beers or using exogenous enzymes during brewing or fermentation don’t require as high of enzyme levels as adjunct brewers that don’t use exogenous enzymes. High enzymatic activity is better for carbohydrate degradation and moderate levels of protein for yeast nutrition during fermentation. Having said this, high levels of protein results in lower malt extract, which is a major economic factor to the brewer.

Malt Quality Analyses

Extract

Whereas yield is the most important trait considered by a producer, extract is one of the most economically valued parameters for maltsters and brewers. It is expressed as a percentage of malt on a dry basis and is essentially composed of carbohydrates that can be broken down into disaccharide maltose and branched dextrins (Burger and La Berge, 1985).

Diastatic Power

Diastatic power (DP) is a measure of the capacity of the malt to convert starch into fermentable sugars (Schwarz and Li, 2011). Some scientists consider DP as a measure of β-amylase activity since this enzyme has a much larger activity than any other starch-degrading enzyme in the determination of DP. However, it does include all starch degrading enzymes. Units of DP are recorded in °ASBC in accordance with the American Society of Brewing Chemists (ASBC) and the current target by AMBA for DP is over 140 °ASBC (ASBC, 2009).

α-Amylase

The dextrinizing capacity of malt is measured in dextrinizing units (DU) and is referred to as α-amylase. Like ß-amylase, this enzyme also degrades starch and larger dextrins. Additionally, it helps to reduce viscosity and provide more substrate for ß-amylase (Schwarz and Li, 2011; ASBC, 2009).

Wort Quality Analyses

Wort Color

Wort color is measured with a spectrophotometer at 430 nm wavelength (Schwarz and Li, 2011). The ASBC method reports these results in °SRM, which is similar to the °Lovibond. The wort color preference ranges from 1.6-2.8 and 1.8-2.5 SRM for adjunct and all malt worts, respectively. The mentioned wavelength is used to analyze pale yellow or golden colored beers (ASBC, 2009).

Kolbach Index

Kolbach index, also known as the ratio of soluble to total protein (S/T), directly measures protein modification (Schwarz and Li, 2011). The measurement is expressed as a percentage (S/T x 100). Malt can be classified as under modified (<35%), well modified (35%-41%), or highly modified (>41% and predominant in North American malt). The recommendation from AMBA is between 38%-45% for two-rowed barley (2014).

Wort β-Glucan

Depending on their molecular weight or size and conformation, wort ß-glucans have been found to have an impact on wort and beer viscosity, slow lautering, and membrane plugging (Schwarz and Li, 2011). The increasing concentration of wort ß-glucan appears to significantly increase wort viscosity and decrease filterability; thus, making it yet another important measurement of quality. The ASBC measures this quality parameter in ppm and the AMBA recommended level is <100 mg L^{-1} for two-rowed barley (2014).

Disease Traits

Deoxynivalenol

Deoxynivalenol is a mycotoxin produced by the pathogen *F. graminearum* that causes FHB. High levels of FHB and DON can negatively impact grain yield and/or grain quality. Furthermore, the products of the fungus can harm animals and humans alike (Paulitz, and Steffenson, 2011). For example, humans who ingest DON can experience acute toxicosis symptoms and animals, such as swine, may experience vomiting and hyperestrogenism. The observation of swine vomiting after ingesting DON has led to its common nickname of “vomitoxin.”. Since these mycotoxins are perceived as problematic by end users and consumers, assays to determine the level of mycotoxin present are now standard tests for barley at the point of purchase.

Spot Blotch

Spot blotch, cause by *Cochliobolus sativus* (Ito & Kuribayashi) Drechs. ex Dastur, is a disease that can cause root rot, leaf spot scaring, and kernel blight. When all these characteristics are present due to the presence of the disease it will impact kernel size and weight (Mathre, 1997). Visual symptoms of this disease on leaves can be described as small round to oblong brown blotches with chlorotic border. The pathogen can survive in the host seed, plant debris, and in the soil (Kiesling, 1985). The current best practices against this disease is the use of resistant cultivars.

Net Blotch

Net blotch has two common forms seen on leaves, spot-form net blotch and net-form net blotch caused by *Drechslera teres* f. sp. *maculata* Smedeg. and *Drechslera teres* f. sp. *teres* (Sacc.) Shoemaker, respectively. Spot-form net blotch is a form of net blotch with dark brown round to elongated lesions that develop into large irregular patches (Liu et al., 2012). The lesion and patches are surrounded by necrosis or a chlorotic halo. When the leaves are severely affected and die, the brown lesions are more visible. Net-form net blotch symptoms are small circular brown lesions that develop into narrow dark brown lesions with longitudinal and transverse lesions creating a net "pattern" within the leaf veins for which the disease was originally named (Liu et al., 2012). A chlorotic halo surrounds the net pattern. When severely affected, the lesions coalesce, and the leaves die. Stems and kernels also can be infected. Both forms of net blotch can impact yield losses whereas net form net blotch can adversely affect malting quality through a reduction of kernel plumpness and decrease malt extract (Liu et al., 2012).

Best Linear Unbiased Prediction

A great challenge that breeders face consistently when evaluating crops across environments and years is the challenge of estimating the population mean because of the unbalanced nature of these data. The evaluation of breeding lines within a year generally begins with balanced datasets. When data from multiple years are used, the data become unbalanced because some lines are not advanced to the next year of testing because of poor performance. The nature of the unbalanced data increases as even more years of data are included in the analyses because fewer lines are advanced from year to year. Traditional analyses of breeding data using mixed models have assumed that entries are a fixed effect and environments are a random effect. A limitation in these traditional analyses is that valuable information on the relationships between sibs or families are not utilized when entries are considered a fixed effect. The values obtained from these analyses are referred to as Best Linear Unbiased Estimates (BLUEs). Assuming entries are a random effect allows for the relationship between sibs or families in the analyses to be utilized. The values obtained from these analyses are referred to as Best Linear Unbiased Predictions (BLUPs). A feature of BLUPs is that the differential between the observed value and the population mean is smaller or "shrunk" as compared to the differentials for BLUEs.

The concern of not using information on the relationship between sibs or families was addressed by Henderson (1975). He expressed a concern that a great deal of the data available to animal breeders for their analyses didn't generally meet the requirements of being from a true random sample because the animals are chosen by selection. To account for this discrepancy, Henderson proposed the use of an unbiased value, the BLUP. The general mixed model for BLUPs can be denoted as:

$$y = X\beta + Zu + e \qquad \text{(Equation 1)}$$

where y is a vector of observations, β is a vector of fixed effects, u is a vector of random effects, and X and Z are incidence matrices. Benardo (2010) expands on utilization of BLUPs in plant breeding.

The estimated predicted difference (EPD) values routinely used by animal breeders are related to BLUPs. Many plant breeders prefer to use values that look more like the ones that are regularly seen in Extension bulletins and advertising materials provided for new cultivars or hybrids. To obtain these types of values from BLUPs, the BLUPs are added to a common value for each entry. In analyses done by JMP or SAS, the BLUP for each entry can be added to the intercept obtained in the analysis to provide a predicted value for each entry that looks similar in scale to the results they typically used for making breeding decisions or for marketing seed.

Genomic Selection

Genomic selection was first proposed by Meuwissen et al. (2001) as an extension of marker assisted selection (MAS) to compensate for its shortcomings. Since its incorporation into plant breeding, MAS has been successful in cases generally associated with the selection of major genes (Dekkers and Hospital, 2002). However, in crop plants a variety of economically important traits are controlled by many small effect genes rather than major genes (Eathington et al., 2007). Heffner et al. (2009) stated that there are limitations to MAS, including that (i) biparental original populations used in many studies are not applicable to most breeding populations and (ii) statistical methods used in MAS are not well suited for improving polygenic traits such as yield. Additionally, the genetic diversity in a biparental population provides insufficient information in order to capture allelic differences within a breeding program. Thus, breeders must perform multiple validation studies and estimate quantitative trait loci (QTL) effects within multiple populations to ensure that gains from MAS are superior to those in traditional phenotypic selection (Bernardo, 2001). This validation process can become an economic constraint to many breeding programs.

Genomic selection, unlike MAS, takes into account the whole genome when associating a trait by estimating marker effects across the whole genome of a breeding population (Ortiz et al., 2014). The estimates are based on a prediction model developed from a TP, which generally includes parental genotypes of a breeding program that have been phenotyped and genotyped. The breeding population (BP) consists of related individuals to the aforementioned TP and are candidates for selection and advancement in a breeding program. The main calculations of genomic selection are the computation of GEBVs for the BP based on the model developed from the TP (Meuwissen et al., 2001).

The confidence of using predicted values for selection are based on statistical models that interpret the accuracy of a predicted value vs. true breeding values; this is known as prediction accuracy. This definition of accuracy is directly proportional to gain from selection when using GEBVs (Jannink et al., 2009). Factors that can affect the accuracy of predicted values are model performances, sample size and relatedness, marker density, gene effects, heritability, and genetic architecture (Ortiz and Desta, 2014).

In genomic selection, BLUPs are utilized to predict the continuous effects across markers that contain both major and minor effects (Bernardo, 2010). Two frequently used procedures for developing genomic selection models are the ridge regression best linear unbiased prediction (RR) and Bayesian methods. The RR method simultaneously estimates all marker effects and shrinks them towards zero. This method assumes that marker effects are random with a common variance (Heffner et al., 2009). By shrinking marker effects towards zero, it implies that all markers may carry the same effect within the genome. This method has proved to be successful and less complicated in terms of necessary computer power and superior accuracy results to other methodologies (Heffner et al., 2009). While the RR may be a simpler method to use, it will inevitably underestimate large effects as it assumes equal and fixed marker effect variances. Bayesian methods, while more complicated, do have the flexibility to model marker effects of different sizes by estimating a separate variance per marker effect.

Genomic selection has been successful in its applications in other crops such as wheat (*Triticum aestivum* L) (Battenfield et al., 2016a). Like barley, wheat has important end-use quality traits related to flour, dough, and loaf traits. Genetic gain was improved up to 2.7 times with the implementation of genomic selection by the CIMMYT bread wheat breeding program for test weight, 1000-kernel weight, hardness, grain and flour protein, flour yield, sodium dodecyl sulfate sedimentation, Mixograph and Alveograph performance, and loaf volume. (Battenfield et al., 2016b).

Genomic Selection in Barley

Genomic selection in barley is currently in use by the breeding program at University of Minnesota (U of M). Sallam et al. (2015) assessed the prediction accuracy of genomic selection in a breeding population consisting of historical sets of breeding lines that were defined as parents or progeny sets from the U of M. The parent set was comprised of 168 breeding lines developed between 1999 and 2004. The progeny consisted of five sets of 96 lines evaluated between 2006 and 2010. The prediction models used to assess the prediction accuracy were the RR model, Gaussian kernel model, Exponential kernel model, and Bayes Cπ. Their results indicated that even though there was no significant difference based on which TP was used (historical vs. contemporary), the contemporary TP generally had higher prediction accuracy than the historical TP (Sallam et al., 2015). This is due to the fact that as lines were developed, the similarity to older cultivars shrank. Habier et al. (2007) believe that the prediction accuracy should be at its highest when the TP is more related to the validation population. The findings by Sallam et al. (2015) indicate that historical unbalanced data can also be used to train prediction models after proper adjustments for spatial variability and trial effects. In terms of models to be used, results indicated that there was no significant difference between models and the simplest one, the RR, was accurate across multiple situations. Sallam and Smith (2016) used the same population data in a comparison of genotypic selection vs. phenotypic selection for yield, FHB resistance, and DON concentration. The results indicated there were no significant difference between phenotypic and genotypic selection; however, genotypic selection did increase genetic similarity and the frequency of favorable alleles. These results suggest that since the cost of genotyping is decreasing, the use of genotypic over phenotypic selection will become more commonly used by breeding programs (Sallam and Smith, 2016).

Another study conducted on barley assessed the potential of genomic selection on malt quality traits by conducting simulations (Schmidt et al., 2016). The populations consisted of released lines or potential candidates of both winter and spring barley. For both growth habits of barley, 12 malt quality traits were studied, which included α-amylase activity, ß-amylase activity, extract, final attenuation, friability, ß-glucan content, Kolbach Index, malt loss, soluble nitrogen, protein content, and viscosity. Of these traits, higher values are desirable with the exception of ß-glucan and viscosity. They found that even with relatively small training sets of 100 individuals, there was a very high prediction ability depending on the trait and its heritability. Broad sense heritability of >0.80 was observed in extract, final attenuation, friability, ß-glucan content, Kolbach Index, and soluble nitrogen for spring barley. Predictive ability, as a measurement of cross validation correlations ranged from 0.4 to 0.8. Results also indicated that increasing the TP size led to higher stability, and that reliability of GEBVs implies that applying genomic selection can be a very powerful and useful tool.

Based on the results from Jung (2015), the NDSU Barley Breeding program designed a SNP chip comprised of 462 SNPs that is used to genotype F_4 and F_5 lines in the winter nursery near Yuma, AZ (Horsley, personal communication, 2020). Selected lines from this nursery are harvested and advanced to the Preliminary Yield Trial (PYT) that is grown in four locations in North Dakota. The number of lines genotyped was 2,100 in 2017 and 2018, and 2,169 lines in 2019. The 81 lines used by Jung (2015) were used as the TP to develop genomic selection models for the malt quality traits ß-glucan, α-amylase, malt extract, and wort protein. These traits were selected as candidates for genomic selection because of the expense and time needed to collect the data. The results for these traits are not usually available until three to nine months following harvest. Results indicate that genomic selection for reduced ß-glucan was successful, but not so for the other traits. In the two years prior to genomic selection for ß-glucan, about one-third of the lines advanced to the PYT had ß-glucan less than ND Genesis. In 2017-2019 when genomic selection was used, the average number of lines in the PYT with ß-glucan levels less than ND Genesis was greater than 75%. Additional research is needed by the NDSU barley breeding program to identify updated TPs and genomic selection models that can be used to expand the successful use of genomic selection to more traits. The NDSU barley breeding program regularly collects phenotype data on over 24 traits each year.

Genomic Selection Models

Bayesian Methods

The Bayes package used in JMP Genomics comes from the BGLR statistical package in R provided by Pérez and De Los Campos (2014). This package was implemented in a unified Bayesian framework for several commonly used parametric and non-parametric methods used for predictions. Bayesian estimation permits separate estimates of variance per marker and assumes a specified prior distribution (Meuwissen et al., 2001). In this case, Bayes B is used during the analysis. Bayes B has an inverse chi-square resulting in a scaled t-distribution with a prior mass at zero allowing markers with no effects. Equation 2 presents the model used where β_j are vectors of effects, $N(\cdot|\cdot, \cdot)$, $\chi\text{–}2(\cdot|\cdot, \cdot)$, $G(\cdot|\cdot, \cdot)$, $Exp(\cdot|\cdot)$, $B(\cdot|\cdot, \cdot)$ denote normal, scaled inverse Chi-squared, gamma, exponential and beta densities, respectively, β_{jk} are fixed effect regression coefficients, π

is the probability of non-null effects, and σ^2_β are variance parameters based on random effects (Pérez and De Los Campos, 2014).

$$p(\beta_j, \sigma^2_\beta, \pi) = \{\Pi_k [\pi N(\beta_{jk}|0, \sigma^2_\beta) + (1 - \pi)1(\beta_{jk} = 0)]\ \chi^{-2}(\sigma^2_{\beta jk}\ |df_\beta, S_\beta)\} \qquad \text{(Equation 2)}$$

$$B(\pi|p_0, \pi_0) \times G(S_\beta|r, s)$$

Ridge Regression

The RR method is known to be the least computationally demanding method for genomic selection. Ridge regression estimates all marker effects, shrinks them toward zero and makes the assumption that markers are random effects with a common variance (Meuwissen et al., 2001). The RR method computations in JMP Genomics are performed using SAS/STAT PROC MIXED. This model provides flexibility in modeling means, variances, and covariances. While this method shrinks all marker effects toward zero it can underestimate some marker effects because the traits of interest are generally quantitative, and most are controlled by minor effect genes.

Partial Least Squares

Partial least squares (PLS) regression is a method developed in the 1960's by Herman Wold as a soft modeling technique (JMP, 2019b). Soft modeling refers to describing a system without any previous model postulation. The PLS method is a regression statistical method that estimates the relationship among variables by modeling the variation of the dependent and the predictor variables concurrently. The method is especially useful for creating models when the number of factors are numerous and collinear (Tobias, 1995). The PLS method extracts back-to-back linear combinations of the predictor variable and maximizes the variance explained in X and Y, and it is used to find the multidimensional course in the X space that explains the maximum multidimensional variance course in Y.

XGBoost Regression

XGBoost is a machine learning method that uses a sparsity-aware algorithm for sparse data and weighted quartile sketch for approximate tree learning (Chen and Guestrin, 2016). Machine learning is a method used in data analyses that automates analytical model building as a branch of artificial intelligence (AI). The idea behind these methods is the potential of AI being capable of learning from experience and adjusting to new inputs (SAS, 2019).

MATERIALS AND METHODS

Plant Material

The current study used three TPs originating from the NDSU Barley Breeding Program. The first TP (Original TP) consisted of 81 two-rowed barley lines from NDSU that were utilized in the USDA-NIFA Barley Coordinated Project (Barley CAP) in 2006-2009. The 81 lines were those among 384 that were identified to have maximum diversity as determined using the software STRUCTURE (Jung, 2015). The list of lines, their pedigree, and the years they were evaluated in the Barley CAP are listed in Appendix A. The second TP (Crossing parent TP TP) consisted of 137 two-rowed parents used by the NDSU barley breeding program from 2008-2016. The list of lines is available in Appendix A. The third TP (Combined TP) included all lines in the previous two TP’s.

Genetic Analysis

Previous to the start of the current study, the Original TP (Jung, 2015) was genotyped by the USDA-ARS Molecular Genotyping Laboratory of Dr. Shiaoman Chao as part of the CAP. The genotype data are from the first of two-barley oligo pool assay platforms (BOPA1 and BOPA2) (Close et al., 2009) containing allele-specific oligos for a set of 3,072 SNPs that were used to genotype all Barley CAP lines. The representative mapping panels were built following the procedure described by Negeri (PhD dissertation, NDSU 2009) that selects a mapping panel of breeding lines that maximizes diversity among lines. The criterion for selection was based on the subpopulation membership coefficient of a line in an inferred subpopulation cluster (Mamidi et al., 2013). The genotype data were obtained from the Hordeum Toolbox database Website (http://hordeumtoolbox.org/).

The Crossing parent TP consists of parents used by the NDSU barley breeding program from 2008-2016. I sowed the Crossing parent TP in the greenhouse at the beginning of this study to provide leaf tissue for DNA extraction. The population was genotyped in Dr. Shiaoman Chao's USDA-ARS laboratory in Fargo using the Illumina 50k (San Diego, CA) Infinium iSelect genotyping array for barley (Bayer et al., 2017).

Phenotypic Data for Breeding Populations

Phenotype data utilized in this study included those for 24 traits (Table 1) in which data are regularly collected on NDSU breeding lines. Data collected from 2006-2018 were used throughout the estimation analyses. Data are available online in the Triticeae Toolbox (T3; http://triticeaetoolbox.org/barley/). "T3 is the web portal for data generated by the USDA-NIFA Triticeae Coordinated Agricultural Project (T-CAP).

Greenhouse Experiments

A randomized complete block design with three replicates was used for each of the disease screening experiments.

Net-Form Net Blotch

The NFNB isolate ND89-19 was used to produce inoculum. The inoculum was grown for 12-14 d in the dark at room temperature and then moved to light for one day. The spores were collected by flooding plates with sterile distilled water, gently rubbing plate surfaces with a rubber policeman to release spores, and pouring the suspension through two layers of cheesecloth. Spore concentration was adjusted to 7,000 spores mL^{-1}.

Plants for inoculation were grown as described for SFNB screening, except the resistant and susceptible check genotypes were ND-B112 and 'Hector', respectively. Cone-tainers were grown in the greenhouse at a room temperature of 20°C±5 with a 14-h photoperiod under 430W

Agrosun lights. Two-week old seedlings were inoculated with an aqueous spore suspension containing two drops of Tween 500 mL^{-1} of solution. The spray solution was applied with an atomizer-pressurized sprayer. Approximately 100 mL of spray solution was applied at 55 kPa to each rack of 98 Cone-tainers until the solution began to bead up and run off the leaf surfaces. To enhance infection, inoculated plants were kept in a mist chamber. Plants were misted for 24 sec every 12 min in the dark for 22-24 h with 100% relative humidity. After inoculation and misting were completed, plants were allowed to dry slowly with lights on, then moved back to the greenhouse. Plants were rated 7 d later for disease infection response (IR) using a 1-10 rating scale, where 1 = resistant and 10 = susceptible (Tekauz, 1985). The evaluation consisted of taking the highest and lowest IR observed. The highest IR was multiplied by 2/3 and the lowest IR was multiplied by 1/3 to give the predominant and less predominant score and both values were summed to provide the final rating.

Spot Blotch

The SB isolate used for screening was SB85-F pathotype 1 (Valjavec-Gratian and Steffenson, 1997). The inoculum was grown under 40-watt cool florescent lights for 12 h and in dark for 12 h, for 10-12 d. Spores were collected by flooding plates with sterile distilled water, gently rubbing plate surfaces with a rubber policeman to release spores and pouring the suspension through two layers of cheesecloth. Spore concentration was adjusted to 8,000 spores mL^{-1}.

Plants for inoculation were grown as described for SFNB screening, except the resistant and susceptible check genotypes were ND-B112 and ND5883, respectively. Cone-tainers were kept in a greenhouse at room temperature (20 °C±5) with a 14-h photoperiod under 430W Agrosun lights. Two-week old seedlings (two to three-leaf stage) were inoculated with an aqueous spore suspension containing 2 drops of Tween 500 mL^{-1} of solution. The spray solution was applied with an atomizer pressurized sprayer. Approximately100 mL of spray solution was applied at 5 kPa rack^{-1} of 98 Cone-tainers until the inoculum beaded and ran off the leaves. To enhance infection, inoculated plants were kept in a mist chamber. Plants were misted for 24 sec every 12 min, in the dark, for 22-24 h with 100% relative humidity. Next, plants were allowed to air dry slowly with lights on and moved back to the greenhouse. Disease ratings were collected on plants after 7 d using a 1-9 rating scale, where 1 = resistant and 9 = susceptible, as described by Fetch and Steffenson (1999). The evaluation consisted of taking the highest and lowest IR observed. The highest IR was multiplied by 2/3 and the lowest IR was multiplied by 1/3, to give the predominant and less predominant score and both were summed to provide the final rating. Then the mean of the three replicates was used in the statistical and AM analysis.

Field Experiments

Six-character environment code designations were used for presenting the results of analyses as follows: the first two digits represent the year (11=2011; 12=2012 and 13=2013); the next two characters are for the locations (NV= Nesson Valley; OS = Osnabrock and LA= Langdon); and the last two digits represent the row type of experiment (57= two-rowed type). Field screening was limited to the two-rowed panel.

Deoxynivalenol accumulation

In order to collect data on DON accumulation, the experimental materials were sown in the NDSU Fusarium head blight nursery at Osnabrock, ND in 2012 and Langdon, ND in 2012 and 2013. Entries were assigned to experimental units (hills) using the repeated augmented block experimented design (repeating four checks every 20 entries), as described by Horsley et al., (2006b). Each augmented block experiment was repeated twice at an environment each year. The grain-spawn inoculation method used was the same as described by Urrea et al. (2002). The DON content was determined in the NDSU Barley and Malt Quality Laboratory of Dr. Paul Schwarz and the threshold of detection was 0.5 µg g^{-1} (Schwarz, 1995).

Foliar diseases

Foliar disease (FD) severity was evaluated using a 1-9 scale (1 = no/low disease damage 9 = severe disease damage). This trait was evaluated in environments where foliar diseases occurred.

Data Analyses

Agronomic Data

Data from the NDSU Barley Breeding Program dating back to 2006 were utilized for analyses. These data are stored in an SQL database that is managed using the software Agrobase (Agronomix, Winnipeg, Manitoba, Canada). Best linear unbiased estimates from each location within a year were utilized to calculate BLUPs across environments using ASReml (VSNi, Hemel Hempstead, England, UK). In these combined analyses, years and locations were considered fixed effects and lines were considered a random effect.

Table 1. Traits included within experiment divided into agronomic, malt quality and disease traits.

Agronomic	Barley and Malt Quality	Disease
Heading date	Barley color	Deoxynivalenol
Height	α-amylase	Foliar disease
Kernel weight	ß-glucan	Net blotch
Lodging	Diastatic power	Spot blotch
Stem breakage	Free amino nitrogen	
Yield	Malt extract	
Moisture	Plump	
	Protein	
	Soluble protein over total protein	
	Test weight	
	Wort clarity	
	Wort color	
	Wort protein	

Malt Quality and Disease Data

Because of the expense of determining DON, and barley and malt quality traits, the samples used for determining DON, and the barley and malt quality traits were composites across replicates for each entry within a location. Calculation of BLUPs for DON and the barley malt quality traits were calculated using these single location values. In these analyses done using JMP-Pro 14.3 (SAS, Cary, NC), location and year were considered fix effects and entry was a random effect. The BLUPs for net blotch and spot blotch were calculated using BLUEs obtained from greenhouse evaluation of seedlings by the barley pathology project in the Department of Plant Pathology at NDSU. Three replicates of each entry are used in these annual disease assessments. The BLUPs were calculated using a mix-model analysis in JMP-Pro where year was a fixed effect and entry was a random effect.

Analyses Using JMP-Genomics

Preparation of Files for Analyses

Relying on documentation manuals in order to run software can be frustrating, so to help users that may use JMP Genomics in the future for their analyses, I summarized the steps I used. I used the Genome Wide Association Studies (GWAS) and Predictive Modeling methods of JMP Genomics for my initial analyses. In order to perform these analyses, the first step is to prepare your phenotype, genotype, and map information so it can be imported into JMP Genomics. Data files with both genotypic and phenotypic information were joined into a single file, so marker names and genotype phenotype data were in columns. This file is referred to by JMP Genomics as the Input File. Next, the Annotation File with columns containing the SNP name, chromosome, map information (map position), and source sequence (ATCG...) was created. After these files were prepared, data were analyzed in JMP Genomics 9 using the steps outlined below. Failure to successfully perform any of these steps will result in the failure of the full analyses to run.

Subset and Reorder Data

The purpose of sub-setting and reordering data in JMP Genomics 9 is to ensure that the genetic information present in the Annotation File corresponds precisely with the information present in the Input File. The number and order of SNPs in the Input File must be the same as the SNPs in the Annotation File. Doing so not only prevents discrepancies of information, but also allows the users to make inferences for genotypes that have both genotypic and phenotypic information and impute genotypes for entries that have missing or no genetic information. This feature helps specify the proportion of genotypes required for each line to be included for further analysis. A default parameter of 0.9 was used during this analysis.

Recoding Genotypes

As the name suggests, this step involved recoding the datasets. In the case of the current study, the genotypic information was recoded by converting AA, AB, and BB genotypes to the numeric values of 0, 1, and 2, respectively. The annotation dataset was recoded to so that each SNP name contained the prefix “nug” in order to simplify further analyses.

Marker Properties

Performing quality control of your marker data to identify markers that should be excluded from use in analyses can be done using Marker Properties. This function calculates marker informativeness, including allele and genotype frequencies, and tests markers for Hardy-Weinberg equilibrium (HWE) using SAS PROC ALLELE. No lines or markers were excluded during this step.

Subset and Reorder Genetic Data

This step is done to ensure, once again, the Information File and the Annotation File have the correct corresponding markers in the same order to proceed with further analysis. Minor allele frequency, which can be described as the alleles that occurs least often in a population from a set of alleles for a given gene or locus, was used to determine lines and markers to remove for further analyses. In this case, markers with a minor allele frequency greater than 0.01, a proportion of missing genotypes less than or equal to 0.10, and a negative log value of HWE lower than 100 were retained for further analyses.

Relationship Matrix

The relationship matrix outputs a heat map that illustrates relationships of samples utilizing the JMP Hierarchical Clustering Platform. Identity by Descent (IBD) values were obtained in this analysis. I used this analysis to identify genetic relationships within the population. IBD values greater or equal to a proportion of 0.25 of alleles can be found in data output provided within JMP. The IBD method is used over identity by state (IBS) as the default method because IBS requires all SNPs to be polymorphic to avoid errors in the distance procedure.

Principal Component Analysis for Population Stratification

Principal component analysis (PCA) was utilized to determine population structure based on SNPs. Another use of PCA is to adjust the stratification of populations and variation in allele frequency that may take place due to familial differences. Principle components with $P \leq 0.10$ based on the multiple testing method were included to adjust for population stratification. A conversion to $\log_{10}$ values was done to transform *p*-values at $P \leq 0.5$ to easily identify peaks of significant value.

Q-K Model Fitness

The Q-K Model Fitness process was utilized to determine which model or combination of models was most appropriate for the mixed model analysis. The models include relationship matrix values (K) and principal component values (Q) calculated in previous steps. Model combinations observed within these analyses include naïve (neither Q or K), K only, Q only, and Q plus K. The best combination of models was determined by using Akaike's Information Criterion (AIC), Akaike's Information Criterion correction (AICc) and Bayesian Information Criterion (BIC) values calculated in the maximum likelihood analyses. These estimates were used to estimate the quality of each model relative to each of the other models. The maximum likelihood technique estimates parameters of a given model by maximizing the likelihood function. The likelihood function is the product of the probability density functions evaluated at observed data values as described in JMP (2019a). The AIC, AICc, and the BIC values are information-based criteria that assess model fit. Both are based on -2LogLikelihood. Smaller AIC, AICc and BIC are indicative of "better" models.

SNP Trait Association

SNP Trait Association is a GWAS analysis to associate or link markers to traits of economic importance. This step within JMP Genomics 9 was specifically designed for very large data sets to seek the association of genetic markers with quantitative and qualitative traits. These analyses are output with $-\log_{10}$ at $P \leq 0.05$.

Q-K Mixed Model

The Q-K Mixed Model process tests for association between traits and SNPs using the results from the Q-K Model Fitness described previously. This test adjusts for population structure and family relatedness as it tests for association between many types of traits and SNP genotypes one SNP at a time (Yu et al., 2006).

Genomic Heritability

Genomic heritability refers to a portion of the phenotypic variation among individuals due to their genetic differences. The genomic heritability value is obtained by dividing the genetic variance of all markers by the phenotypic variance. In JMP Genomics 9, genomic heritability estimates the genetic variance explained by marker variables using a mixed model framework as described in (Yang et al., 2010).

Genomic Bayesian Regression (GBR)

The Bayes package used in JMP Genomics comes from the BGLR statistical package in R provided by Pérez and De Los Campos (2014). Files prepared in previous steps containing traits and SNPs in columns were selected as input. For initial analysis, Forest predictor reduction with a maximum number of filtered predictors of 1,000 was used under the *Predictor Reduction* tab. The predictors chosen were those with the most significant *t* and Fisher exact tests. Under the *Analysis tab*, Bayes B with 10,000 iterations, 2,000 burn samples, a thinning rate of five, and an expected proportion of the total variance explained by the regression model of 0.5 were the selected options. Additionally, variables were considered to be continuous. Once an initial test is run for each trait, the top two performing models (best combination of highest correlation and lowest error) were rerun using different levels of Forest predictor reduction (1000, 800, 500, 200, 100) to determine the minimum number of markers that could be used without losing power in the model.

Partial Least Squares

Partial least squares regression is a method developed in the 1960's by Herman Wold for multivariate analyses he referred to as "soft" modeling (Tobias, 1995). Files prepared in previous steps containing traits and SNPs in columns are selected as input. For initial analysis, Forest predictor reduction with a maximum number of filtered predictors of 1000 was selected under the

Predictor Reduction tab. The predictors chosen were those with the most significant *t* and Fisher exact tests. Under the *Analysis tab*, variables were considered continuous, and proportional prior probabilities and three PLS components were the selected options. Once an initial test was run for each trait, the top two performing models were rerun using different levels of Forest predictor reduction (1000, 800, 500, 200, 100) to verify the minimum number of markers that could be used without losing power in the model.

Ridge Regression

The RR method computations in JMP Genomics are performed using SAS/STAT PROC MIXED. Files prepared in previous steps containing traits and SNPs in columns are selected as input. For initial analysis, Forest predictor reduction with a maximum number of filtered predictors of 1000 was selected under the *Predictor Reduction* tab. The predictors chosen were those with the most significant *t* and Fisher exact tests. Under the *Analysis tab*, variables were considered continuous; and 0.5 asymmetric loss fitting proportion, proportional prior probabilities, and Dot Kernel function were the selected options. The Dot Kernel function corresponds to the same structure induced by random effects, which is the outer dot product of the Z matrix. The asymmetric loss fitting proportion value (0.5) becomes the weight placed on positive residuals or under-predictions. Negative residuals or over-predictions were then weighted as one minus the specified value (0.5). Once an initial test was run for each trait, the top two performing models were rerun using different levels of Forest predictor reduction (1000, 800, 500, 200, 100) to verify the minimum number of markers that could be used without losing power in the model.

XG Boost

XGBoost is a machine learning method that uses a sparsity-aware algorithm for sparse data and weighted quartile sketch for approximate tree learning (Chen and Guestrin, 2016). Files prepared in previous steps containing traits and SNPs in columns were selected as input. For initial analysis, Forest predictor reduction with a maximum number of filtered predictors of 1000 was used under the *Predictor Reduction* tab. The predictors chosen were those with the most significant *t* and Fisher exact tests. Under the *Analysis tab*, gbtree for booster type, 10 boosting iterations, and reg:linear for learning objective with default values were selected. Once an initial test was run for each trait, the top two performing models were rerun using different levels of Forest predictor reduction (1000, 800, 500, 200, 100) to verify the minimum number of markers that could be used without losing power in the model.

Cross Validation Model Comparison

Cross-validation was implemented to train and develop the prediction models for each TP. This process was performed by randomly selecting one (1/K) of the observations at random as the TP and the remaining (1-1/K) were used for validation, where K was the number of times the TP was subdivided. Under the *Analysis* tab, selected options used were random partition as the hold out method, K for K-Fold or 1/K Hold-Out as the hold out size, where K was the number of folds or groups in a partition. Selected values were three for K and 10 for random hold-out iterations. To compare models for my study, I used Hsu's MCB method. Hsu's MCB is a multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best. In my analyses, the best results refer to the highest mean correlation values. This method creates a confidence interval for the difference between each level mean and the best of the remaining level means. If an interval has zero as an end point, there is a statistically significant difference between the corresponding means.

RESULTS AND DISCUSSION

Training populations for genomic selection must have both phenotypic and genotypic data and be representative of selection candidates in breeding programs (Heffner et al., 2009). The current study used three TPs originating from the NDSU Barley Breeding Program. The first TP (Original TP) consisted of 81 two-rowed barley lines from NDSU that were utilized in the USDA-NIFA Barley Coordinated Project (Barley CAP) in 2006-2009. The 81 lines were those identified to have maximum diversity as determined using the software STRUCTURE (Jung, 2015). The second TP (Crossing Parents TP) consisted of 137 two-rowed parents used by the NDSU barley breeding program from 2008-2016. The third and final population consisted of the combination of both previously mentioned populations (combined TP). The combined TP has 188 lines. Once data processing was finished, however, the population was decreases to 179 lines. This decrease was based on the proportion limits of marker frequency and missing values that could cause errors if maintained in further analyses. The first step in my research was to determine which TP of the three to use for predictive modeling based on the information derived from analyses on relationships for each TP.

Relationship Matrix to Determine the Relationship Between Lines

Heat Map

The three TPs used during this research can be expected to have an ancestral relationship because the barley genotypes comprising the populations are all from the NDSU breeding program and they have been bred for malting purposes. Years of intensive selection have likely fixed segments within the genome that are relevant to agronomic and malting quality traits, and disease resistance. The heat maps in Figures 1-3 can be used to identify the relationship across the samples within each population.

The square symmetric matrix in each figure represents the genetic relation of all possible individuals using the IBD metric. This IBD metric estimates the probability of two individuals sharing an allele that is derived from the same ancestor at a locus (Oliehoek et al., 2006). The colors within the heat maps illustrate the computed genetic metric for pairs of samples. The dendrograms to the right and below each heat map provide a view of the clustering history of the genotypes. The genotypes clustered together show similar patterns of relationship. The color key on the right side of each figure groups genotypes using a clustering algorithm of the genotype data utilized during the analysis. Within the heat map, the red or close to red colors indicate a higher level of relationship and the blue or close to blue colors represent a more distant relationship.

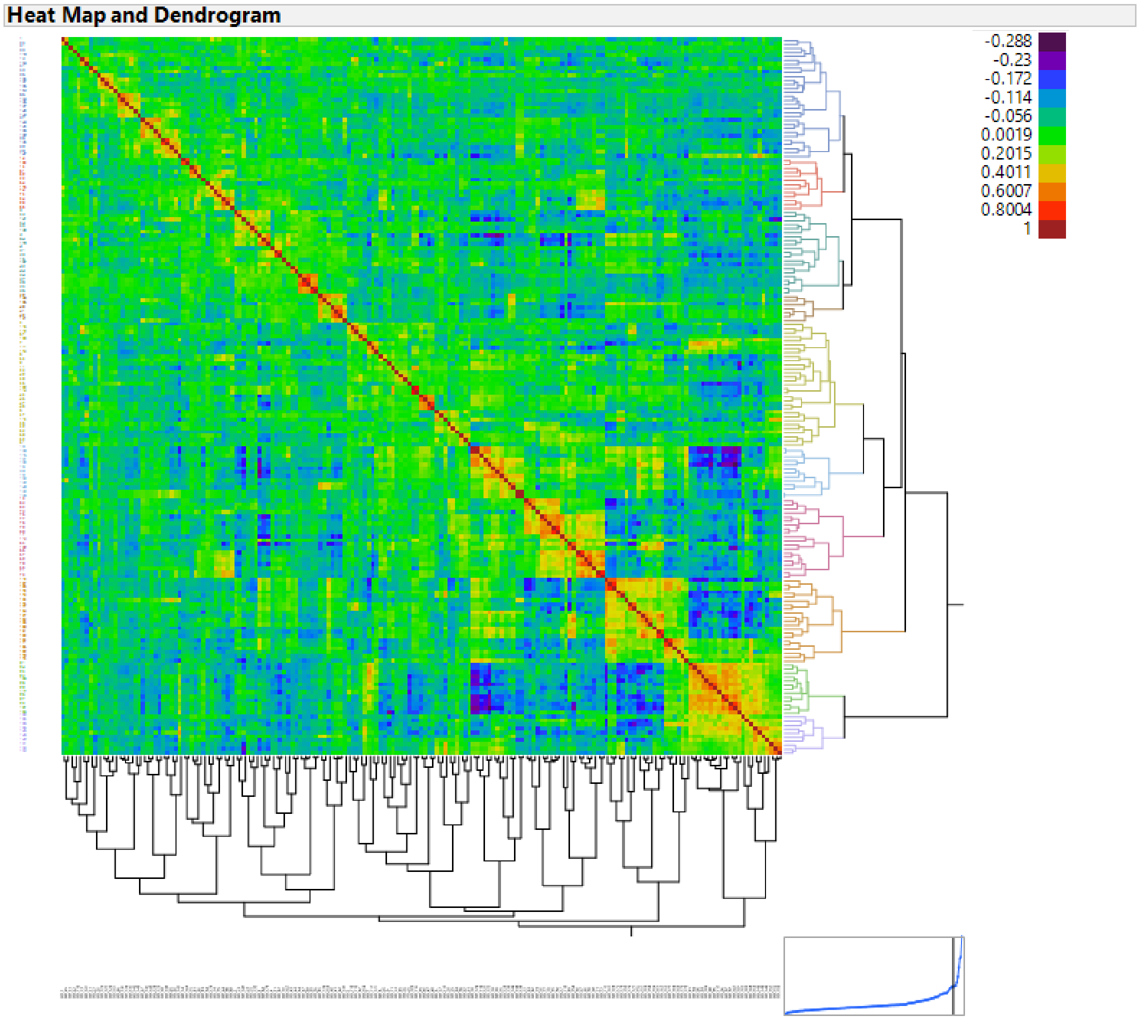


Figure 1. Relationship matrix heat map for the combined training population. The colors on the right side of the dendrogram group genotypes determined by a clustering algorithm by the SNP variable used during the analysis. Within the heat map, the red or close to red colors indicate a higher level of relationship and the blue or close to blue colors represent a more distant relationship.

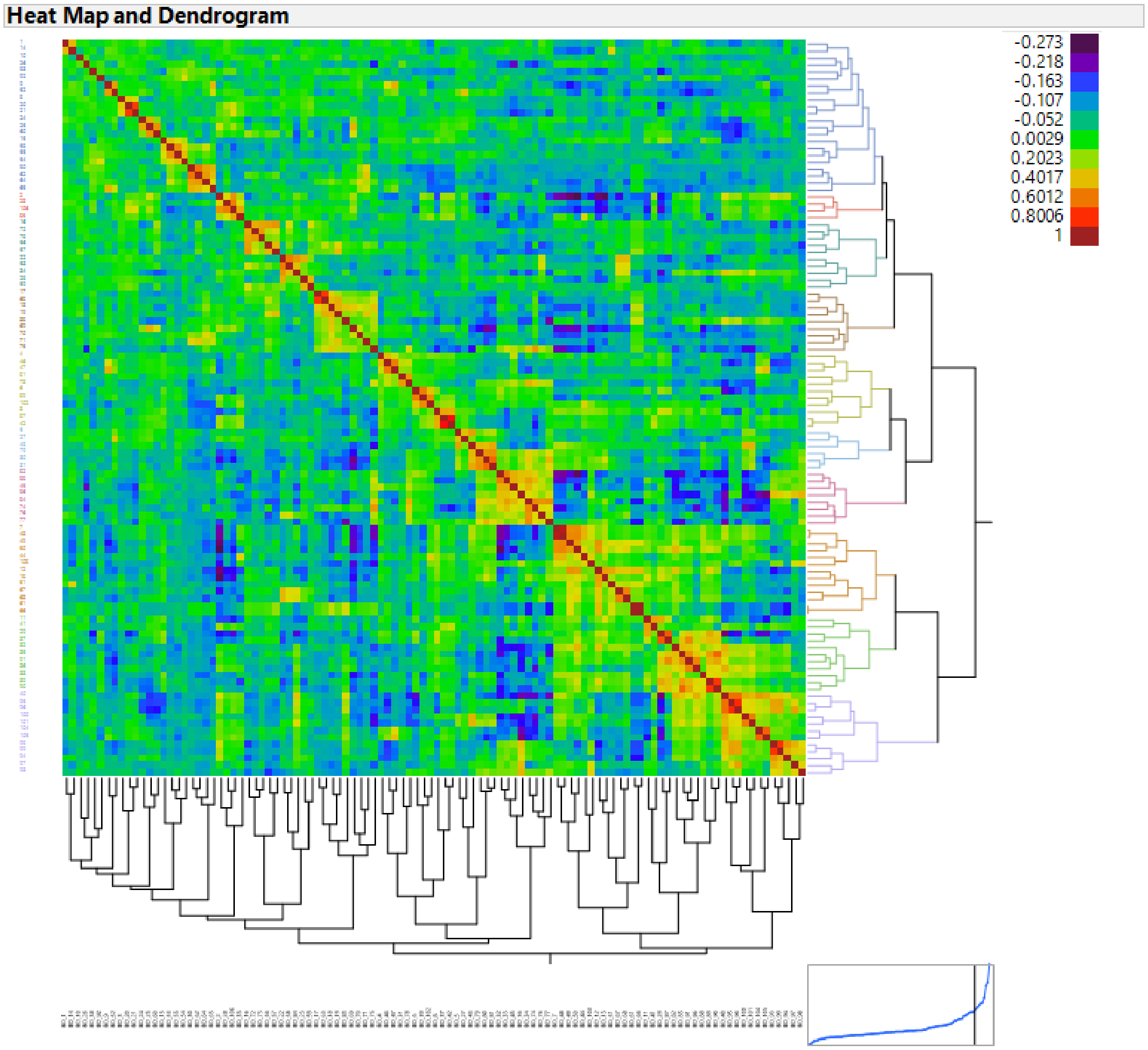


Figure 2. Relationship matrix heat map for the crossing parents training population. The colors on the right side of the dendrogram group genotypes determined by a clustering algorithm by the SNP variable used during the analysis. Within the heat map, the red or close to red colors indicate a higher level of relationship and the blue or close to blue colors represent a more distant relationship.

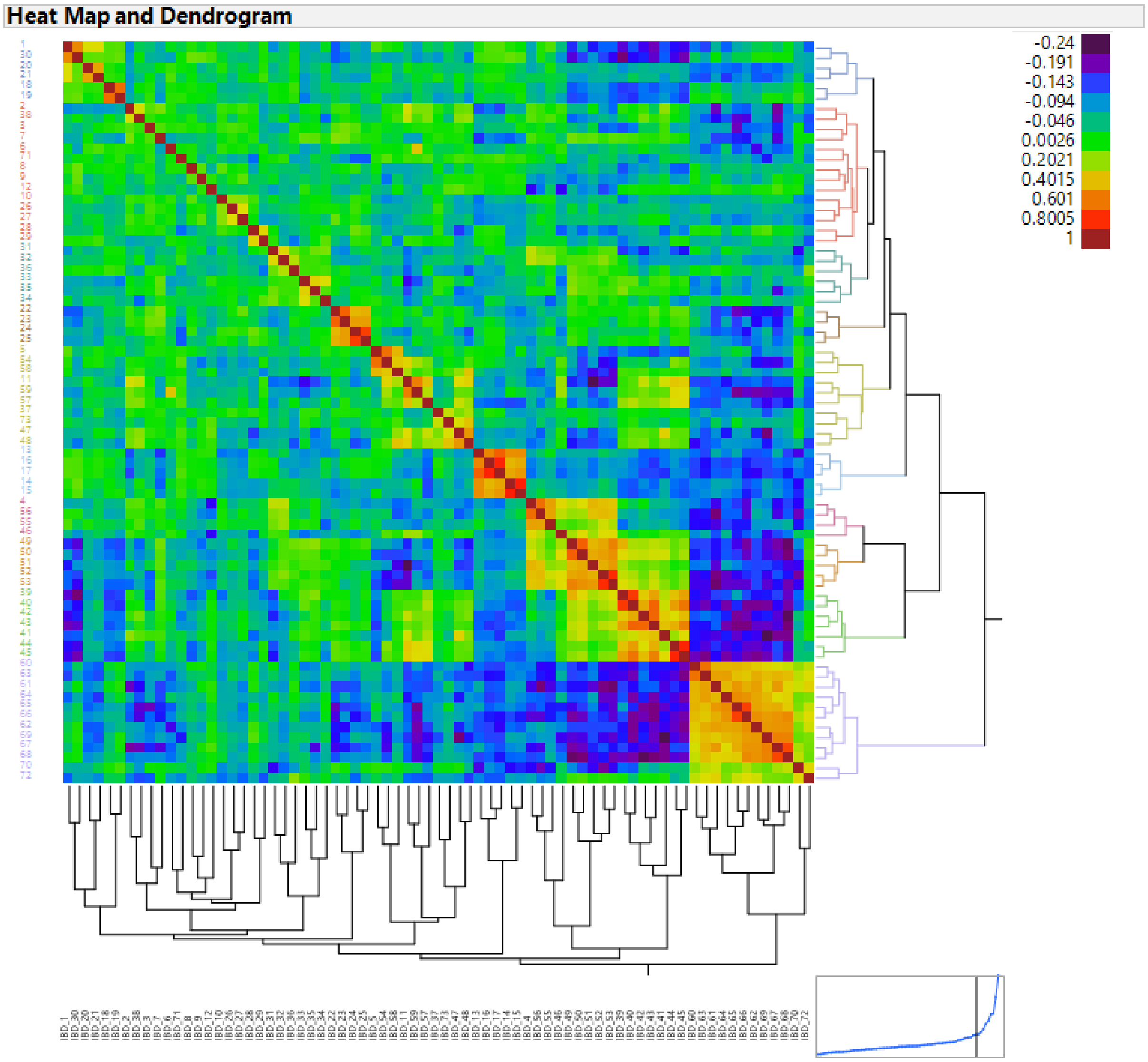
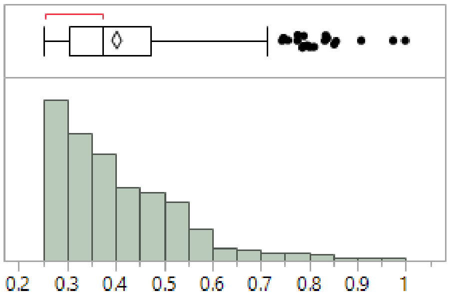


Figure 3. Relationship matrix heat map for the original training population. The colors on the right side of the dendrogram group genotypes determined by a clustering algorithm by the SNP variable used during the analysis. Within the heat map, the red or close to red colors indicate a higher level of relationship and the blue or close to blue colors represent a more distant relationship.

As displayed in Figures 1-3, the higher incidence of the blue color in the heat map indicates that lines in the original TP (Figure 3) appear to be more unrelated than the lines in the crossing parent and combined TP. This is an expected result as the original TP was selected by Negeri (20090 using the software Structure to contain a set of lines from the original 384 lines that have maximum diversity. Even with a higher amount of blue coloring within the heat map, it should be noted that there is also a larger presence of red along the diagonal as well when compared to the combined (Figure 1) and crossing parents TP (Figure 2). The appearance of the original TP having more diversity from viewing the heat map alone could be due to its smaller population size compared to the other two TPs. A small population size may be incapable of capturing enough of the variation that is needed for a TP.

IBD Distributions

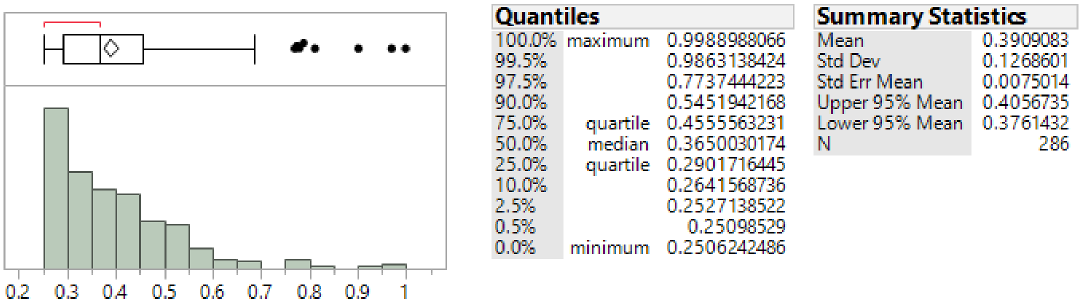
The relationship matrix results from JMP Genomics provide histograms that represent the distribution or count of genotypes above the IDB threshold. For my analysis, I used the default value of 0.25 for the threshold. In addition, the results identify the amount of highly related genotypes and contain the quantiles and summary statistics of the distribution of the IBD values. The higher the mean value within each histogram the higher the relationship in general within the specific population. Figures 4-6 contain data pertaining to the different populations analyzed within this experiment.



Quantiles		
100.0%	maximum	0.9991171192
99.5%		0.890480574
97.5%		0.7622204098
90.0%		0.5568022717
75.0%	quartile	0.4728497434
50.0%	median	0.3724435656
25.0%	quartile	0.3025012708
10.0%		0.2706414452
2.5%		0.2555357182
0.5%		0.2534162568
0.0%	minimum	0.251136628

Summary Statistics	
Mean	0.4014746
Std Dev	0.1274622
Std Err Mean	0.0049354
Upper 95% Mean	0.4111653
Lower 95% Mean	0.3917838
N	667

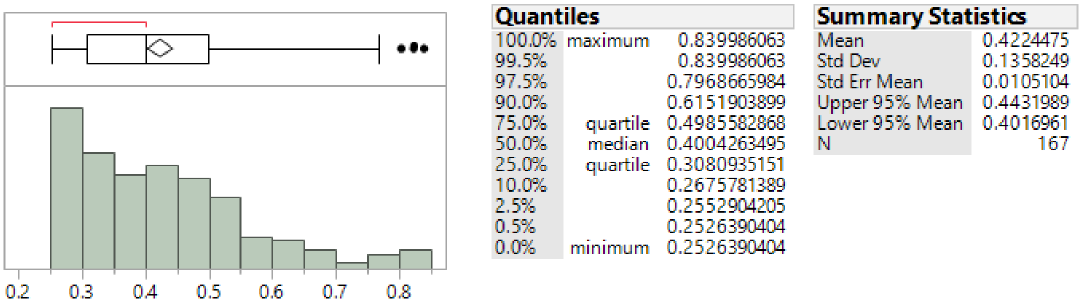
Figure 4. Distribution of IBD values from the combined population. A histogram counts the distribution of the sample of pairs with an IBD value above the threshold of 0.25 as well as a box plot with outliers. The table demonstrate the quantile and summary statistics of the distribution of IBD values for pairs of samples.



Quantiles		
100.0%	maximum	0.9988988066
99.5%		0.9863138424
97.5%		0.7737444223
90.0%		0.5451942168
75.0%	quartile	0.4555563231
50.0%	median	0.3650030174
25.0%	quartile	0.2901716445
10.0%		0.2641568736
2.5%		0.2527138522
0.5%		0.25098529
0.0%	minimum	0.2506242486

Summary Statistics	
Mean	0.3909083
Std Dev	0.1268601
Std Err Mean	0.0075014
Upper 95% Mean	0.4056735
Lower 95% Mean	0.3761432
N	286

Figure 5. Distribution of IBD values for the crossing parents. A histogram counts the distribution of the sample of pairs with an IBD value above the threshold of 0.25 as well as a box plot with outliers. The table demonstrate the quantile and summary statistics of the distribution of IBD values for pairs of samples.



Quantiles		
100.0%	maximum	0.839986063
99.5%		0.839986063
97.5%		0.7968665984
90.0%		0.6151903899
75.0%	quartile	0.4985582868
50.0%	median	0.4004263495
25.0%	quartile	0.3080935151
10.0%		0.2675781389
2.5%		0.2552904205
0.5%		0.2526390404
0.0%	minimum	0.2526390404

Summary Statistics	
Mean	0.4224475
Std Dev	0.1358249
Std Err Mean	0.0105104
Upper 95% Mean	0.4431989
Lower 95% Mean	0.4016961
N	167

Figure 6. Distribution of IBD values for the original population. A histogram counts the distribution of the sample of pairs with an IBD value above the threshold of 0.25 as well as a box plot with outliers. The table demonstrate the quantile and summary statistics of the distribution of IBD values for pairs of samples.

The combined TP had a mean of 0.40, the crossing parent TP had a mean of 0.39, and the original population had a mean of 0.42. As mentioned previously, it was unexpected that the original population was identified as having more related individuals than the crossing parents due to the purpose of its development. With the finding of this initial analyses of relationships within the populations and the recommended characteristics needed in a TP, further results in my research were obtained using analyses done using the combined TP.

PCA for Population Stratification

PCA is used to better understand the structure of a given population based on SNPs. The scree plots in Figure 7 can be used to determine the number of principal components to retain in the GWAS analysis to account for population structure. The Y-axis shows the proportion of the variance explained by the principal components and the X-axis indicates the number of principal components. The point where the plot of the proportion of the variation begins to level off is matched up with the value on the X-axis. The value of the X-axis is the number of principal components that should be used to account for structure in the GWAS analysis. The proportional variation began to level off at the fourth principal component.

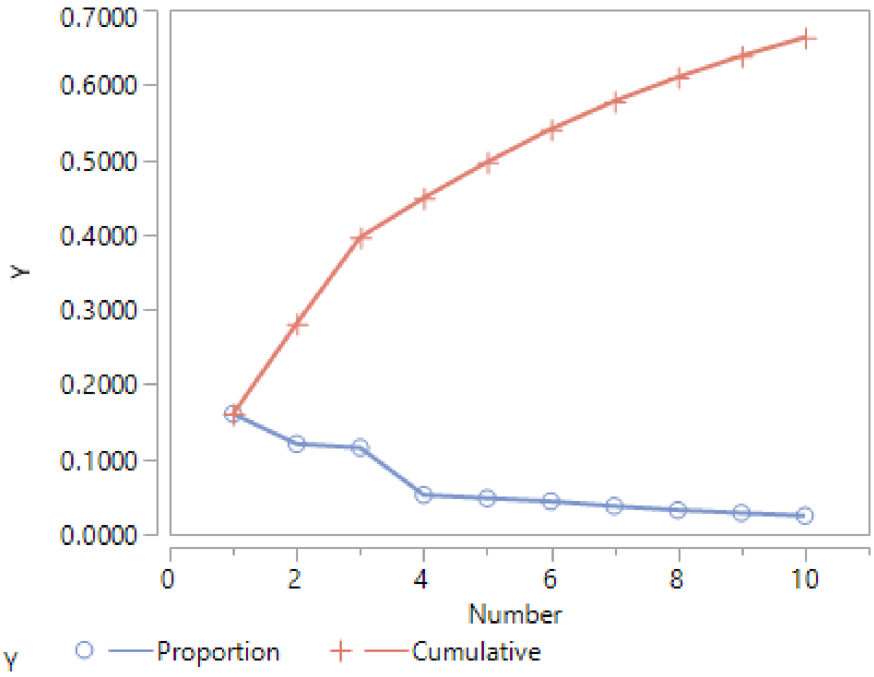


Figure 7. Scree plot for the combined population of the eigenvalue for the ith principal component versus the proportion of variation explained by the principal components.

Q-K Model Fitness

Figures 8-10 depict the Q-K model fitness for the combined TP. The Y-axis depicts the values used within each trait and the X-axis contains every combination of the models, which includes the naïve model, K only, Q only, and Q+K. The best model for each trait is the one that has the lowest -2LogLikelihood, AIC, AICC, and BIC values. AIC has the potential of overfitting when there are small sample sizes; thus, the use of AICc is used to address this issue. Based on the results, I concluded that the Q+K model was best for all traits.

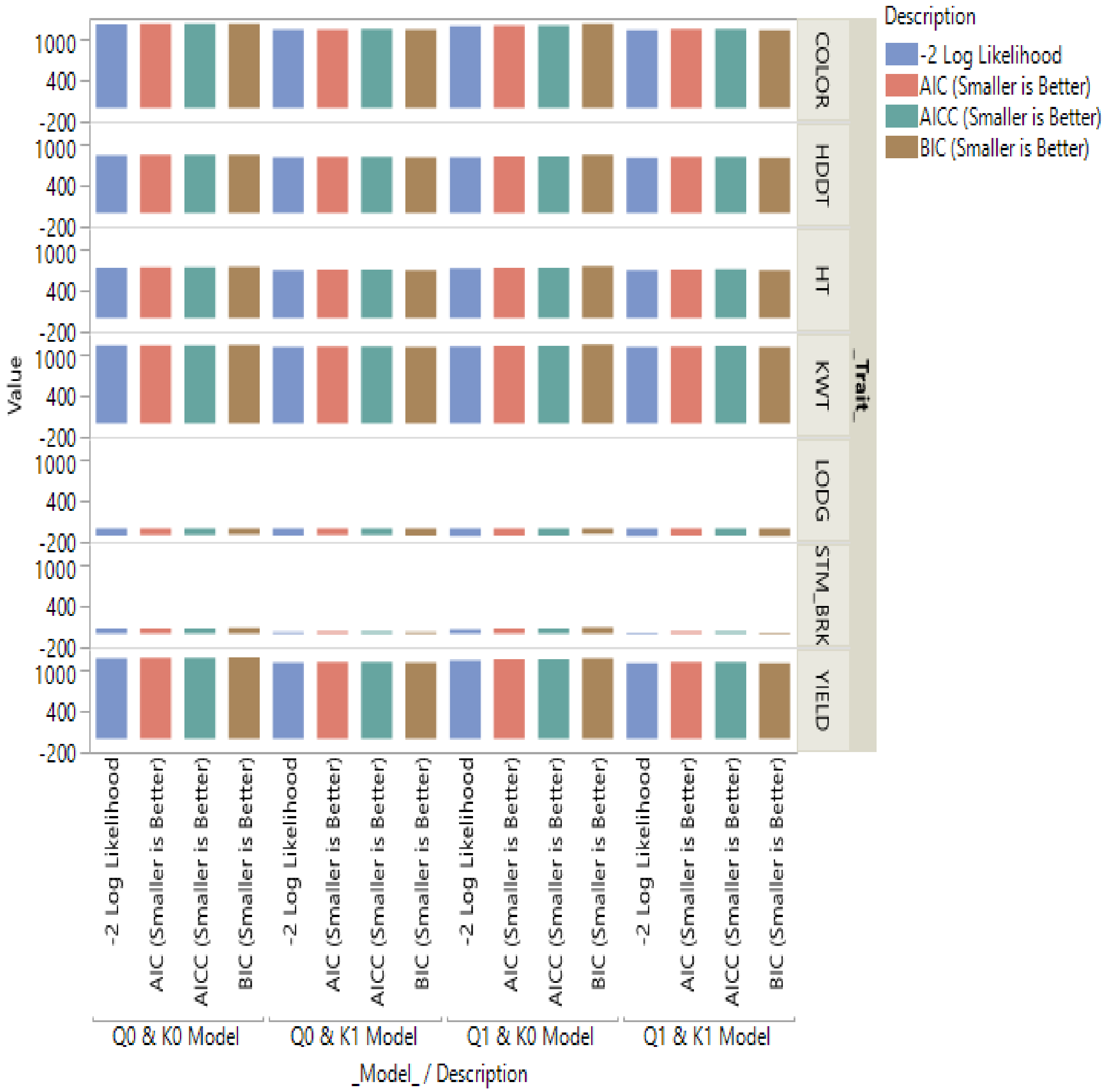


Figure 8. Q-K model fitness for analysis of agronomic traits using the combined TP. The Q0 & K0 model is the naïve model, the Q0 & K1 model is one where only kinship is addressed, the Q1 & K0 model is one where only structure is addressed, and the Q1 & K1 model is one where kinship and structure were addressed. Color is barley color, HDDT=heading date, HT=plant height, KWT=1000-kernel weight, LODG=lodging, and STM_BRK=stem breakage.

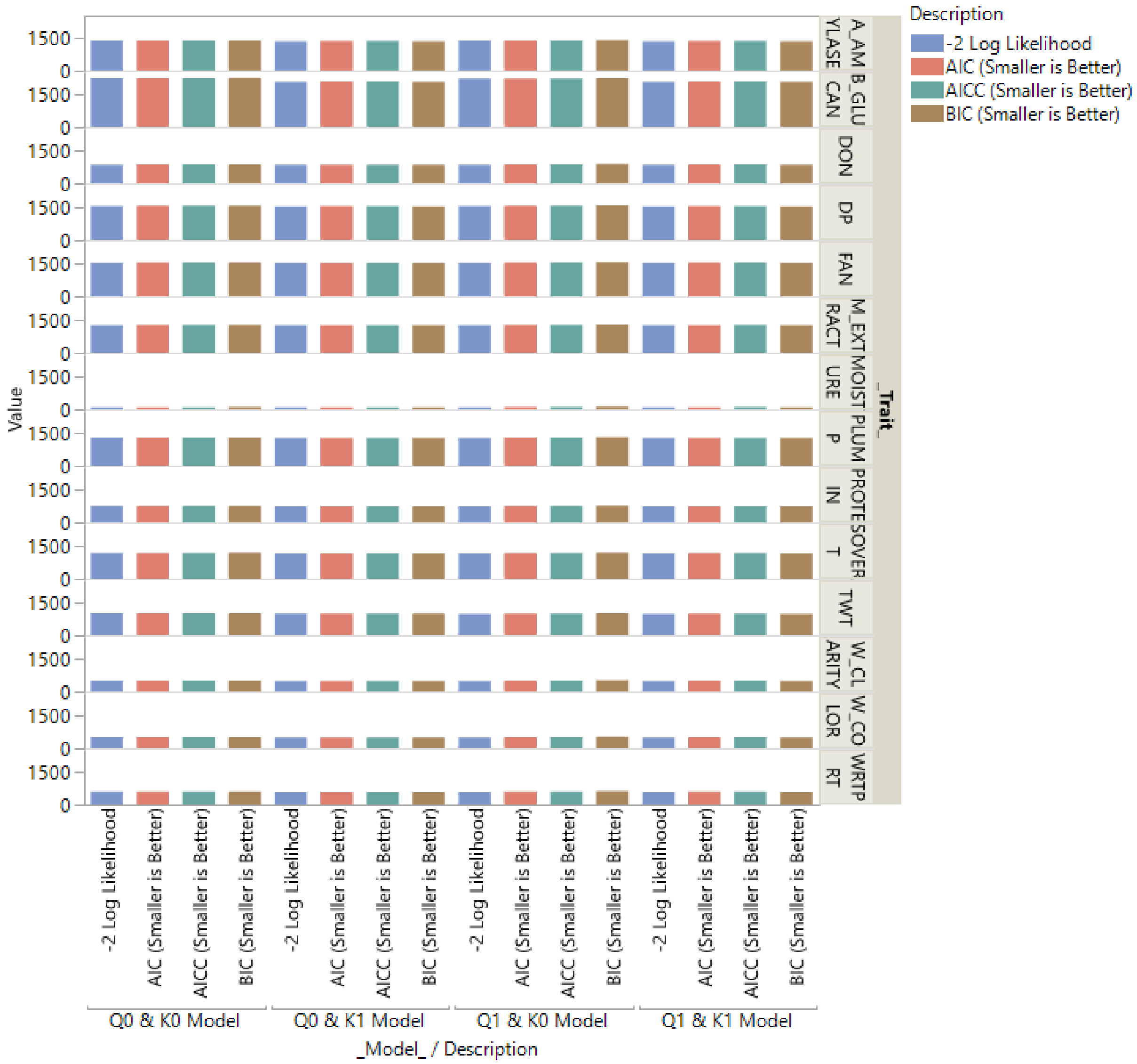


Figure 9. Q-K model fitness for analysis of malt quality traits using the combined TP. The Q0 & K0 model is the naïve model, the Q0 & K1 model is one where only kinship is addressed, the Q1 & K0 model is one where only structure is addressed, and the Q1 & K1 model is one where kinship and structure were addressed. A_Amylase=α-amylase, B_glucan=ß-glucan, MOISTURE=malt moisture, PLUMP=kernel plumpness, PROTEIN=barley protein, SOVERT=S/T, TWT=test weight, W_CLARITY=wort clarity, W_COLOR=wort color, and WRTPRT=wort protein.

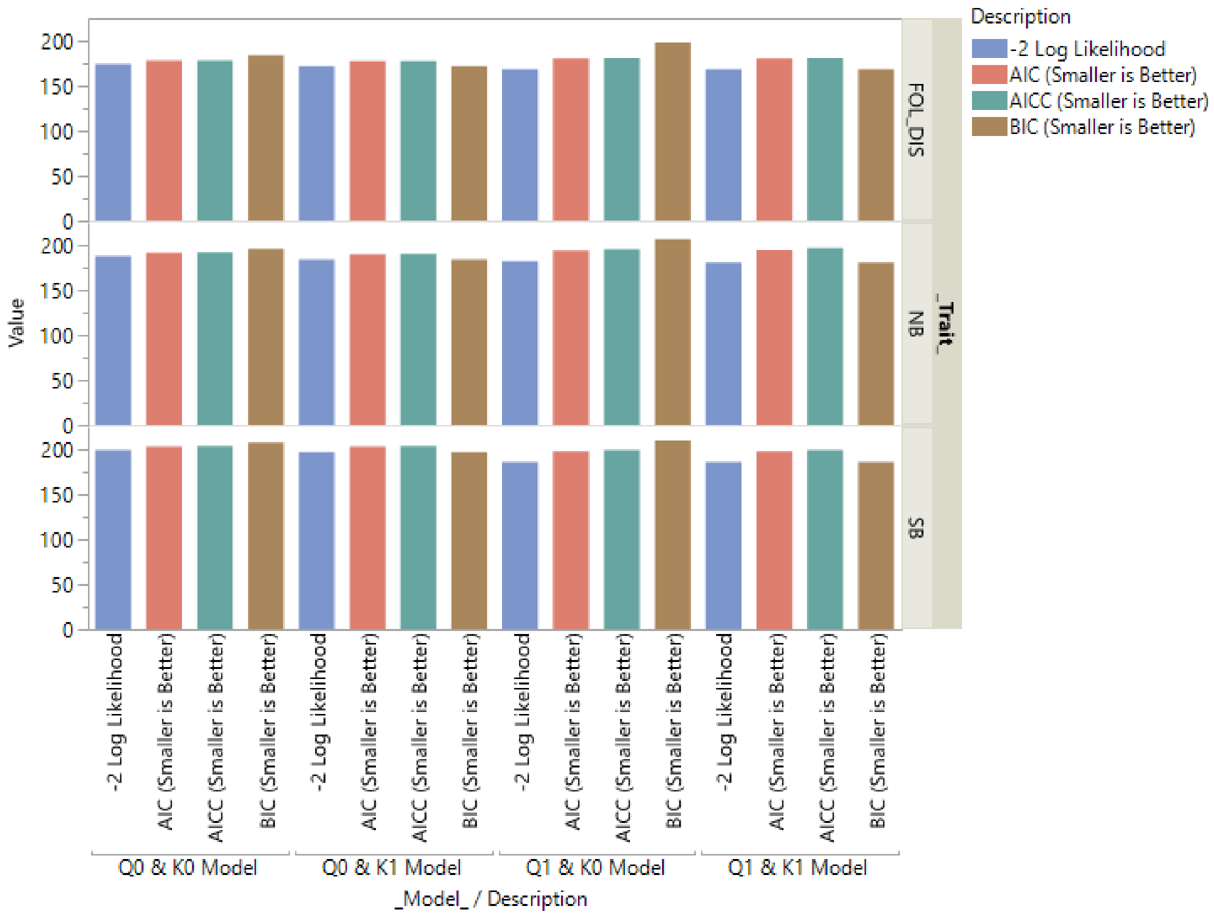


Figure 10. Q-K model fitness for analysis of disease resistance traits using the combined TP. The Q0 & K0 model is the naïve model, the Q0 & K1 model is one where only kinship is addressed, the Q1 & K0 model is one where only structure is addressed, and the Q1 & K1 model is one where kinship and structure were addressed. FOL_DIS=foliar disease, NB=net blotch, and SB=spot blotch.

SNP-Trait Association

Figure 11 illustrates the number of significant markers on each chromosome that were identified in the GWAS analyses for each trait. With years of crossing by the NDSU barley breeding program that utilized mostly parents from within the program, it interesting to find a large number of significant markers when we would expect many regions of the genome to be fixed. Although encouraging, these results are reflective of the current population and may not be applicable to other populations as this can be a flaw of association studies. Significant markers identified in this GWAS analysis will be compared to those obtained in the predictive modeling analyses to follow; however, the primary criterion for determining a marker relevancy for a trait will be the frequency value obtained in cross validation model comparison.

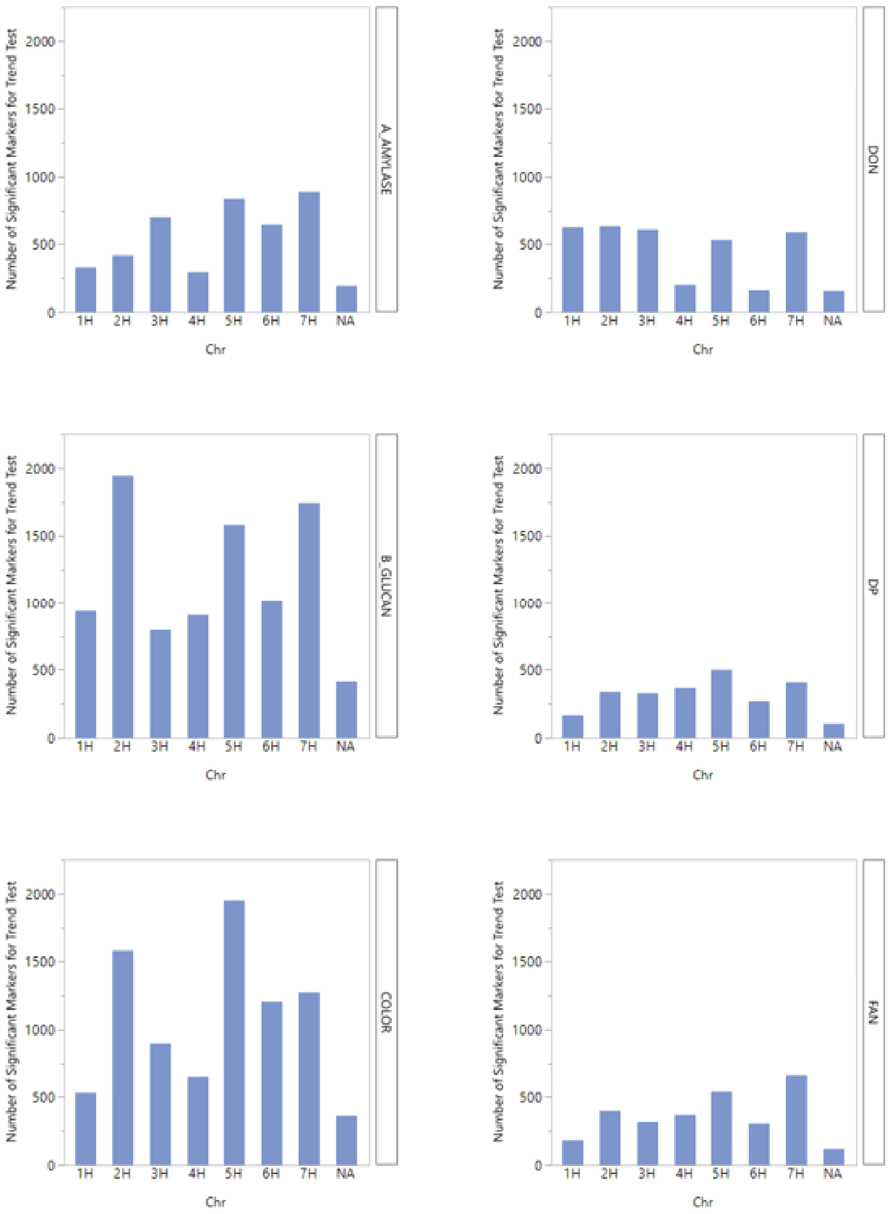


Figure 11. Number of significant SNP-Trait Associations (*P*≤0.05) identified on each chromosome. A_Amylase=α-amylase, DON= deoxynivalenol, B_glucan=ß-glucan, DP=diastatic power, Color is barley color, FAN=free amino nitrogen FOL_DIS=foliar disease, KWT=1000-kernel weight. HDDT=heading date, LODG=lodging, HT=plant height, MOISTURE=malt moisture, PROTEIN=barley protein, NB=net blotch, and SB=spot blotch, PLUMP=kernel plumpness, SOVERT=S/T, STM_BRK=stem breakage, W_COLOR=wort color, TWT=test weight, WRTPRT=wort protein, and W_CLARITY=wort clarity.

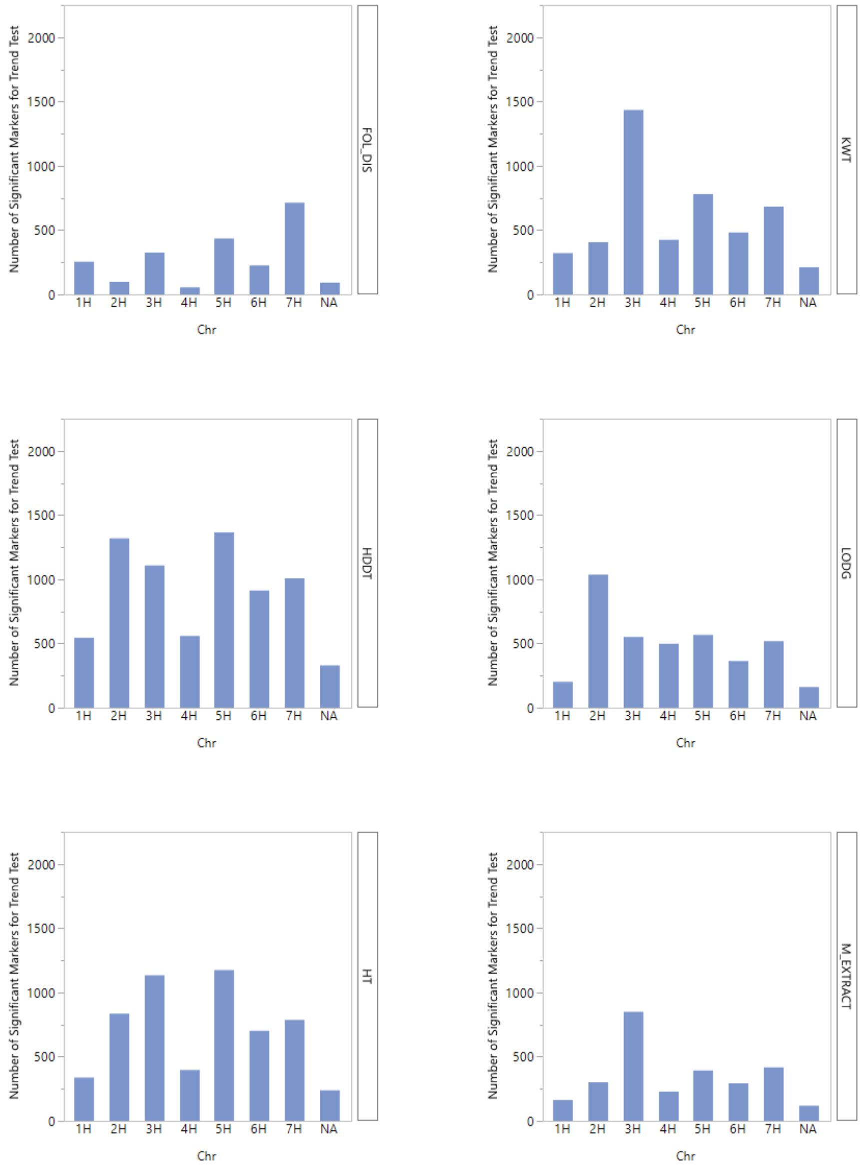


Figure 11. Number of significant SNP-Trait Associations ($P \leq 0.05$) identified on each chromosome (continued). A_Amylase=α-amylase, DON= deoxynivalenol, B_glucan=ß-glucan, DP=diastatic power, Color is barley color, FAN=free amino nitrogen FOL_DIS=foliar disease, KWT=1000-kernel weight. HDDT=heading date, LODG=lodging, HT=plant height, MOISTURE=malt moisture, PROTEIN=barley protein, NB=net blotch, and SB=spot blotch, PLUMP=kernel plumpness, SOVERT=S/T, STM_BRK=stem breakage, W_COLOR=wort color, TWT=test weight, WRTPRT=wort protein, and W_CLARITY=wort clarity.

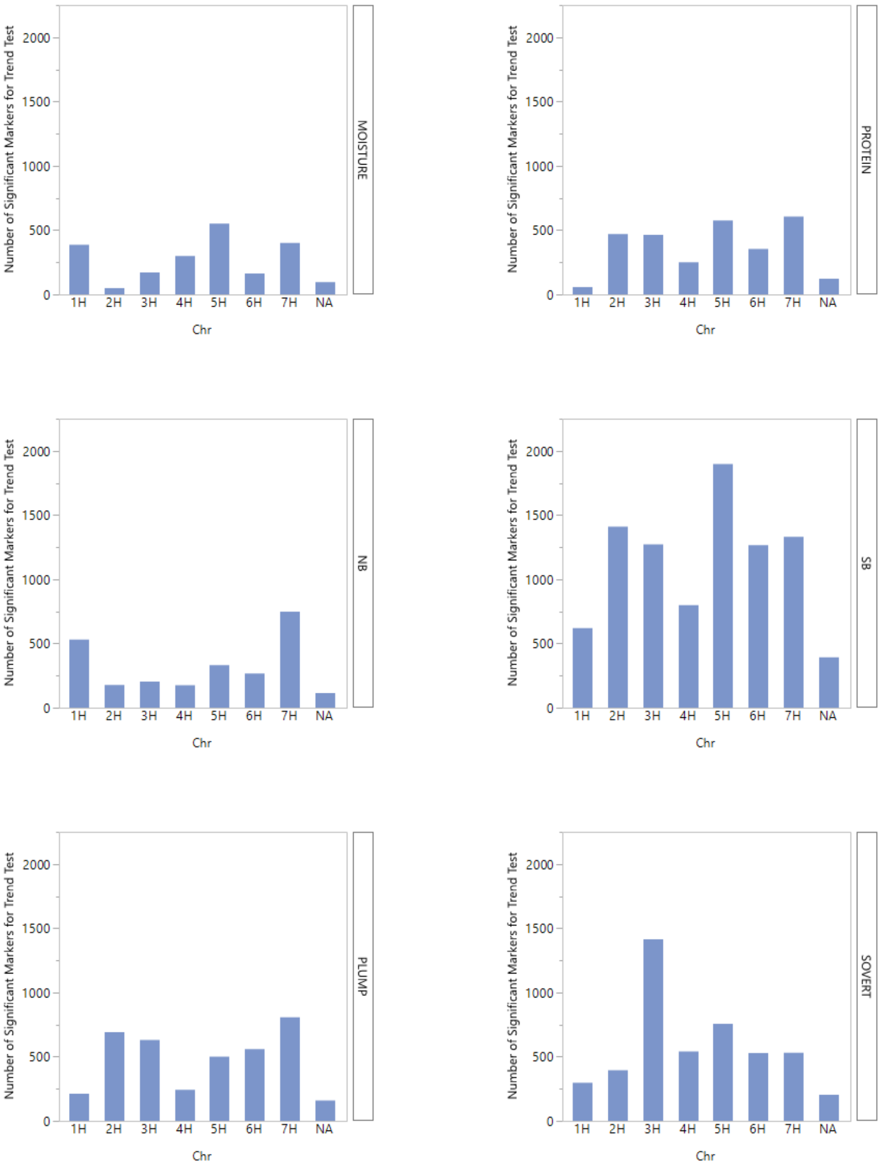


Figure 11. Number of significant SNP-Trait Associations ($P \leq 0.05$) identified on each chromosome (continued). A_Amylase=α-amylase, DON= deoxynivalenol, B_glucan=ß-glucan, DP=diastatic power, Color is barley color, FAN=free amino nitrogen FOL_DIS=foliar disease, KWT=1000-kernel weight. HDDT=heading date, LODG=lodging, HT=plant height, MOISTURE=malt moisture, PROTEIN=barley protein, NB=net blotch, and SB=spot blotch, PLUMP=kernel plumpness, SOVERT=S/T, STM_BRK=stem breakage, W_COLOR=wort color, TWT=test weight, WRTPRT=wort protein, and W_CLARITY=wort clarity.

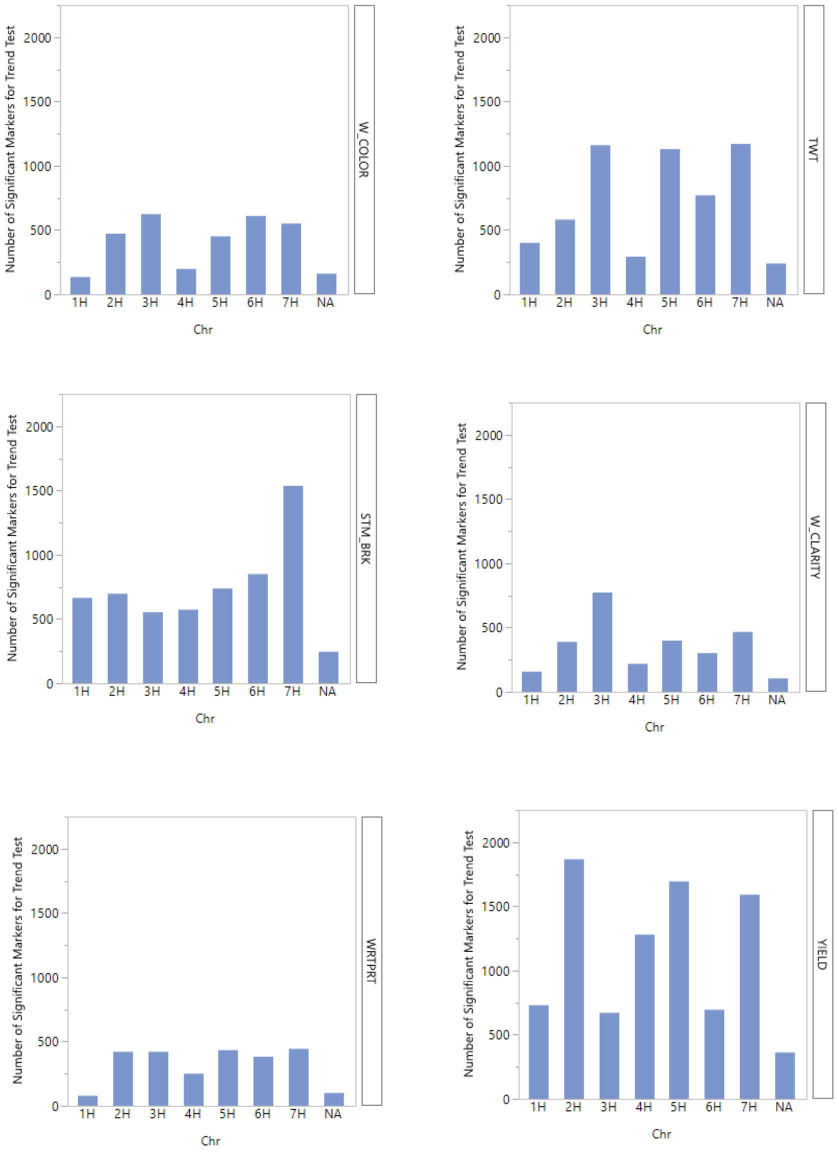


Figure 11. Number of significant SNP-Trait Associations (P≤0.05) identified on each chromosome (continued). A_Amylase=α-amylase, DON= deoxynivalenol, B_glucan=ß-glucan, DP=diastatic power, Color is barley color, FAN=free amino nitrogen, FOL_DIS=foliar disease, KWT=1000-kernel weight. HDDT=heading date, LODG=lodging, HT=plant height, MOISTURE=malt moisture, PROTEIN=barley protein, NB=net blotch, and SB=spot blotch, PLUMP=kernel plumpness, SOVERT=S/T, STM_BRK=stem breakage, W_COLOR=wort color, TWT=test weight, WRTPRT=wort protein, and W_CLARITY=wort clarity.

Genomic Heritability

Figure 12 contains the total genomic heritability calculated for each trait. A trait can be considered heritable when it can be transmitted from parent to progeny. In this vein, genomic heritability refers to the portion of the phenotypic variation among individuals due to their genetic differences. This information is valuable in that it helps to predict the advancements that can be made in crossing and selection based on the heritability for trait. Heritability is calculated by JMP Genomics by dividing the genetic variance of all markers by the phenotypic variance. Heritability values of each trait can be associated to multiple factors including the relationship within the populations, the experiment for each line, and experimental error associated to each experiment. Predictive modeling has been found to be more effective in traits that contain higher heritability. Linkage disequilibrium (LD), the nonrandom association of alleles at different loci in a population, is found more often in dense marker coverage. Using all markers to estimate predictions can lead to finding more QTL in LD and thus maximizing the number of QTL whose effects will be captured by markers (Heffner et al., 2009). Calus and Veerkamp (2008) found that for high heritability traits there is a lower requirement of marker density vs. low heritability traits. In my analyses, the highest heritability values were found for ß-glucan, barley color, height and yield.

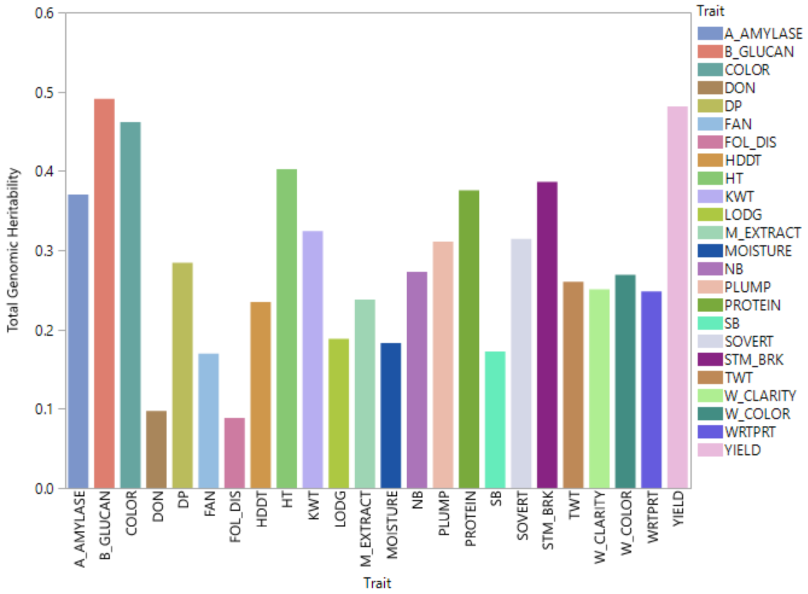


Figure 12. Total genomic heritability determined using the combined training population. A_Amylase=α-amylase, B_glucan=ß-glucan, Color is barley color, DON= deoxynivalenol, DP=diastatic power, FAN=free amino nitrogen, FOL_DIS=foliar disease, HDDT=heading date, HT=plant height, KWT=1000-kernel weight, LODG=lodging, M_EXTRACT=malt extract, MOISTURE=malt moisture, NB=net blotch, PLUMP=kernel plumpness, PROTEIN=barley protein, SB=spot blotch, SOVERT=S/T, and STM_BRK=stem breakage, TWT=test weight, W_CLARITY=wort clarity, W_COLOR=wort color, and WRTPRT=wort protein.

Predictive Modeling

Predictive modeling can obtain predictors for genomic selection using the continuous data of this study and the genotype data obtained using the 50k Illumina Infinium iSelect genotyping array for barley. A goal of my research was to identify the training population and the predictive modeling method that was best for each trait of the 24 traits. The first goal is complete, and I will use the combined TP for subsequent analyses for predictive modeling. Identifying the best model required predictive modeling with cross-validation to train and develop the prediction models. Cross validation was performed by randomly selecting one (1/K) of the observations at random as the TP and the remaining (1-1/K) were used for validation, where K was the number of times the TP was divided into. For these analyses, I used a K value of three with 10 iterations. The greater the similarity of correlation between model subsets to the correlation between the true breeding values in the TP and the expected GEBVs in the breeding population, the higher the precision and reliability of the prediction model (Desta and Ortiz, 2014).

Prediction models vary in terms of assumptions due to differences between traits (Desta and Ortiz, 2014). The standard linear model equation is formulated as seen in Equation 1 where y is a vector of trait phenotype, μ is the overall phenotype mean, k represents the locus, X_k is the allelic state of the locus k, β_k is the marker effect at locus k, and $e \sim (0, \sigma_e^2)$ is the expectation of a vector of random residual effects and the residual variance σ_e^2. For X_k, the allelic state of individuals was coded as a matrix of 0, 1, or 2 values for the diploid genotypic value of AA, AB or BB, respectively.

I tested four models, RR, GBR, PLS and XGBoost. All models were run individually on all 24 traits in which the NDSU barley breeding program routinely collects data in order to verify model capabilities for future use. As described in the *Genomic Selection* section, RR is capable of estimating all marker effects concurrently and shrinks marker effects towards zero; therefore, making the assumption that marker effects are random with a common variance (Meuwissen et al., 2001). Having said this, this assumption does not conclude that all markers have the same effect, rather all effects are shrunken towards zero (Heffner et al., 2009). The RR method may lead to underestimating larger effects within the genome. Bayesian methods can assist in remedying this issue, as they estimates separate variances for each marker via an inverse chi-square on marker variances resulting in a scaled *t*-distribution for marker effects (Desta and Ortiz, 2014). The PLS method is a regression method that estimates the relationship among variables by modeling the variation of the dependent and the predictor variables concurrently. In doing so, PLS extracts back-to-back linear combinations of the predictor variable and maximizes the variance explained in X and Y. This is used to find the multidimensional course in the X space that explains the maximum multidimensional variance course in Y. Finally, XGBoost is a machine learning method using a sparsity-aware algorithm for sparse data and a weighted quantile sketch for approximate tree learning (Chen and Guestrin, 2016).

Model Comparisons

In order to determine which model was the best for each trait, it was necessary to first run each of the four models individually and then to compare the results. The Cross-Validation Model Comparison process in JMP Genomics assists with the comparison of each model by dividing the data set into two groups: one as a tester and the other as a training group. Models are fitted with the training set and then validated with the predictor variables using the test group.

Whisker and box plots of root mean square error (RMSE) values for each model were generated by JMP Genomics and they were used as one tool to identify the best models (Figures 13-76). The figures have a solid black line across them that is the threshold in which you want the mean RMSE value for a model to be below. The solid black horizontal line is the mean among cross validation iterations of the performance criterion estimated without any model. The dashed horizontal lines above and below the solid line are the levels of the whiskers in a box plot for these no-model estimates. I considered models with a mean above the threshold as unacceptable. The box plots within each model display how each model performs across cross validation iterations. The center horizontal line of the plot measures overall performance while the spread within the red box plot shows the variability of predictions. A smaller spread is indicative of more consistent models, when model variability reached over the threshold value these traits were dropped for further analyses. The next component of model comparisons I used to select the best model was to calculate the correlation between the values in the training set and test group for each model and trait. When fitting a model using the entire data set, the model uses only the samples within the data set; thus, resulting in a higher correlation. When that model is used to predict values on a data set other than the TP, it is possible that these correlations may be smaller as they are attempting to mimic real world situations by estimating a mean of many correlations. To compare models for my study, I used Hsu's MCB method. Hsu's MCB is a multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best (Hsu, 1996). In my analyses, the best results refer to the highest mean correlation values. This method creates a confidence interval for the difference between each level mean and the best of the remaining level means. If an interval has zero as an end point, there is a statistically significant difference between the corresponding means. The right side of the figures for the RMSE whisker plots and the correlation plots have the plots for the Hsu multiple comparisons. The circles in the plots represent approximate estimates for determining any statistically significant differences between the models.

The final step in identifying the model to use for genomic selection of actual breeding lines was to identify the model and the minimum number of markers that need to be used for each trait. In this step of the process, the top two models of candidate traits were reanalyzed using five different levels of Forest max predictor reduction to verify if within each model there would be any significant difference between the number of significant markers used and the correlation of the prediction results. The number of SNP markers chosen for each model were 100, 200, 500, 800, and 1000. In the output from JMP Genomics, Hsu's multiple comparisons circles are displayed on the right of each figure and can be used as a rough guide to determine significant differences between models. The purpose of selecting the minimal number of markers to include on the new SNP chip for effectively predicting each trait is to reduce costs of designing the new chip. The cost of including a SNP on the new chip is between $9-$10 per marker.

In the following section of predictive modeling I selected the top two performing models for traits that are candidates for genomic selection. For those traits considered to be candidates, I determined the model to use and the minimum number of markers needed for predicting the trait phenotype.

Agronomic Traits

Barley Color

Buyers of malting barley discount barley that is discolored. Although all models had mean RMSE values for color below the threshold, the goal of this section was to select the top two models for each trait. For this trait, GBR and RR both had the lowest RMSE and highest correlation combination values in comparison to all models (Figure 13 and 14 respectively). The correlation values for the GBR and RR models were nearly 0.55, with RR having a slightly higher value.

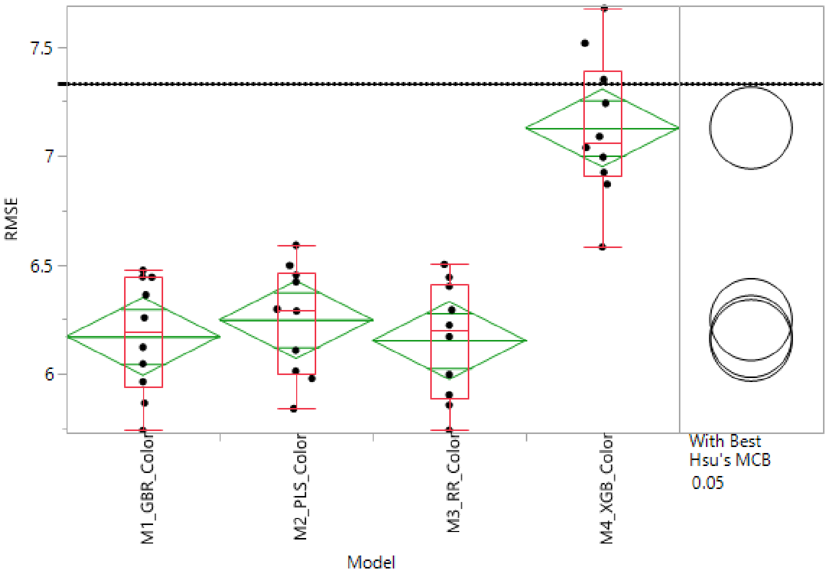


Figure 13. Whisker and box plot of root mean square error (RMSE) values for barley color (color) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

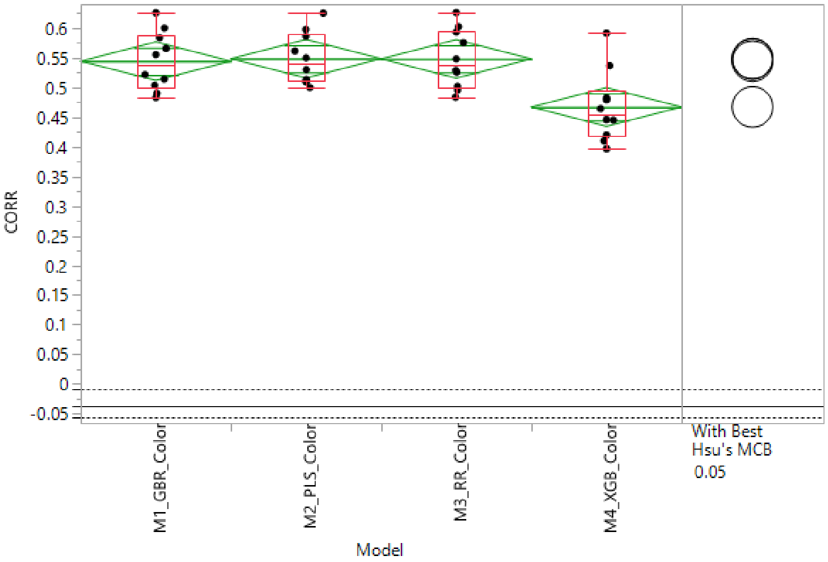


Figure 14. Whisker and box plot of correlation values for barley color (color) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

In the analyses to determine the minimum number of markers needed to predict barley color, no further improvement in RMSE or correlation values were obtained when more than 500 markers were used (Figures 15 and 16). In fact, the results for both models were nearly identical. I chose the GBR model with at least 500 markers as the model to use because Bayesian estimation permits separate estimates of variance per marker while RR makes the assumption that markers are random effects with a common variance and RR may underestimate large effects (Meuwissen et al., 2001).

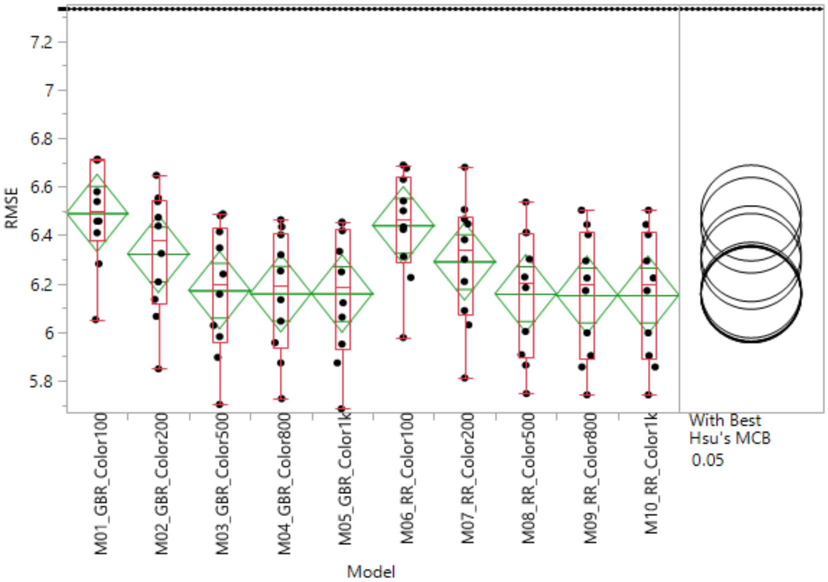


Figure 15. Whisker and box plot of root mean square error (RMSE) values for barley color (color)for two different models (M1_GBR=Bayesian B and M2_RR=ridge regression), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

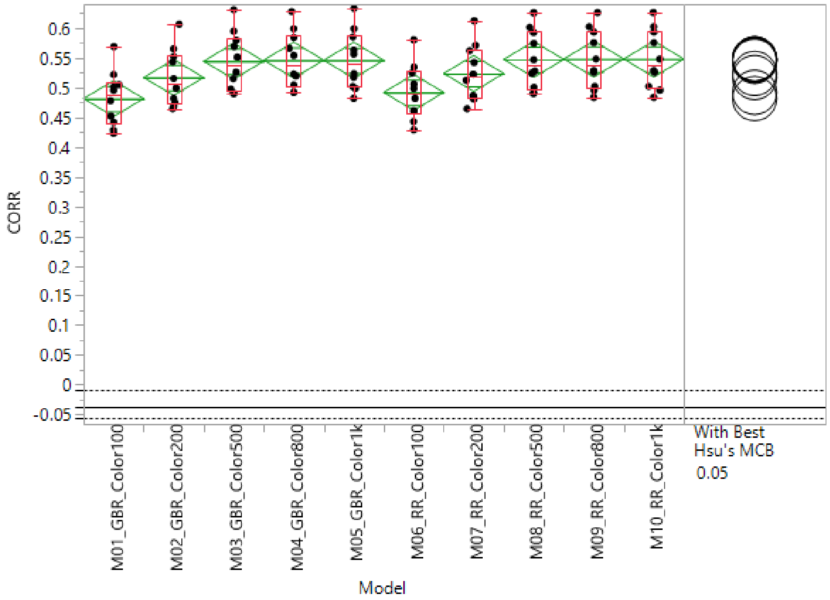


Figure 16. Whisker and box plot of correlation values for barley color (color) for two different models (M1_GBR=Bayesian B and M2_RR=ridge regression), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

Heading Date

Barley growers in North Dakota have expressed concern with the late maturity of the available two-rowed malting barley cultivars as compared to six-rowed barley. Thus, selection for earlier heading is an important selection criterion for the NDSU barley breeding program. Three of the four models had mean RMSE values below the threshold. The GBR and RR models again had the lowest RMSE and highest correlation values (Figures 17 and 18). The correlation for both models was around 0.43. When the analysis for GBR and RR was redone using different numbers of markers, no improvements in RMSE or correlation values were observed when more than 500 markers were used (Figures 19 and 20). I selected GBR with a minimum of 500 markers as the model to use for predicting HDDT.

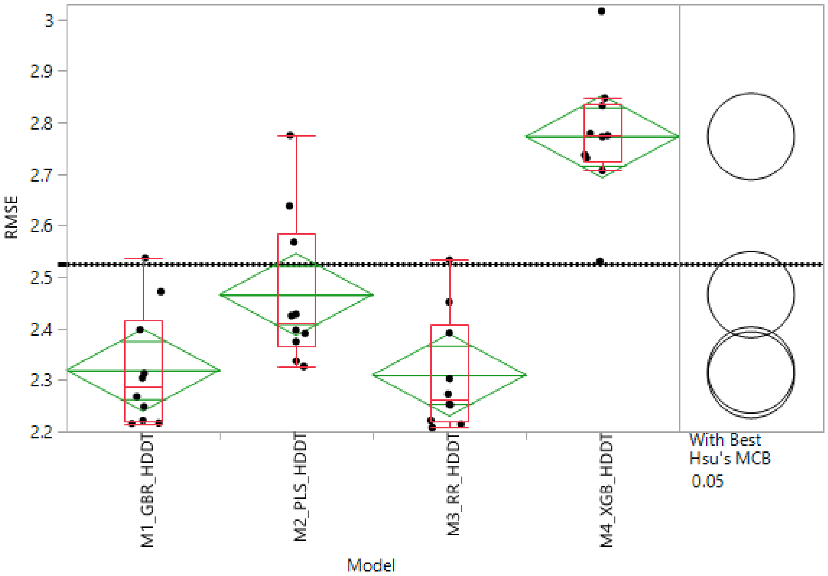


Figure 17. Whisker and box plot of root mean square error (RMSE) values for heading date (HDDT) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

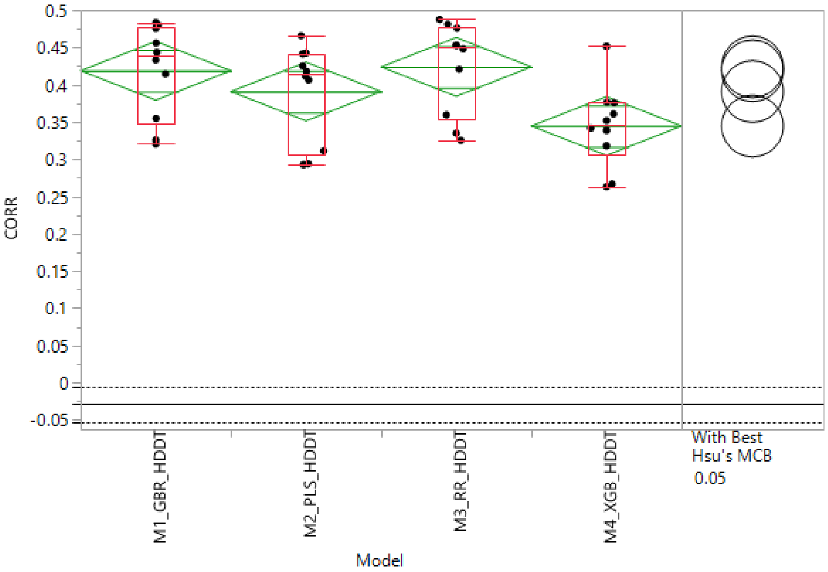


Figure 18. Whisker and box plot of correlation values for heading date (HDDT) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

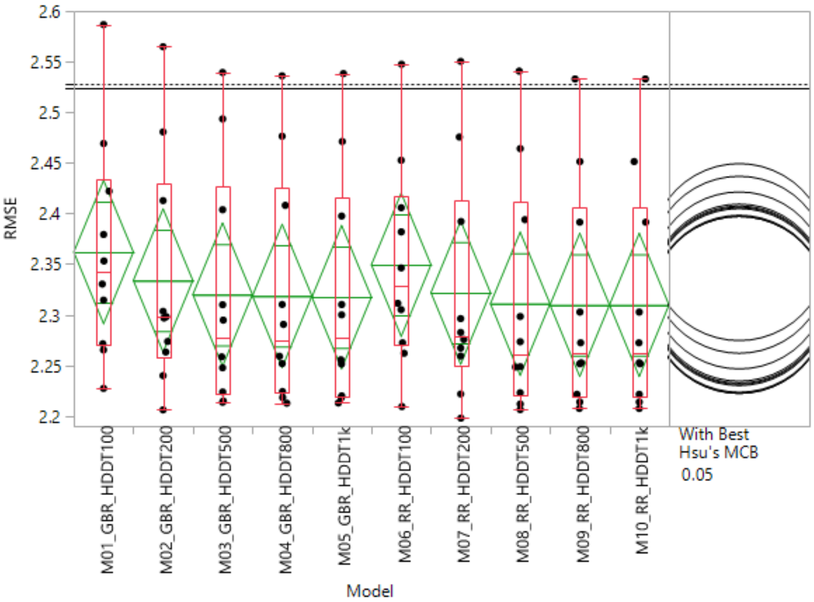


Figure 19. Whisker and box plot of root mean square error (RMSE) values for heading date (HDDT) for two different models (M1_GBR=Bayesian B and M2_RR=ridge regression), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

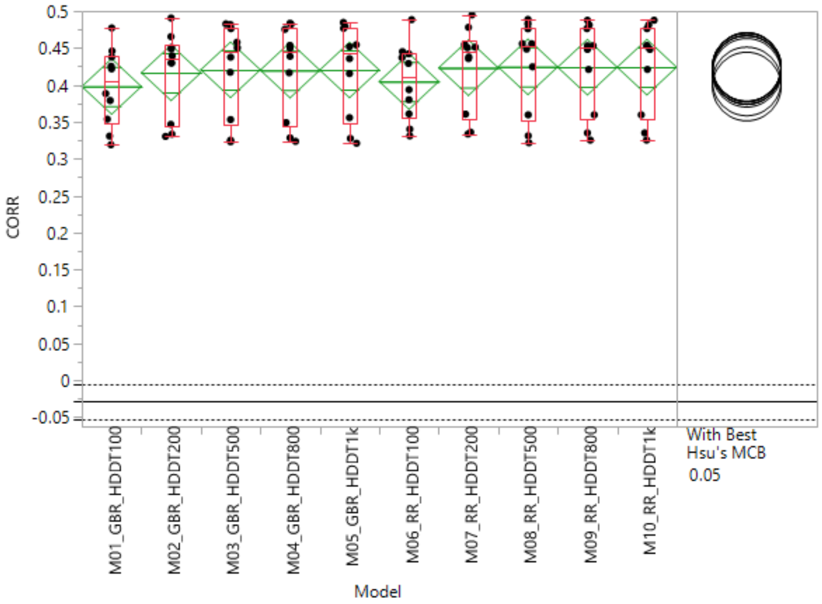


Figure 20. Whisker and box plot of correlation values for heading date (HDDT) for two different models (M1_GBR=Bayesian B and M2_RR=ridge regression), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

Height

North Dakota barley growers have expressed concerns that plant height of the available two-rowed barley cultivars is unacceptably tall. A goal of the NDSU barley breeding program is to breed for shorter two-rowed cultivars with improved straw strength. The mean RMSE values were below the threshold for GBR, PLS and RR (Figure 21). Even though GBR and RR performed better that PLS in terms of RMSE, there were no significant differences between the three models according to Hsu’s multiple comparison. The greatest correlation value of 0.49 was observed for the PLS model (Figure 22). The correlations of 0.47 were only slightly lower for the GBR and RR models. Based on the lower RSME values for the GBR and RR models and nearly identical correlation values for all three models, I chose the GBR and RR models for the next analyses to determine the minimum number of markers needed for prediction and RR.

For both models, no further improvement in RMSE or correlation values were obtained when more than 500 markers were used (Figures 23 and 24). As I did for barley color and HDDT, I chose the GBR model with at least 500 markers as the model to use because Bayesian estimation permits separate estimates of variance per marker (Meuwissen et al., 2001).

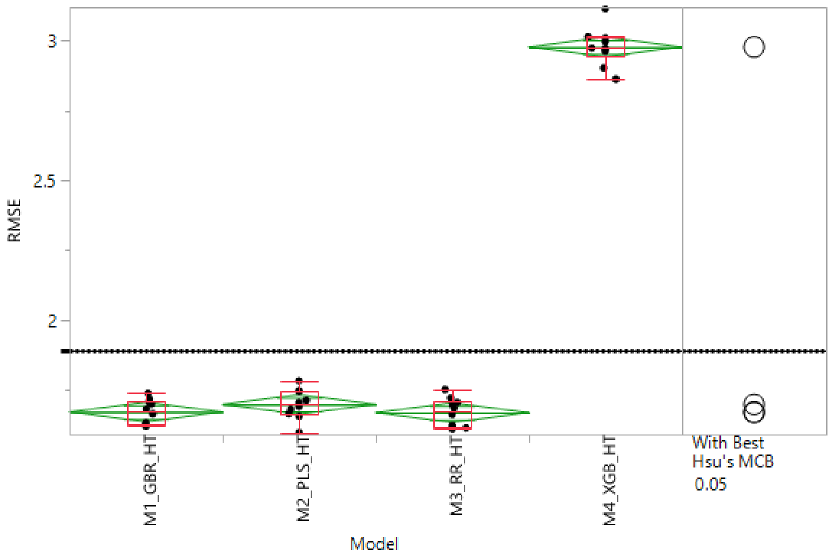


Figure 21. Whisker and box plot of root mean square error (RMSE) values for height (HT) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

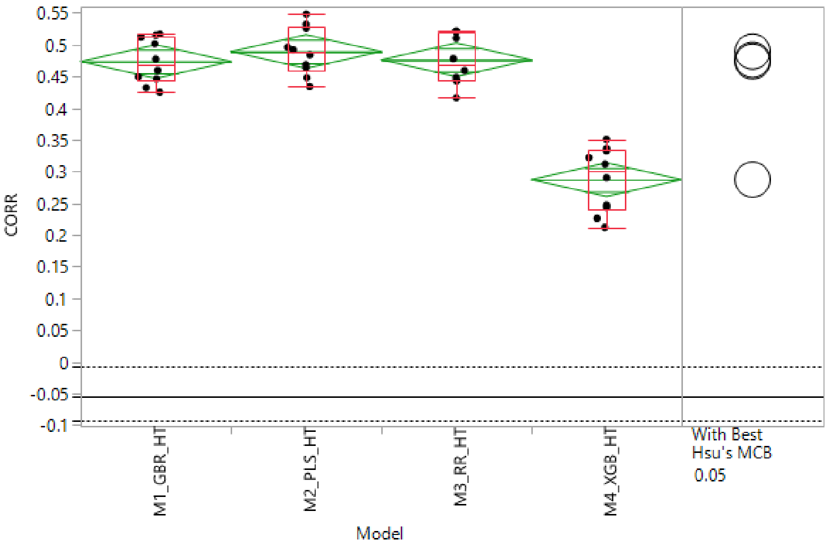


Figure 22. Whisker and box plot of correlation values for barley height (HT) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

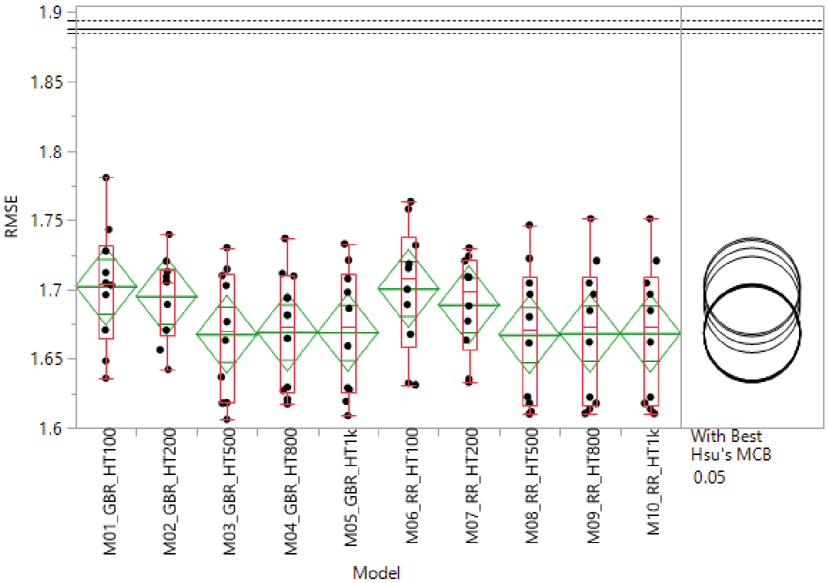


Figure 23. Whisker and box plot of root mean square error (RMSE) values for height (HT) for two different models (M1_GBR=Bayesian B and M2_RR=ridge regression), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

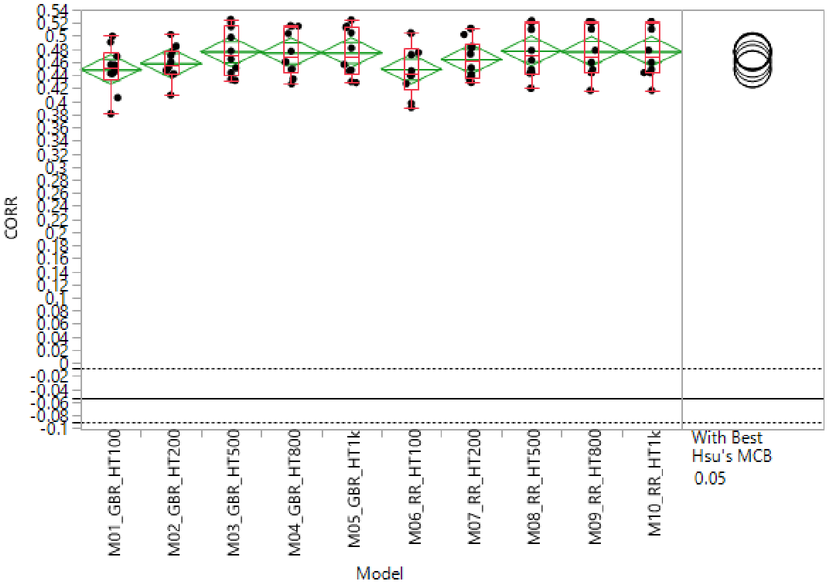


Figure 24.Whisker and box plot of correlation values for barley height (HT) for two different models (M1_GBR=Bayesian B and M2_RR=ridge regression), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

Kernel Weight

Selection for greater kernel weight is desired. RMSE values below the threshold were observed for the GBR and RR models (Figure 25) and the correlation for these two models was around 0.33. None of the correlation values for the four models were significantly different from each other (Figure 26). In the analyses using different numbers of markers (Figure 27 and Figure 28), there were no significant differences between models and levels within models for both RMSE and correlation values. However, numerically the RMSE values for the GBR model were slightly less than those from the RR. Thus, I recommend the use of the GBR model with a minimum of 500 markers for KWT.

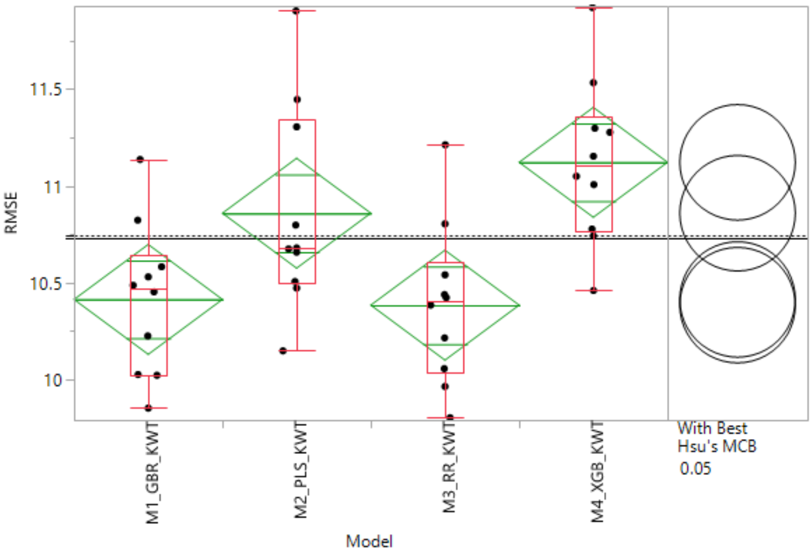


Figure 25. Whisker and box plot of root mean square error (RMSE) values for kernel weight (KWT) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

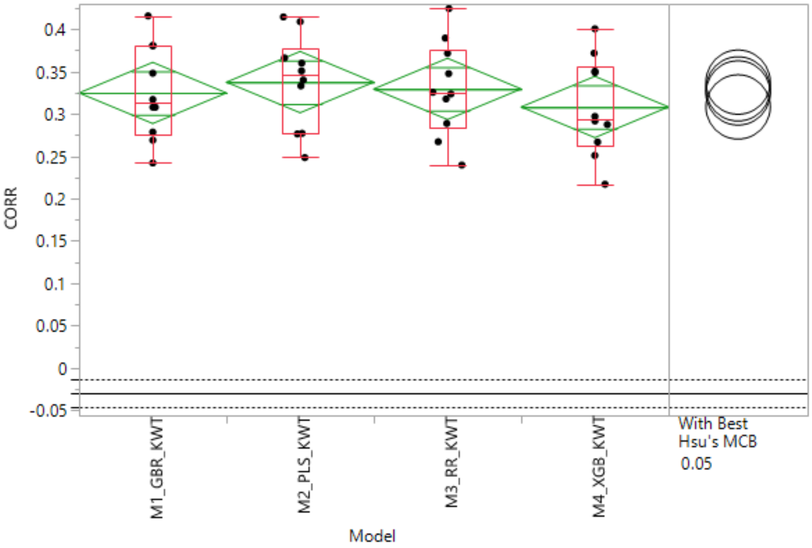


Figure 26. Whisker and box plot of correlation values for barley kernel weight (KWT) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

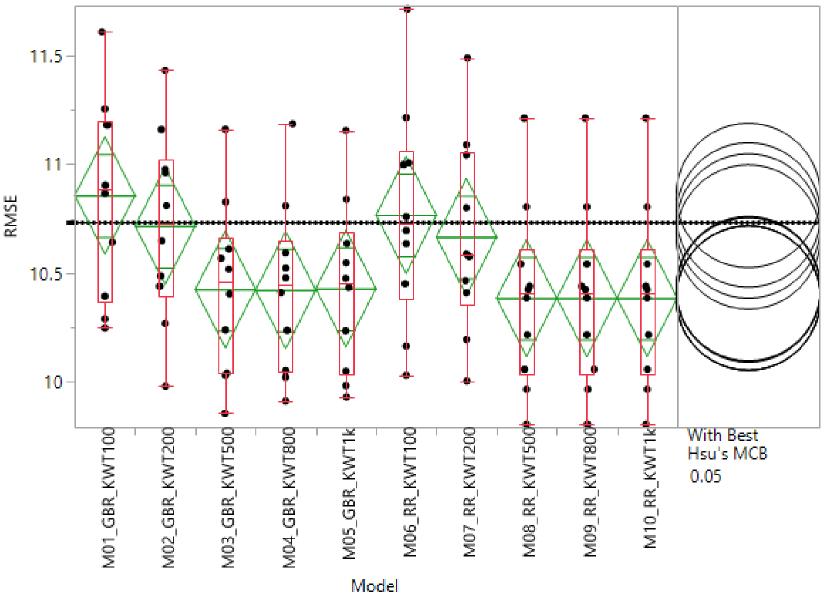


Figure 27. Whisker and box plot of root mean square error (RMSE) values for kernel weight (KWT) for two different models (M1_GBR=Bayesian B and M2_RR=ridge regression), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

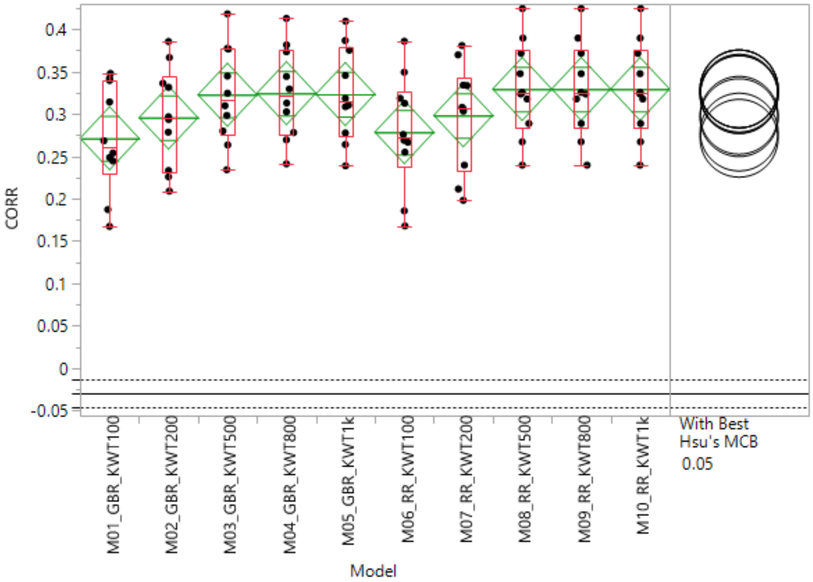


Figure 28. Whisker and box plot of correlation values for kernel weight (KWT) for two different models (M1_GBR=Bayesian B and M2_RR=ridge regression), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

Lodging

As stated earlier, plants with shorter and stronger straw are desired; hence, better resistance to lodging is needed. As seen in Figure 29, none of the models had a mean RMSE value below the threshold. Likewise, the correlation values were at or below 0.10. Given these results, I conclude that lodging is not a candidate for genomic selection on the NDSU barley breeding program at this time.

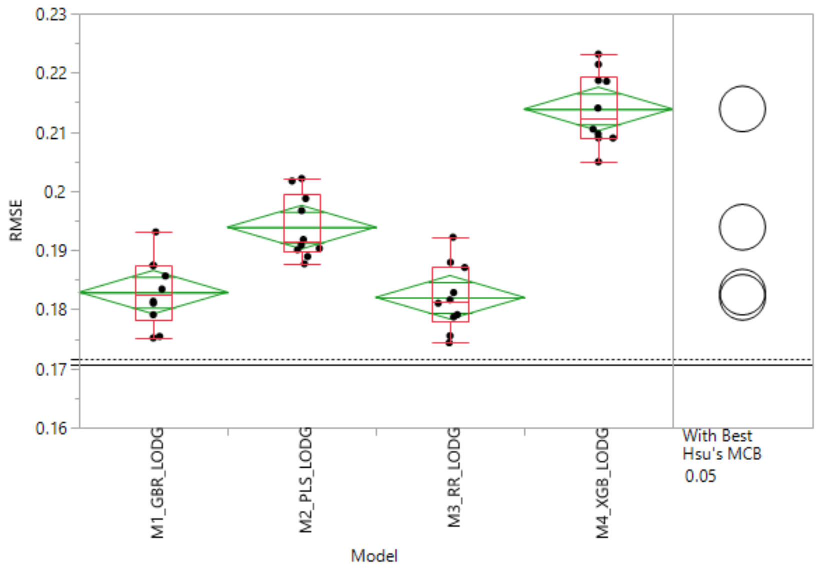


Figure 29. Whisker and box plot of root mean square error (RMSE) values for Lodging for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

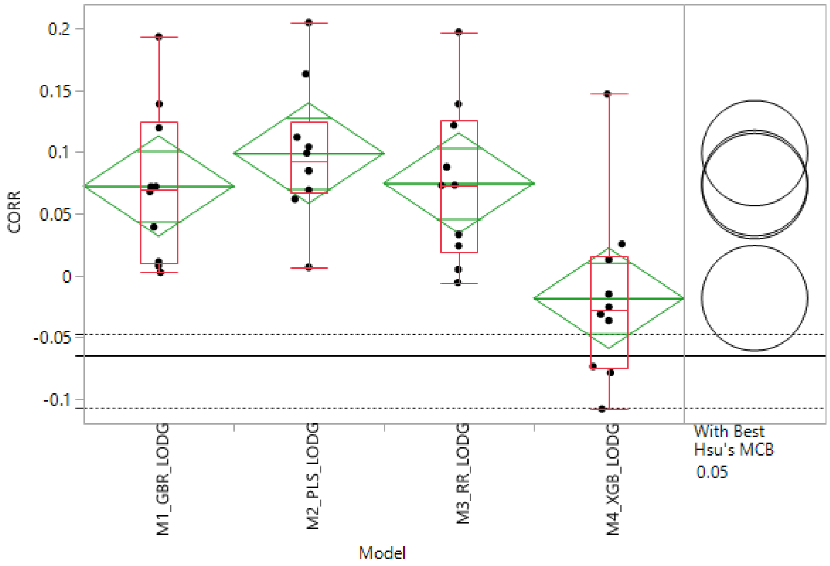


Figure 30. Whisker and box plot of correlation values for barley Lodging for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

Stem Breakage

Data on stem breakage is collected immediately prior to harvest. Cultivars that stand at harvest maturity are desired to facilitate direct combining. Stem breakage had three similarly performing models in terms of RMSE and correlation values. GBR, PLS, and RR had an acceptable RMSE (Figure 31) and correlation above 0.45 (Figure 32). In such close situations in terms of model selection, model selection can be based on known advantages known between models. Ridge regrtession has the computationally efficient analysis performance without losing any significant power whereas GBR will be able to more accurately estimate marker influences throughout the genome for this trait. Since computational power is in new computers is often not limiting, the selected models for STM_BRK are GBR and PLS, GBR for its accuracy and PLS since it has the highest combination of low RMSE and highest correlation.

When looking at the analyses to determine the minimum number of markers to use, there were no significant differences between models or levels within models, as seen in Figure 33 and Figure 34. The best combination of highest correlation and lowest RMSE were seen for the PLS model with 500 or more markers.

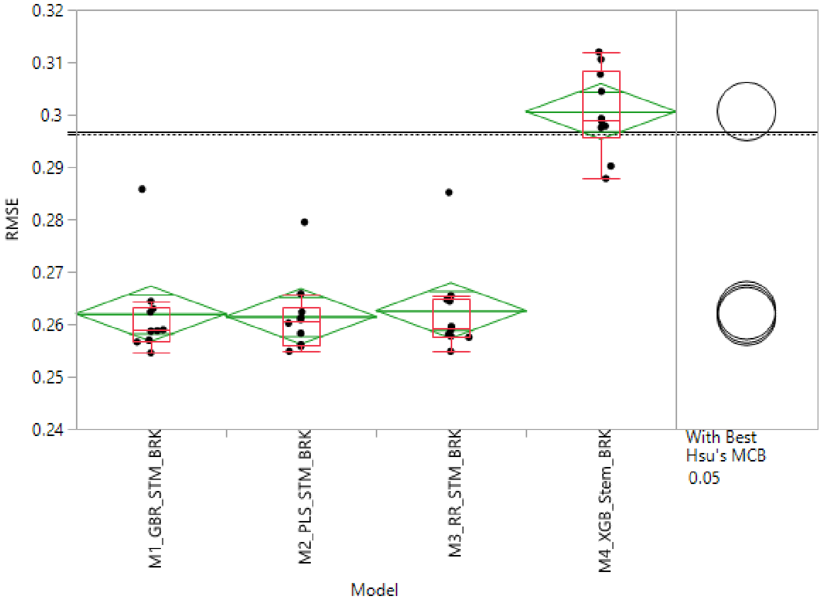


Figure 31. Whisker and box plot of root mean square error (RMSE) values for stem breakage for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

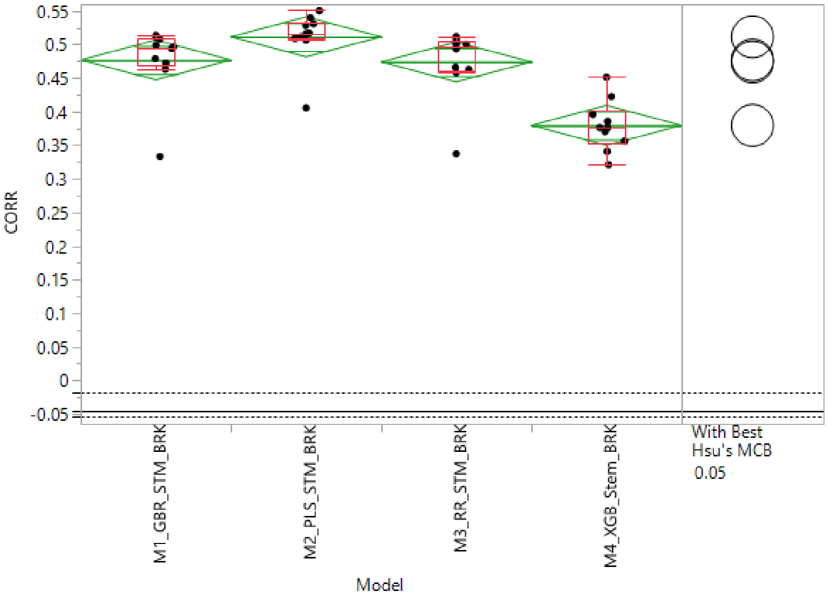


Figure 32. Whisker and box plot of correlation values for barley stem breakage (STM_BRK) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

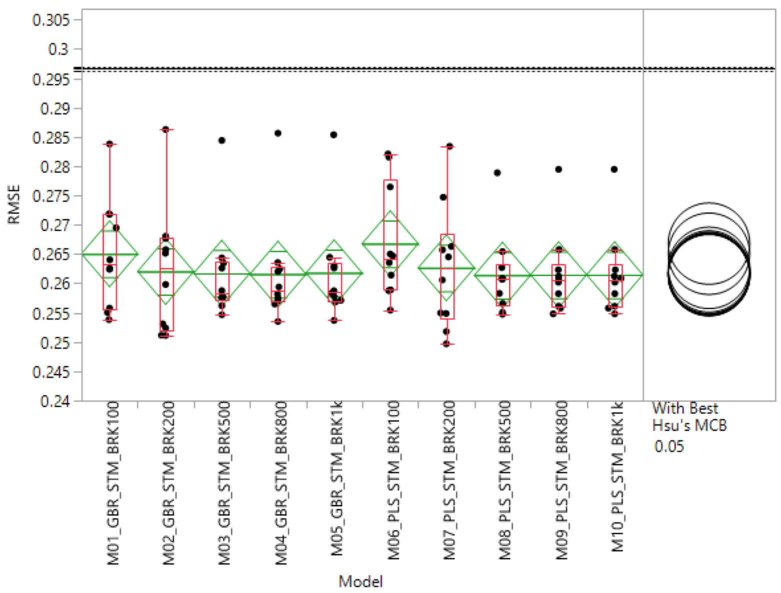


Figure 33. Whisker and box plot of root mean square error (RMSE) values for stem breakage (STM_BRK) for two different models (M1_GBR=Bayesian B and M2_PLS=Partial Least Squares), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

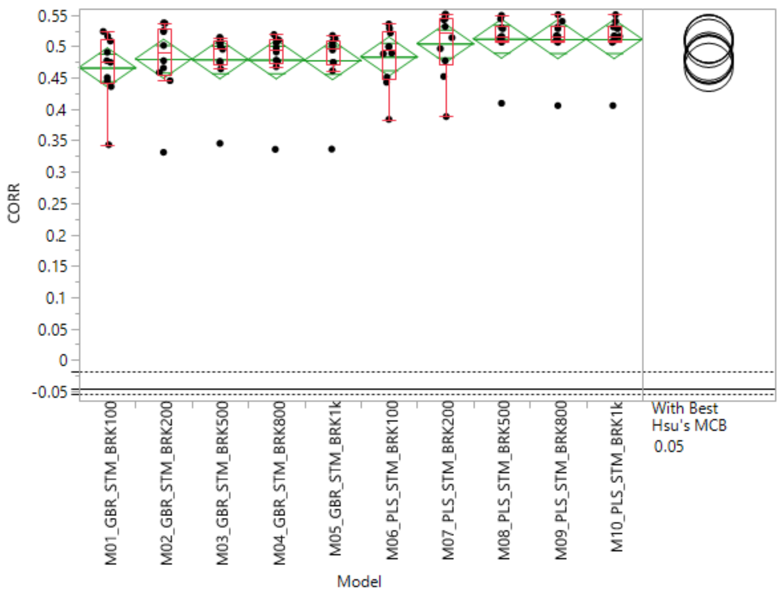


Figure 34. Whisker and box plot of correlation values for stem breakage (STM_BRK) for two different models (M1_GBR=Bayesian B and M2_PLS=Partial Least Square), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

Yield

Yield for barley is the most important trait economically for the producer. The models using GBR, PLS and RR had a mean RMSE below the threshold value (Figure 35) for yield. Having said this, the mean RMSE of both GBR and RR were the best performing models in comparison to the rest. Correlation values were about 0.53 for the GBR and RR models (Figure 36).

In the analyses to identify the minimum number of markers to use for prediction, there was no significant difference between models or levels within models (Figure 37 and Figure 38). For both models, no further improvement in RMSE or correlation values were obtained when more than 500 markers were used. Given the RSME and correlation values are similar for both models, I chose the GBR model with at least 500 markers as the model to use because Bayesian estimation permits separate estimates of variance per marker (Meuwissen et al., 2001).

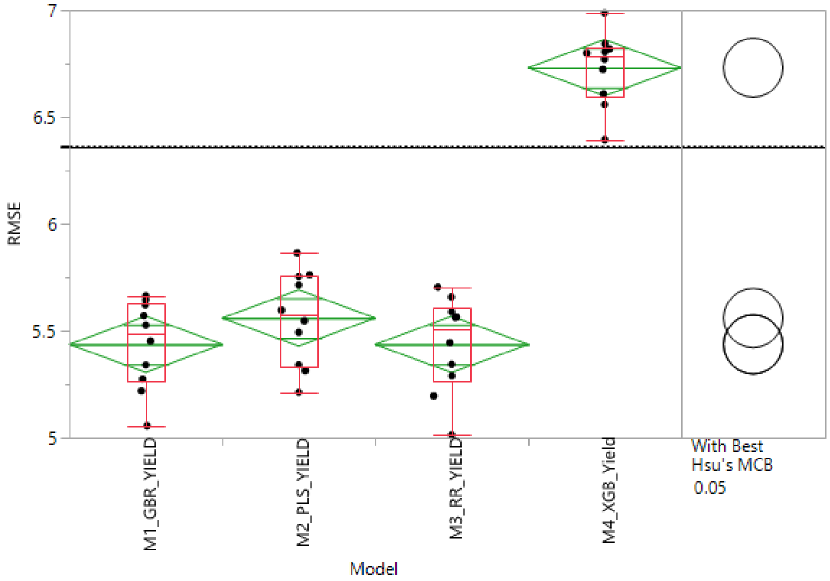


Figure 35. Whisker and box plot of root mean square error (RMSE) values for yield for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

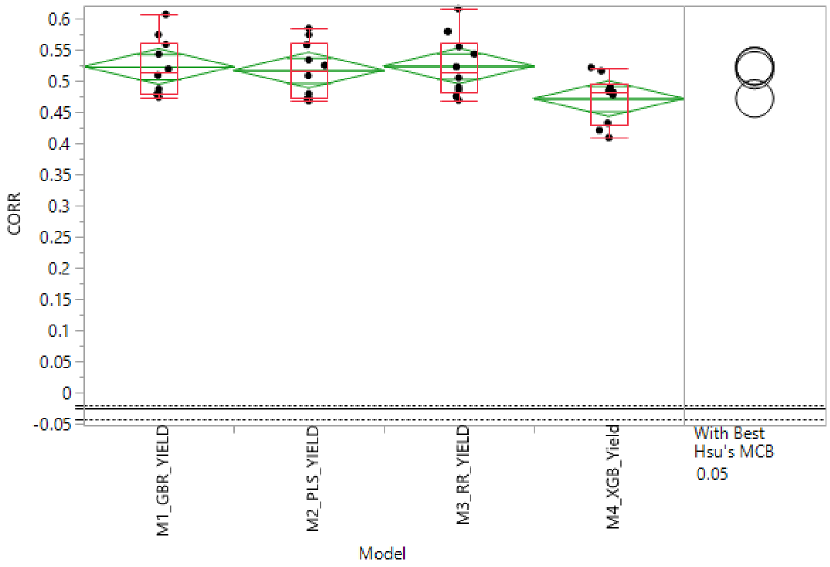


Figure 36. Whisker and box plot of correlation values for barley yield for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

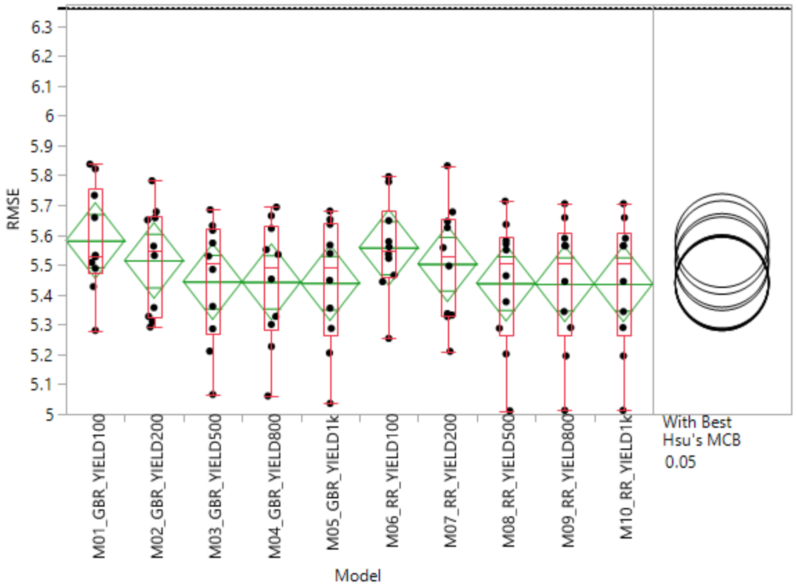


Figure 37. Whisker and box plot of root mean square error (RMSE) values for yield for two different models (M1_GBR=Bayesian B and M2_RR=ridge regression), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

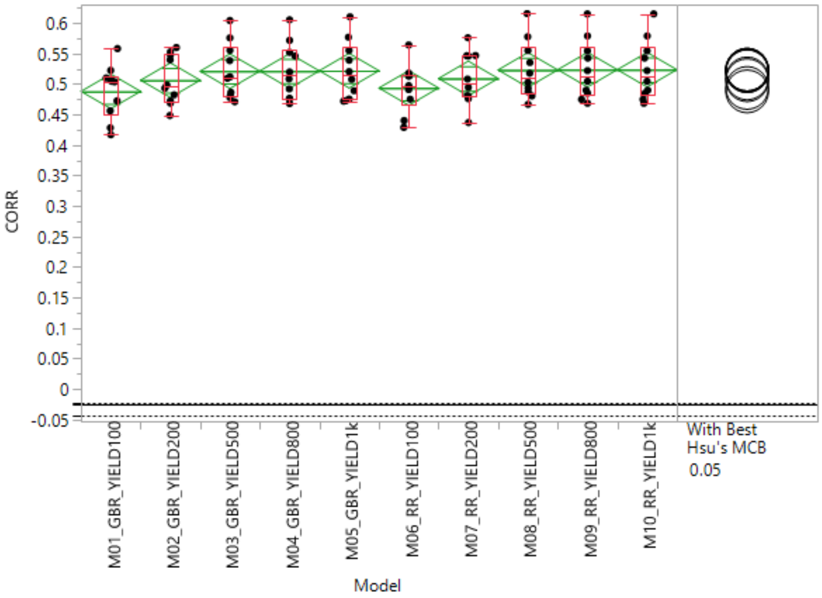


Figure 38. Whisker and box plot of correlation values for yield for two different models (M1_GBR=Bayesian B and M2_RR=ridge regression), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

Moisture

Grain moisture at harvest is an important selection trait for the NDSU barley breeding program as many producers have expressed concerns with the later maturity of currently grown two-rowed cultivars compared to the six-rowed cultivars they previously grew. None of the models had mean RMSE values for moisture below the threshold (Figure 39) and correlations values were all below 0.3 (Figure 40). Given this information, moisture is not a candidate for genomic selection based on the phenotype data used for this study.

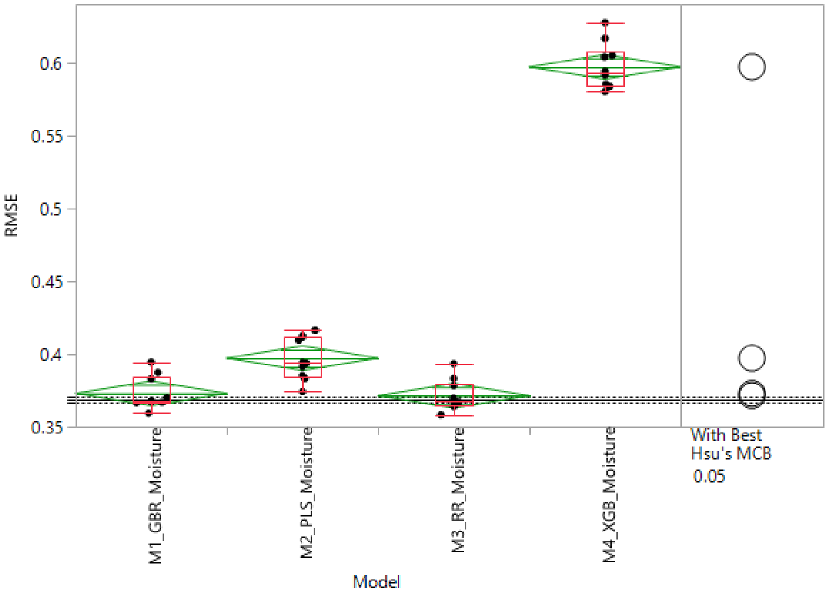


Figure 39. Whisker and box plot of root mean square error (RMSE) values for grain moisture for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

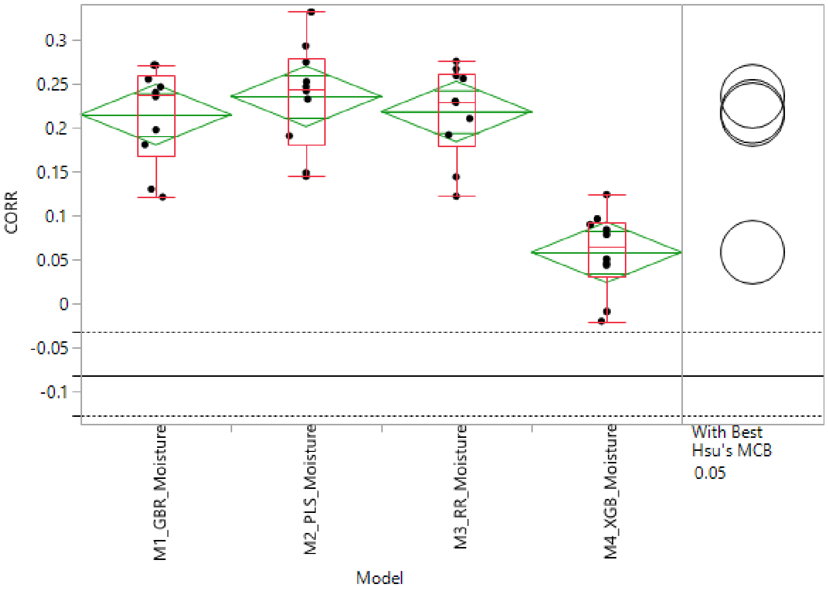


Figure 40. Whisker and box plot of correlation values for barley grain moisture for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

Barley and Malt Quality Traits

α -Amylase

The level of α-amylase needed in malt is dependent on the type of beer produced. Adjunct beers require higher levels of α-amylase than all malt beers because they have adjuncts (corn or rice) that need to be broken down using enzymes in the malt. So, depending on the target for the cultivar, lower or higher levels of α-amylase may be desired. Three of the models for α-amylase had mean RMSE values below the threshold, GBR, PLS, and RR (Figure 41). Of the three models, the lowest RMSE values were observed for GBR and RR. The greatest correlation values for α-amylase were observed for the GBR and PLS models, with the correlation for RR only a bit lower. The correlation value for GBR and RR was 0.45 (Figure 42). Based on the RMSE and correlation results, the models selected as the best performing models for α-amylase were GBR and RR.

As the number of markers for prediction was increased from 100 to 200, the RSME decreased slightly and the correlation values increased slightly for both the GBR and RR models (Figure 43). No further changes in the RSME or correlation values appeared to occur when the number of markers was increased from 200 to 1,000 (Figures 43 and 44). Given the RSME and correlation values were similar for both models, I chose the GBR model with a minimum of 500 markers for the reasons stated earlier.

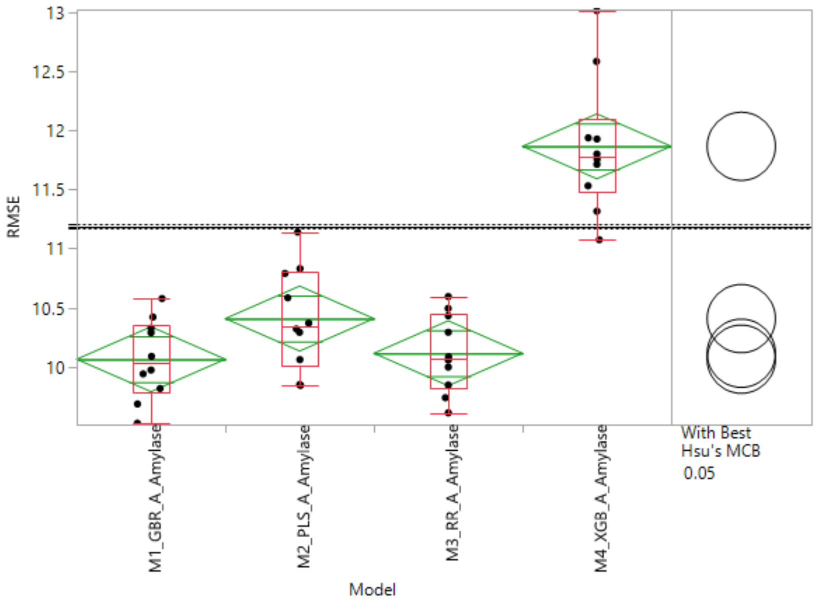


Figure 41. Whisker and box plot of root mean square error (RMSE) values for α amylase for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

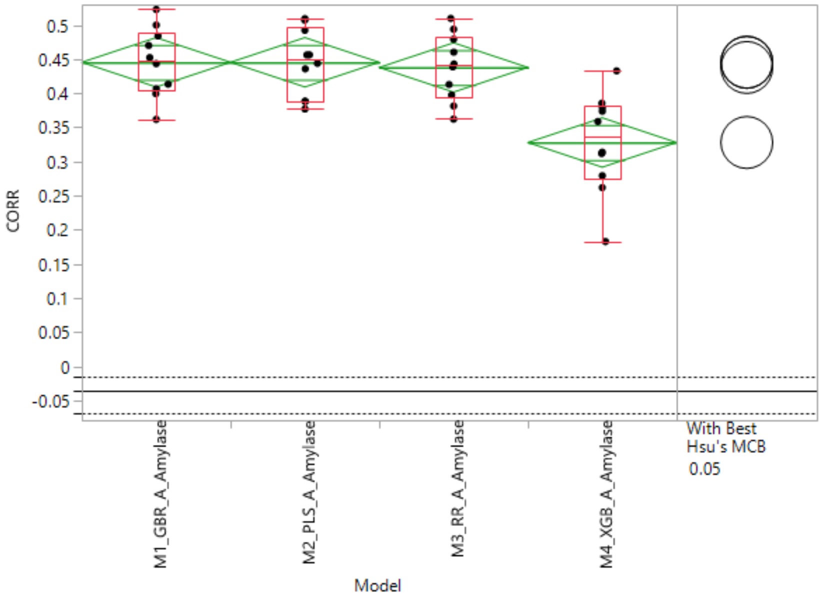


Figure 42. Whisker and box plot of correlation values for barley α amylase (A_Amylase) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

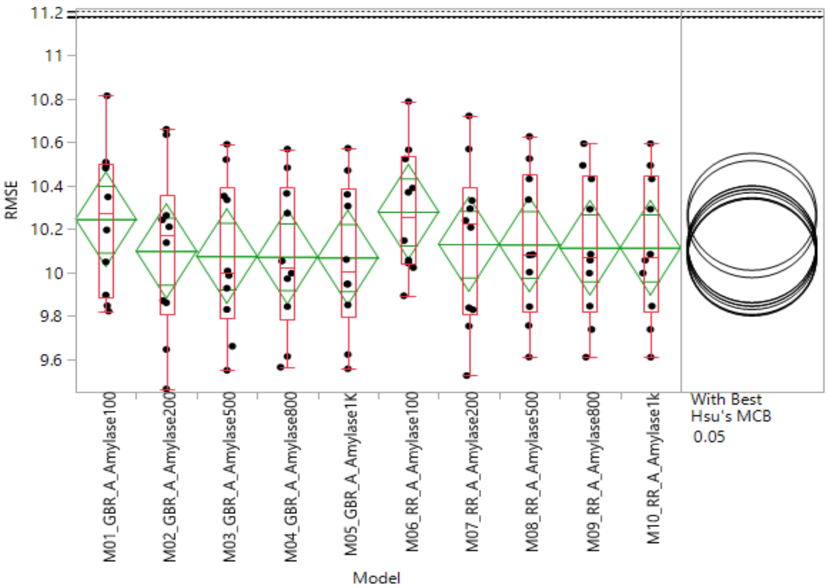


Figure 43. Whisker and box plot of root mean square error (RMSE) values for α amylase (A_Amylase) for two different models (M1_GBR=Bayesian B and M2_RR=ridge regression), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

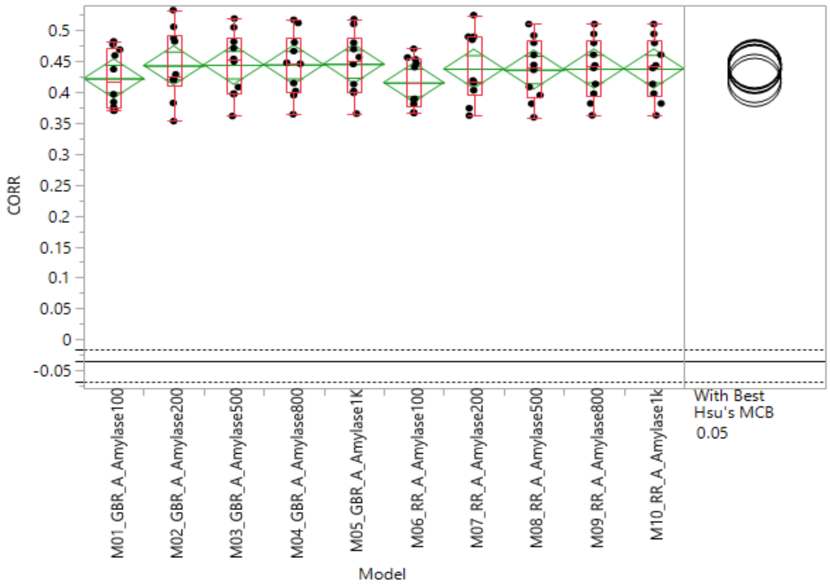


Figure 44. Whisker and box plot of correlation values for α amylase (A_Amylase) for two different models (M1_GBR=Bayesian B and M2_RR=ridge regression), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

ß-glucan

Selection for reduced ß-glucan levels is desired. High levels of ß-glucan can slow down the filtering or lautering of wort during brewing. The two models selected for ß-glucan are GBR and PLS based on the RMSE (Figure 45) and correlation values (Figure 46). The correlation for GBR was nearly 0.75, which suggests that genomic selection for ß-glucan has good potential.

In the analysis to determine the minimum number of markers to use for predictors, no significant differences between the models and levels per model were observed (Figures 47 and 48); yet, the numerical values for GBR were slightly lower. Therefore, I suggest using GBR and a minimum of 500 markers for predicting ß-glucan.

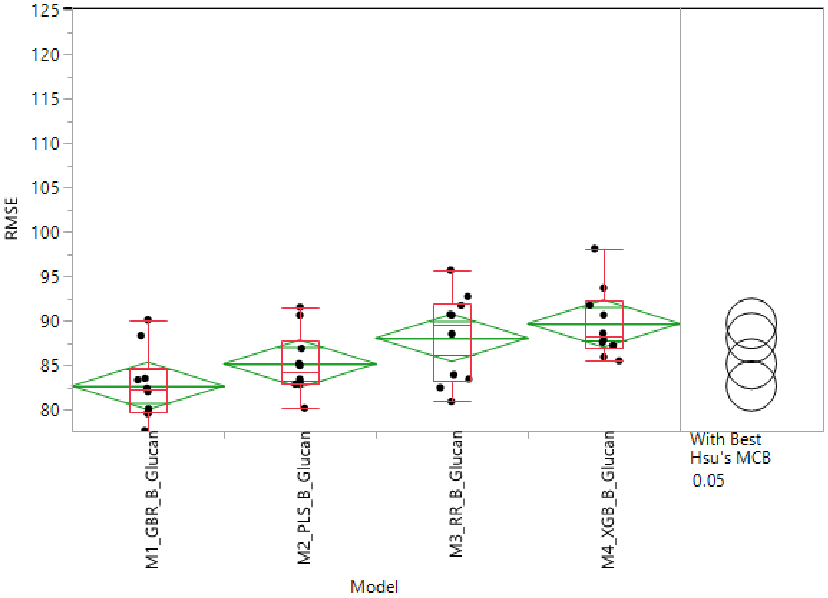


Figure 45. Whisker and box plot of root mean square error (RMSE) values for ß-glucan for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

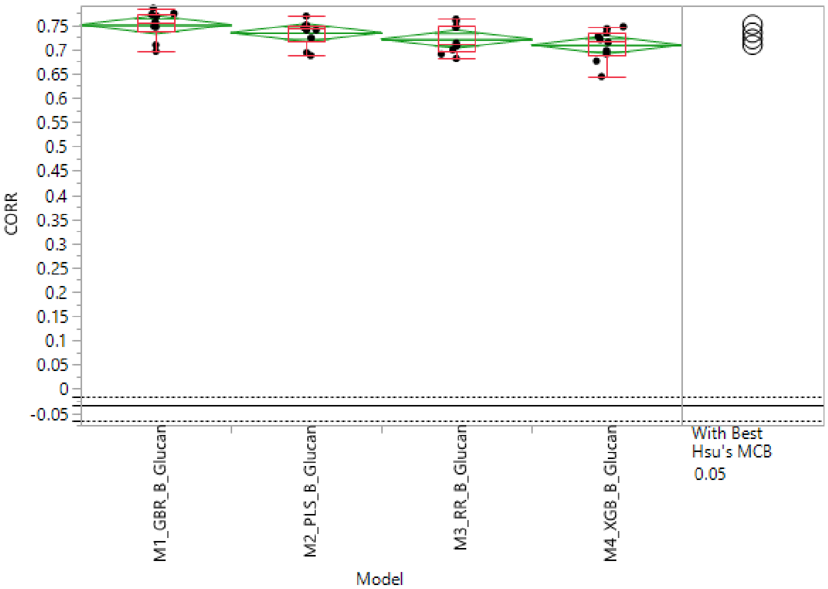


Figure 46. Whisker and box plot of correlation values for barley ß glucan (B_Glucan) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

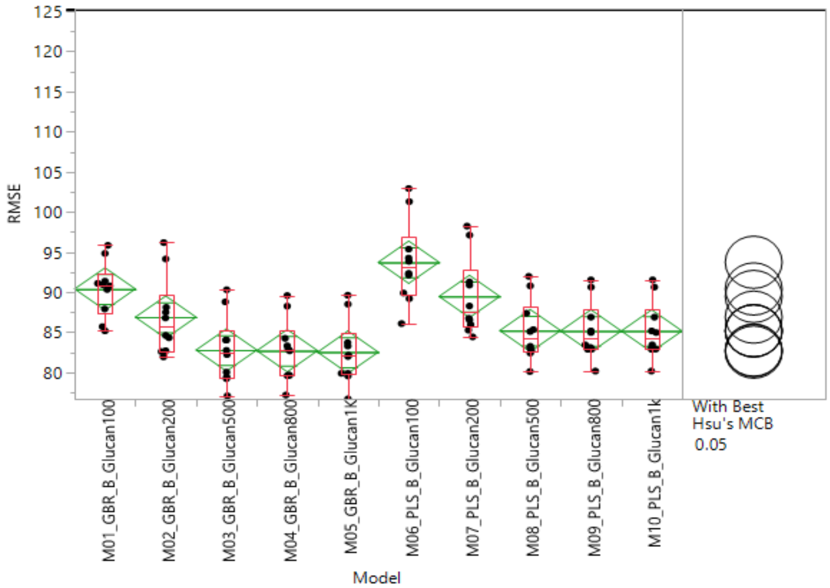


Figure 47. Whisker and box plot of root mean square error (RMSE) values for ß glucan (B_Glucan) for two different models (M1_GBR=Bayesian B and M2_PLS=Partial Least Square), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

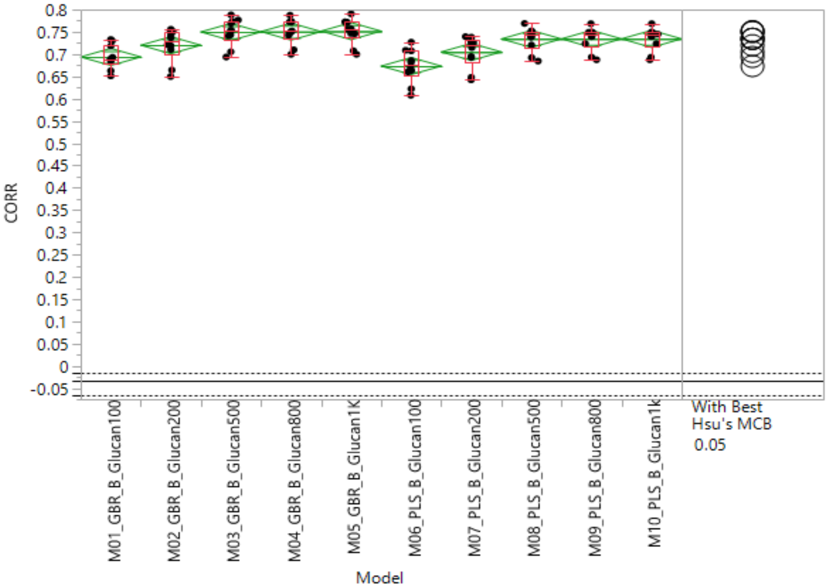


Figure 48. Whisker and box plot of correlation values for ß glucan (B_Glucan) for two different models (M1_GBR=Bayesian B and M2_RR=ridge regression), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

Diastatic Power

Like α-amylase, the level of DP in malt is dependent on the type of beer produced. Adjunct beers require higher levels of DP than all malt beers because they have adjuncts that need to be broken down by enzymes in the malt. So, depending on the target for the cultivar, lower or higher levels of DP may be desired. The mean RMSE values for GBR and RR were the least and below the threshold (Figure 49). The mean RMSE for PLS was also below the threshold; however, since its range falls slightly above the threshold it was not used even though it had a slightly higher correlation (Figure 50) than RR. The correlation for RR was around 0.35.

There were no significant differences between GBR and RR models or level of predictors per model in the analyses to determine the minimum number of markers to use for predicting DP (Figure 51 and 52). Additionally, there were no further improvements in the RMSE or correlation values observed when more than 500 markers are used. Numerically, the RMSE values are slightly lower, and the correlation values were slightly higher for the GBR models; thus, I suggest the GBR model with a minimum of 500 markers be used for genomic selection of DP.

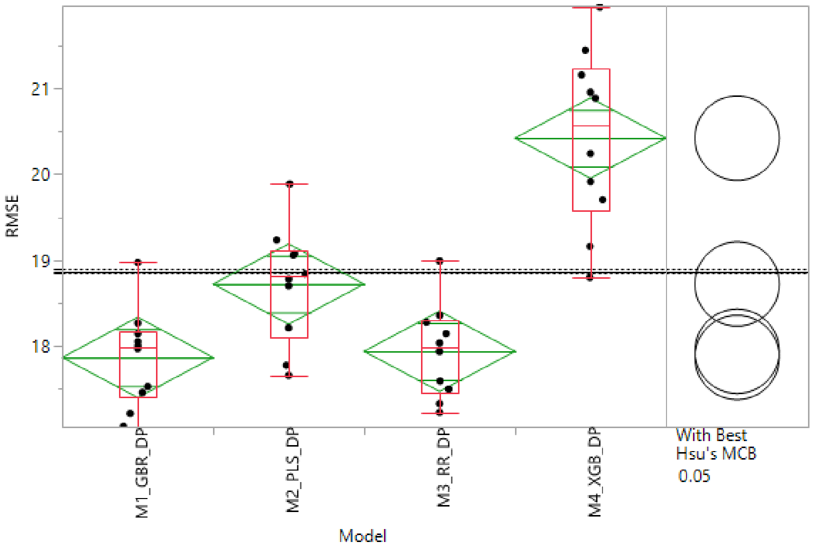


Figure 49. Whisker and box plot of root mean square error (RMSE) values for diastatic power (DP) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

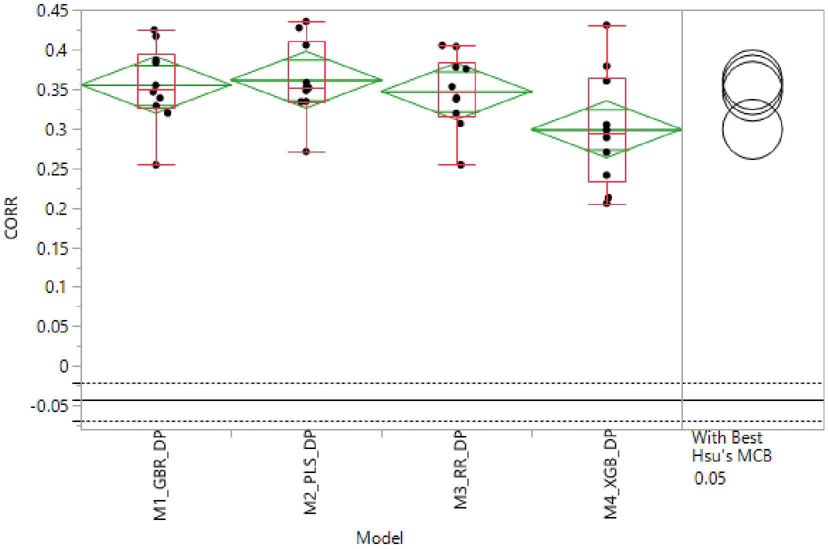


Figure 50. Whisker and box plot of correlation values for barley diastatic power (DP) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

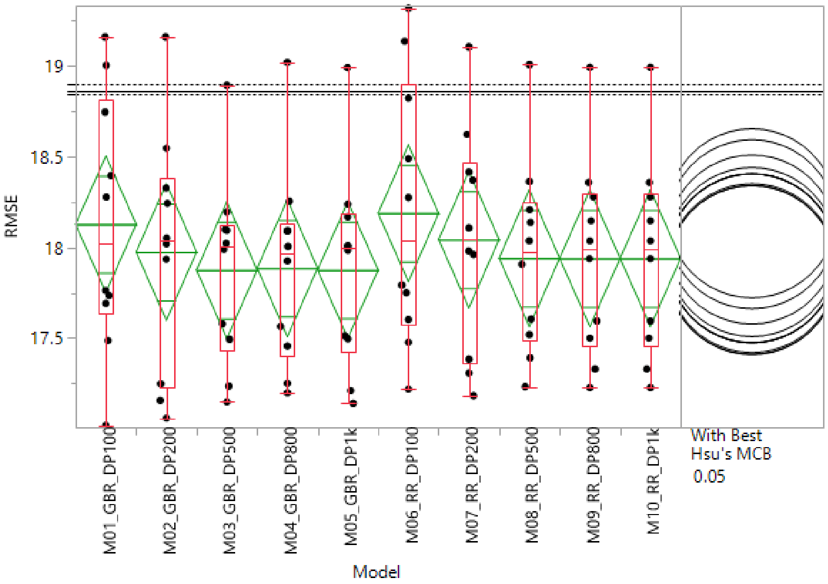


Figure 51. Whisker and box plot of root mean square error (RMSE) values for diastatic power (DP) for two different models (M1_GBR=Bayesian B and M2_RR=ridge regression), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

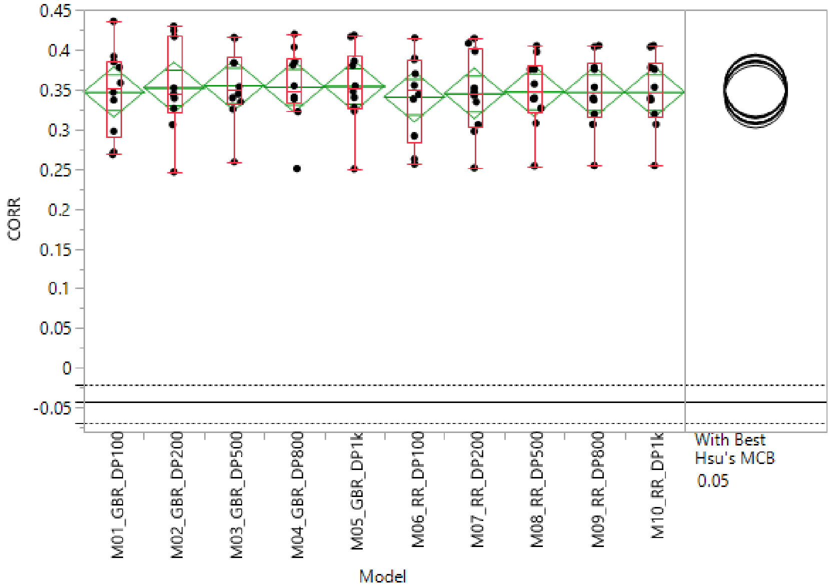


Figure 52. Whisker and box plot of correlation values for diastatic power (DP) for two different models (M1_GBR=Bayesian B and M2_RR=ridge regression), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

FAN

Free amino nitrogen is another trait that has differential requirements for adjunct and all malt brewers. Production of adjunct beers requires higher FAN levels than that needed for all malt beers. None of the models had a mean RSME below the threshold and the highest correlation value was below 0.25 (Figures 53 and 54). Given the high RSME values and the low correlations, FAN is not a candidate trait for genomic selection at this time.

The unacceptably high RSME values and lower correlation values for this and some of the traits may be due to the nature of how the phenotypic values for the values were calculated. The lines in the combined TP were never grown together in a single experiment, but across several years where the checks Conlon and Pinnacle always appeared. To determine if the unbalanced data may be a cause of the lower correlation values, the entire combined TP should be phenotyped using trials grown at multiple locations across years. These data should then be used for predictive modeling analyses to see if more favorable RMSE correlation values are obtained as compared to the ones I obtained in my research.

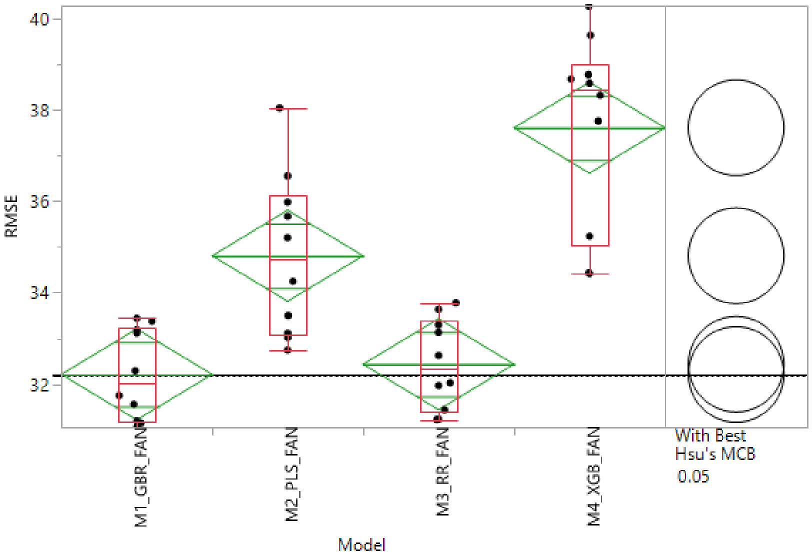


Figure 53. Whisker and box plot of root mean square error (RMSE) values for free amino nitrogen (FAN) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

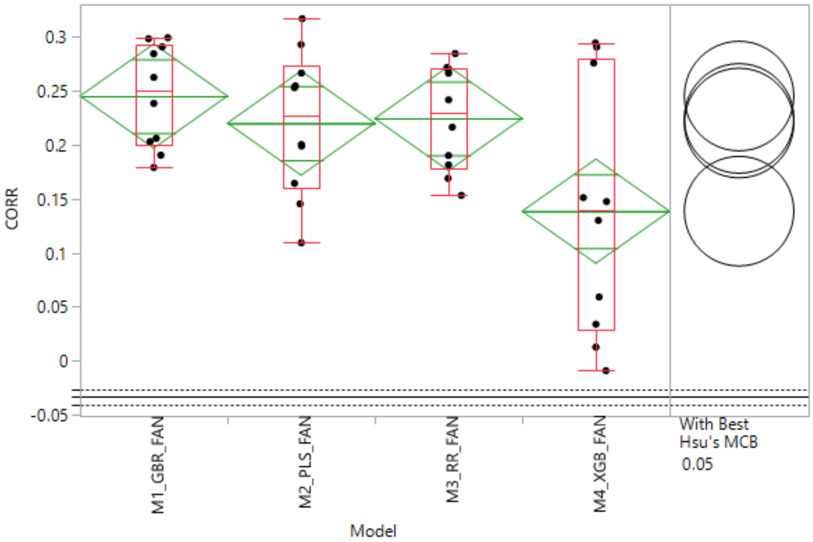


Figure 54. Whisker and box plot of correlation values for barley free amino nitrogen (FAN) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

Malt Extract

Malt extract can be viewed as the maltsters' yield; thus, it is of economic importance to the maltster and brewer. The GBR and RR models were the only ones to have mean RMSE values below the threshold (Figure 55). However, the correlation values were moderately low, approximately 0.27 for both these models (Figure 56).

In the analyses to determine the minimum of markers needed for predictions, the mean RMSE values for the GBR and RR models didn't drop below the threshold until 200 or more markers were used (Figure 57). Furthermore, the RMSE and correlation values showed no further improvement past the use of 500 markers and the numerical values for both traits were similar (Figures 57 and 58). Given the RSME and correlation values are similar for both models, I chose the GBR model with a minimum of 500 markers for the reasons stated earlier for barley color and other traits.

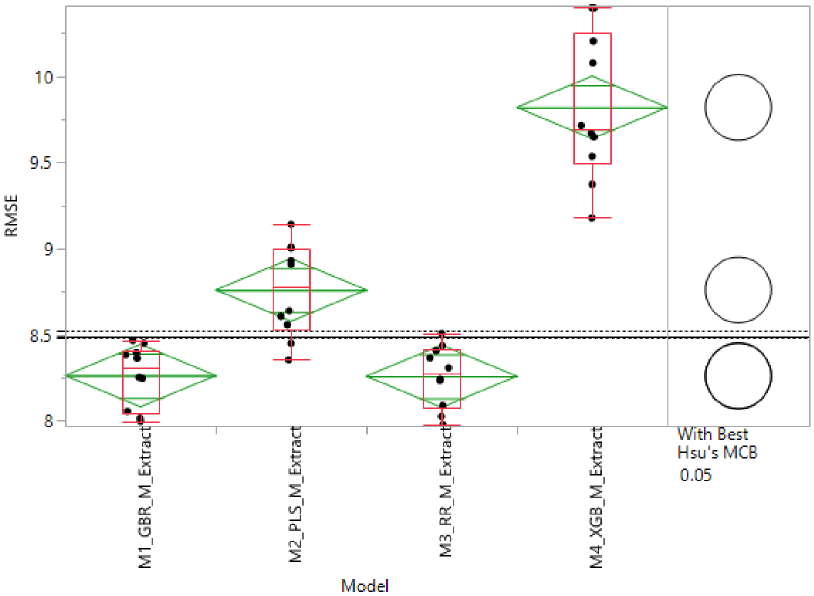


Figure 55. Whisker and box plot of root mean square error (RMSE) values for malt extract for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

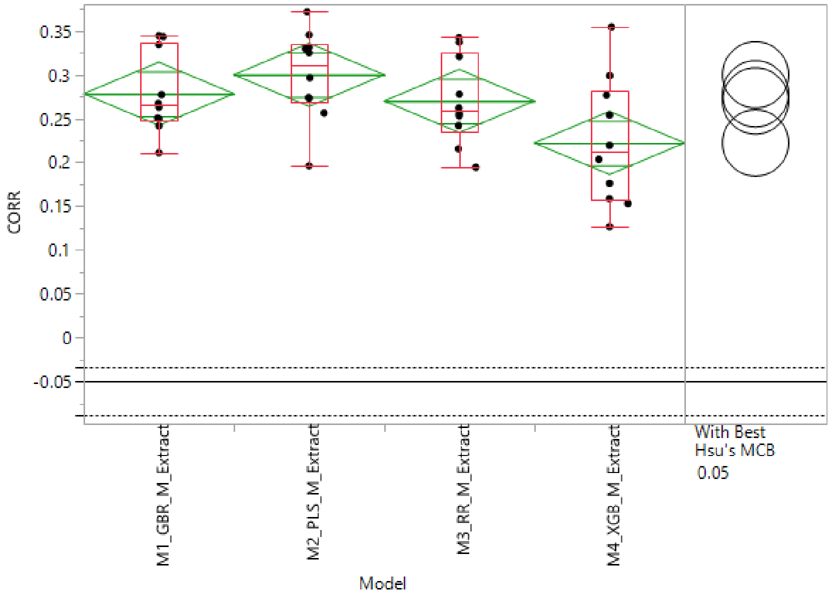


Figure 56. Whisker and box plot of correlation values for barley malt extract (M_Extract) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

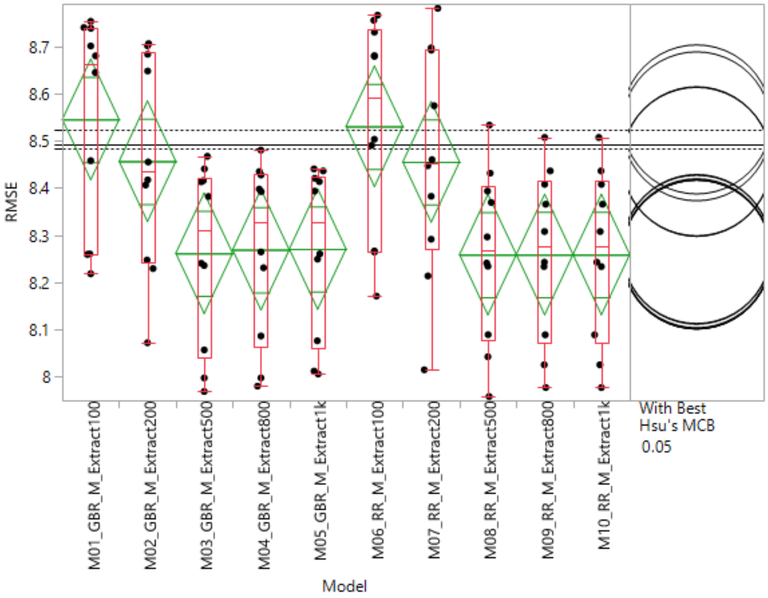


Figure 57. Whisker and box plot of root mean square error (RMSE) values for malt extract (M_Extract) for two different models (M1_GBR=Bayesian B and M2_RR=ridge regression), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

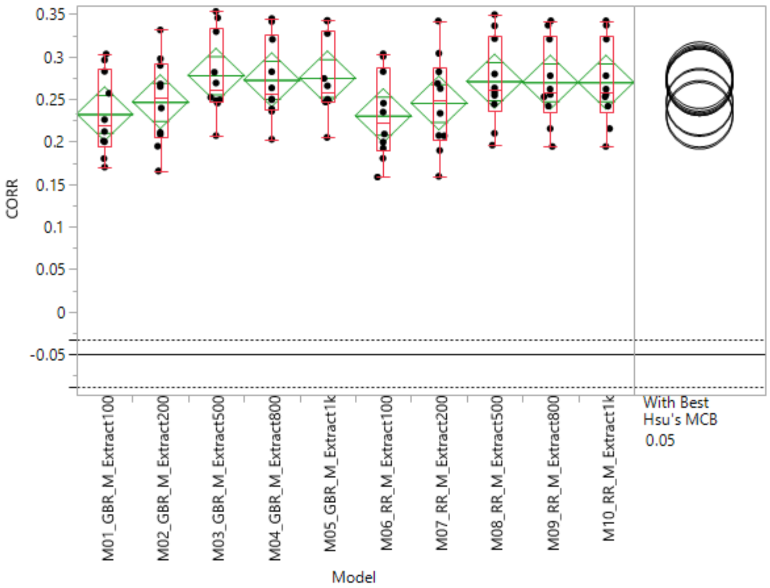


Figure 58. Whisker and box plot of correlation values for malt extract (M_Extract) for two different models (M1_GBR=Bayesian B and M2_RR=ridge regression), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

Plump

Plump kernels are an indirect measurement of the potential extract and starch content within the grain. It is a useful trait to visually determine if the grain will potentially have higher levels of extract in the malt house. During my analyses, GBR and RR had mean RMSE (Figure 59) values below the threshold and mean correlation values ranged from 0.20 – 0.30 (Figure 60). However, this trait will not be taken into frther consideration for further analyses since a portion the variation in the RMSE values for these models goes over the threshold, and more importantly, the correlation values are low.

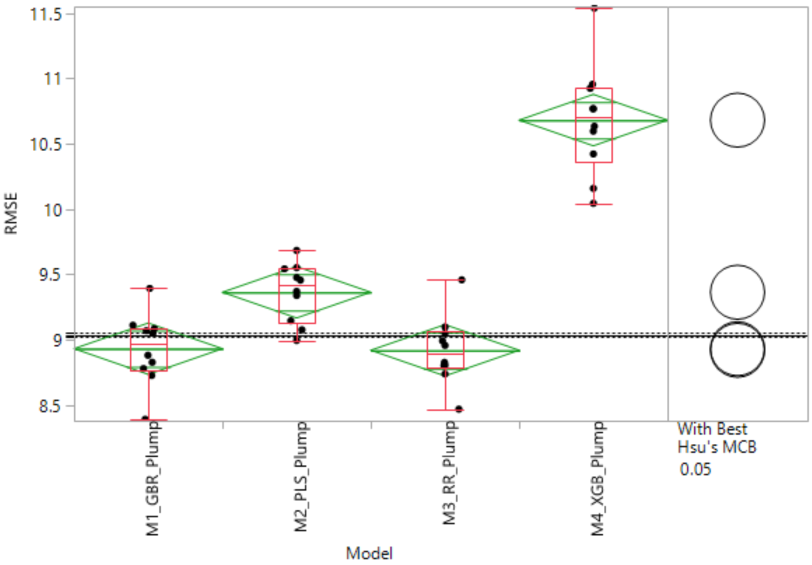


Figure 59. Whisker and box plot of root mean square error (RMSE) values for plump kernels for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

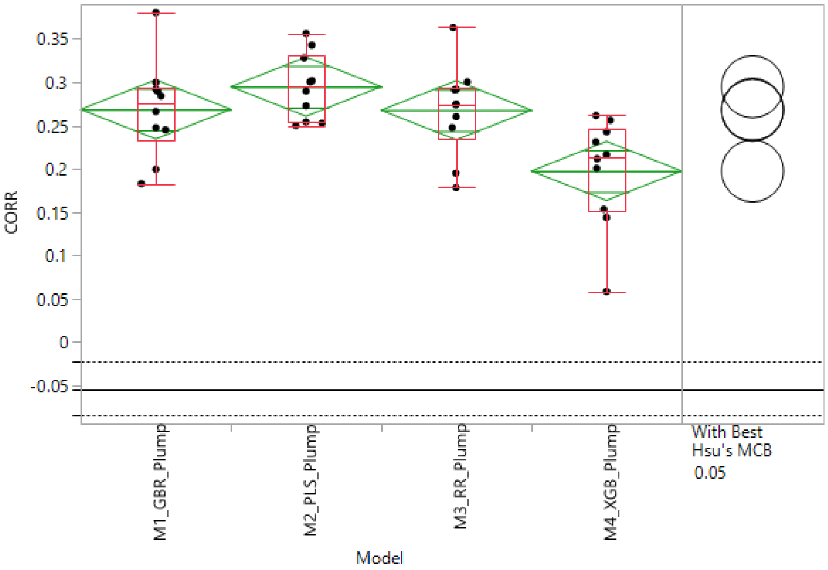


Figure 60. Whisker and box plot of correlation values for barley plump kernels (Plump) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

Protein

Grain protein is another trait that is dependent on whether the malt made from the cultivar will be used for brewing an adjunct or all malt beer. Brewers making an adjunct beer prefer grain protein ≤ 12.8% while brewers making an all malt beer prefer protein levels ≤ 11.5%. Models for protein that had an acceptable RMSE are GBR and RR (Figure 61). The highest correlation was also seen in the GBR model (Figure 62); however, based on Hsu's MCB there were no significant differences between the correlation values for GBR and RR.

In the analyses to determine the minimum number of markers to use for predicting protein, the mean RMSE value for the GBR model was at the threshold for 200 markers and below the threshold for 500 or more markers (Figure 63). The mean RMSE values for the RR model were below the threshold when 200 or more markers were used. There was no improvement in RMSE or correlation when 500 or more markers were used (Figures 63 and 64). I suggest the use of the RR model for protein since its RMSE values are slightly less numerically than those obtained for the GBR model.

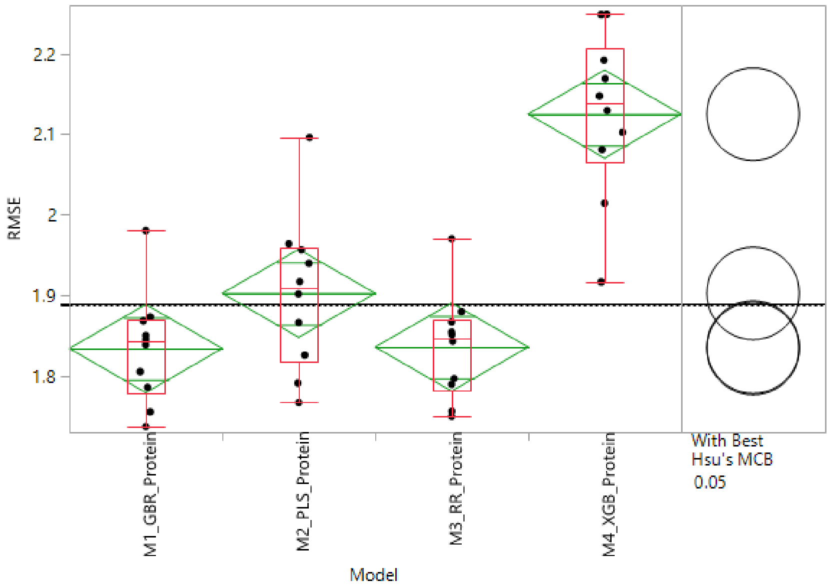


Figure 61. Whisker and box plot of root mean square error (RMSE) values for protein for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

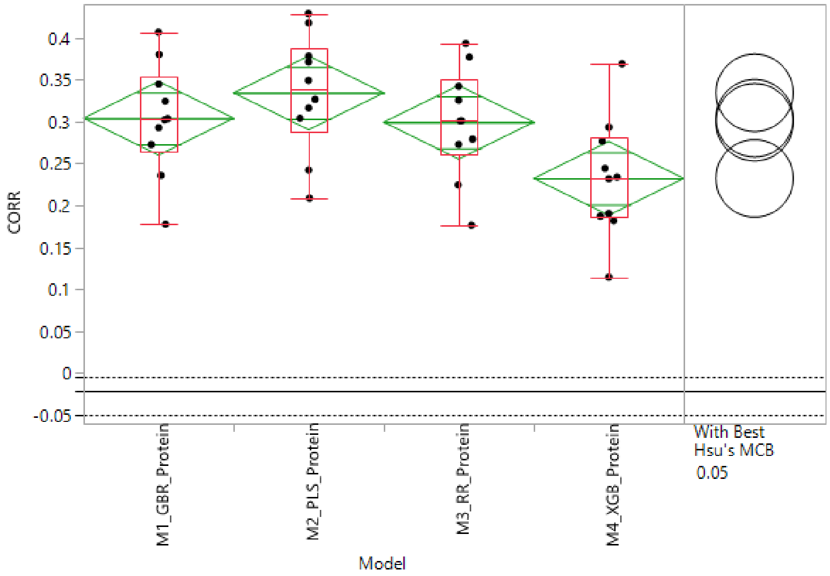


Figure 62. Whisker and box plot of correlation values for barley protein for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

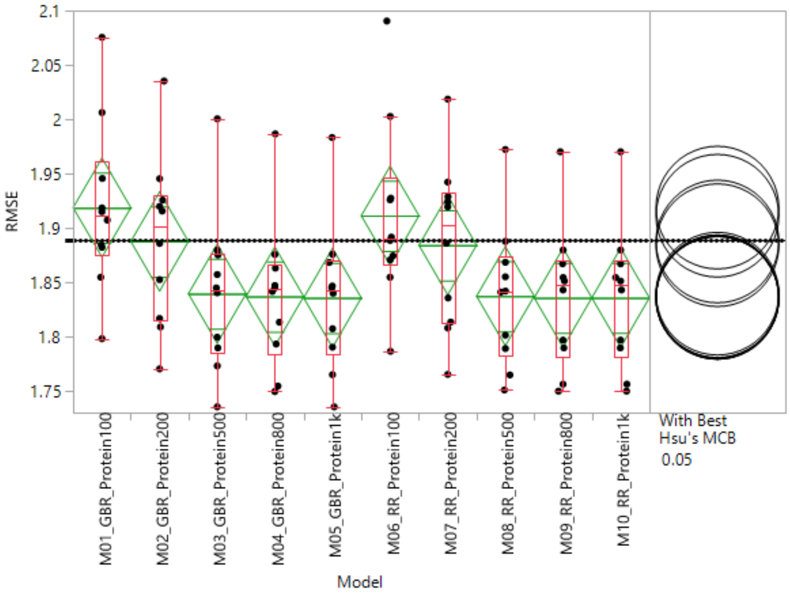


Figure 63. Whisker and box plot of root mean square error (RMSE) values for protein for two different models (M1_GBR=Bayesian B and M2_RR=ridge regression), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

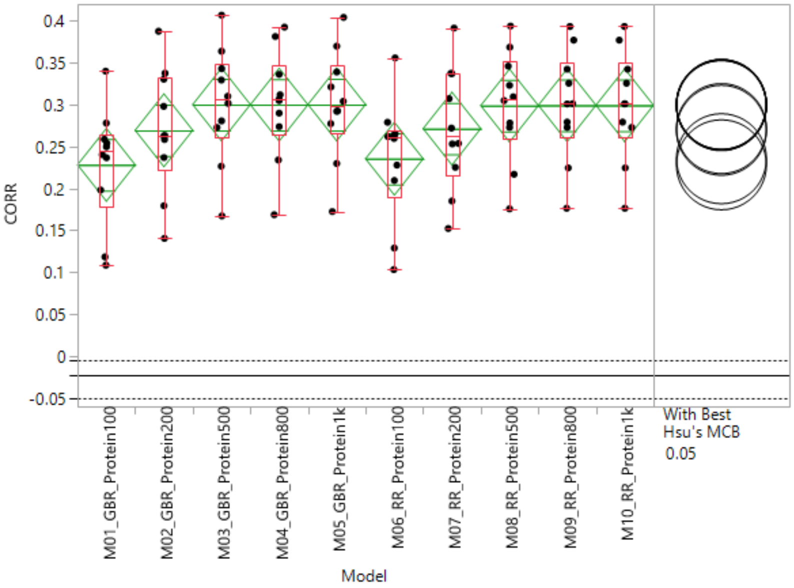


Figure 64. Whisker and box plot of correlation values for protein for two different models (M1_GBR=Bayesian B and M2_RR=ridge regression), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

S/T

Selection for S/T is not as straightforward as for other traits because the desired level falls within the range of 38-47%. Cultivars with values either below or above this range are not desired. The models using GBR, PL, and RR had mean RMSE values below the threshold for S/T (Figure 65). Furthermore, there were no significant differences between the correlation values of the aforementioned models (Figure 66). The best performing models in terms of RMSE were GBR and RR. The correlation value for PLS of 0.34 is slightly higher than those for GBR and RR (0.33); however, based on Hsu's MCB none of the values were significantly different. Thus, I used the GBR and RR models for my next analyses.

In the analyses to determine the minimum number of markers needed for prediction, mean RMSE values for the GBR and RR models were below the threshold when 100 or more markers were used (Figure 67). No improvement in RMSE or correlation values were observed when 500 or more markers were used (Figure 68). Given the RSME and correlation values are similar for both models, I chose the GBR model with a minimum of 500 markers as the model to use for the same reason I indicated for other traits, such as barley color.

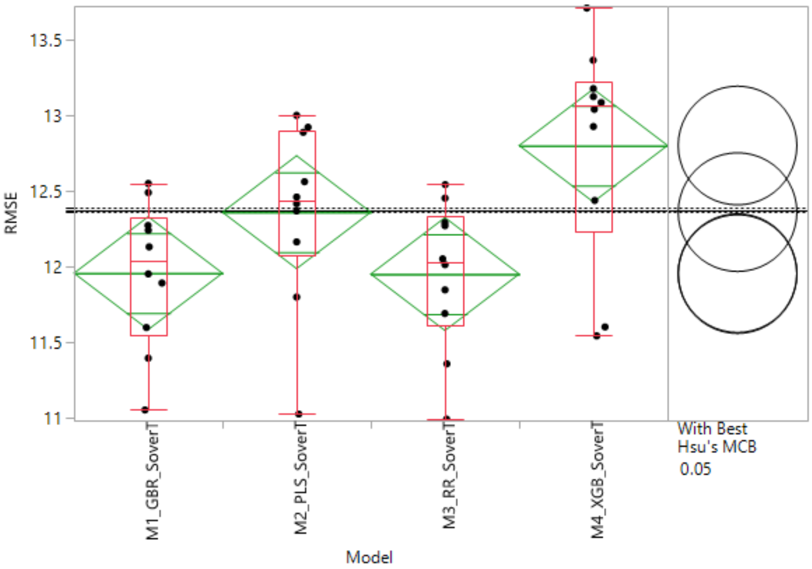


Figure 65. Whisker and box plot of root mean square error (RMSE) values for soluble protein over total protein (SoverT)) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

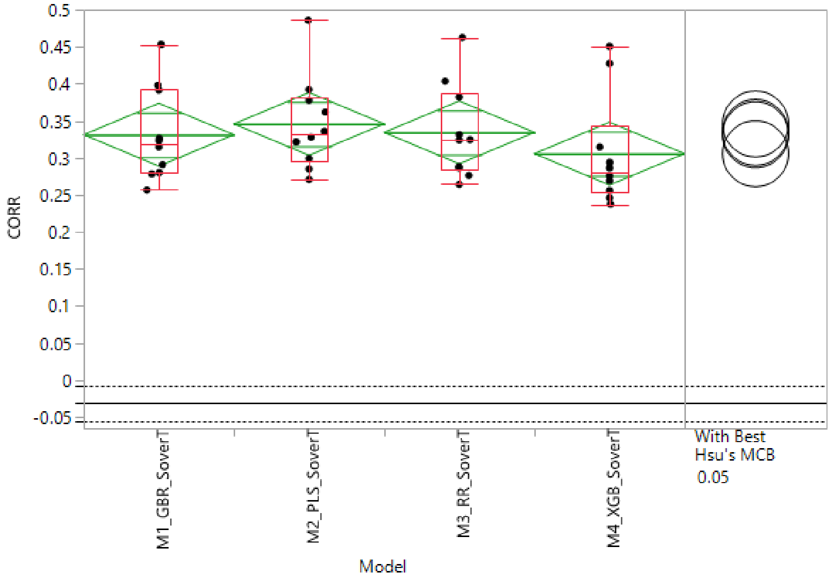


Figure 66. Whisker and box plot of correlation values for barley soluble protein over total protein (SoverT) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

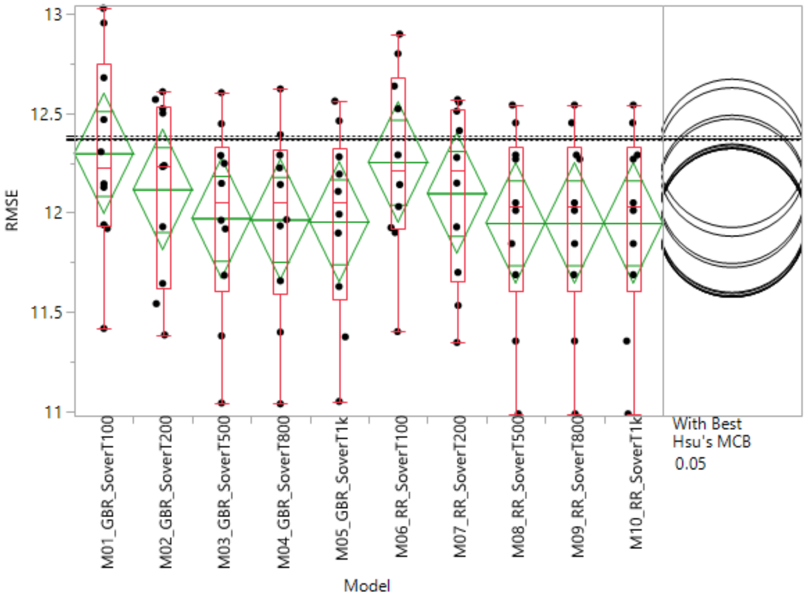


Figure 67. Whisker and box plot of root mean square error (RMSE) values for soluble protein over total protein (SoverT) for two different models (M1_GBR=Bayesian B and M2_RR=ridge regression), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

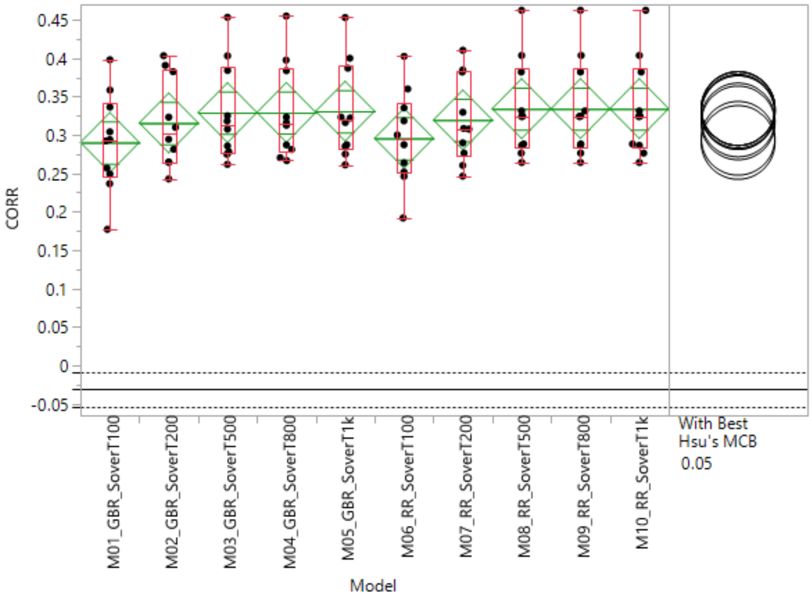


Figure 68. Whisker and box plot of correlation values for soluble protein over total protein (SoverT) for two different models (M1_GBR=Bayesian B and M2_RR=ridge regression), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

Test weight

Test weight above 60.8 kg hL^{-1} is desired for barley. Models for test weight with mean RSME values below threshold were GBR and RR (Figure 69) and the correlation values were 0.28 and 0.27 for the GBR and RR models, respectively (Figure 70). Given the low correlation values and the fact that a large portion of the whisker and box plots for RSME were above the threshold, I chose not to consider test weight for genomic selection.

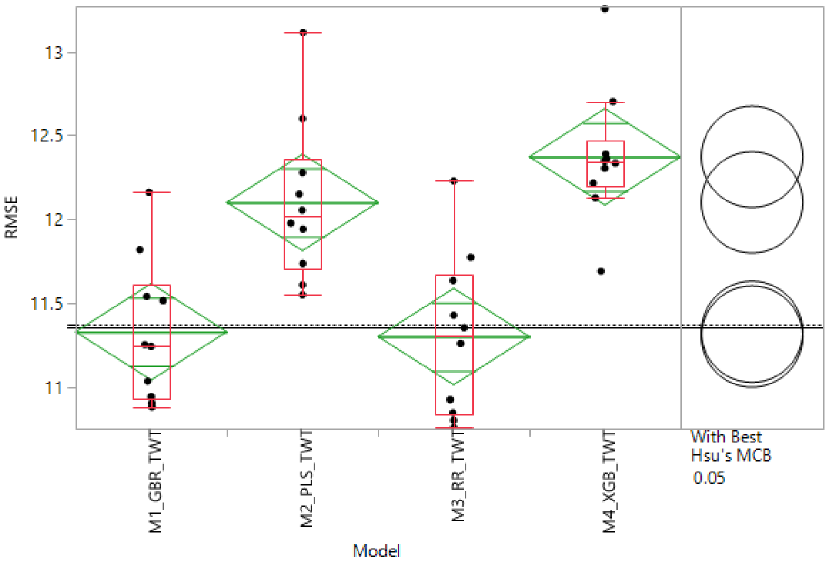


Figure 69. Whisker and box plot of root mean square error (RMSE) values for test weight (TWT) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

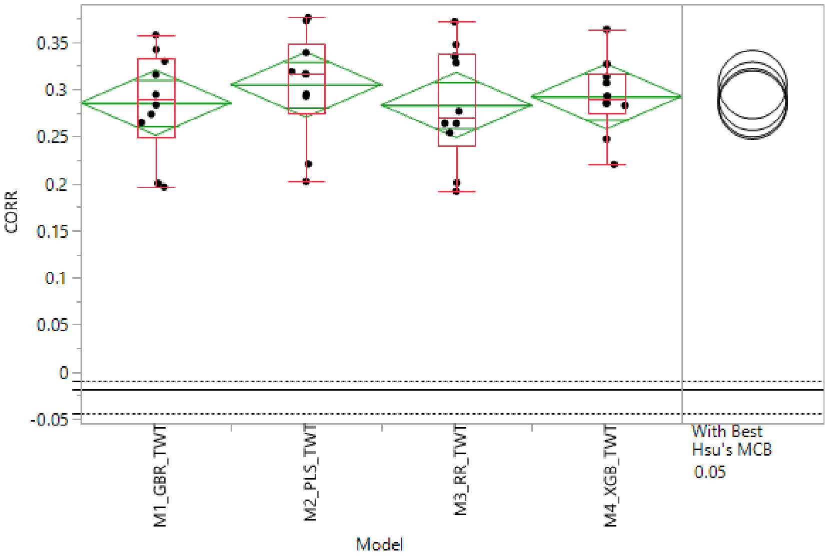


Figure 70. Whisker and box plot of correlation values for barley test weight (TWT) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

Wort Clarity

Lower wort clarity values are desired in selection. The models for GBR and RR had mean RSME values below the threshold (Figure 71). The correlation values for both these models was 0.24 (Figure 72). As was done for test weight, given the low correlation values and the fact that a large portion of the whisker and box plots for RSME were above the threshold, I chose not to consider wort clarity for genomic selection.

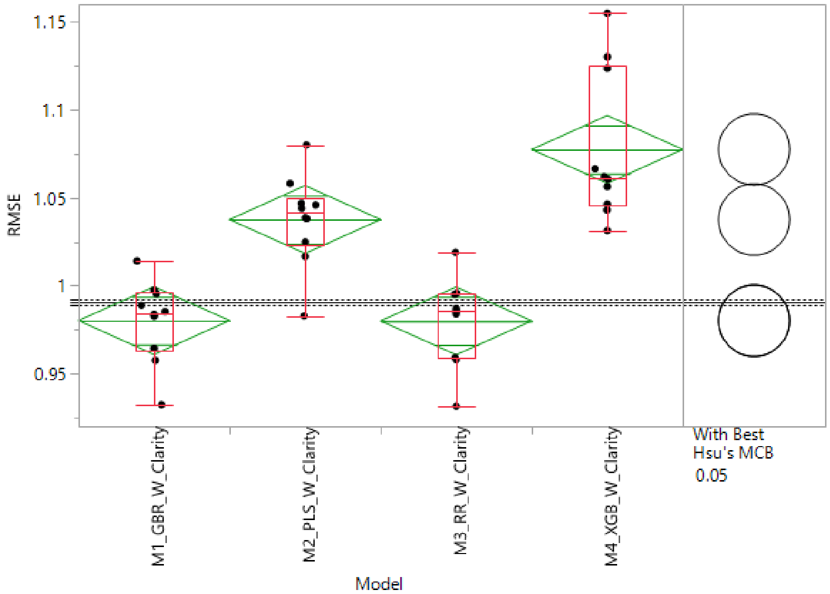


Figure 71. Whisker and box plot of root mean square error (RMSE) values for wortt clarity for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

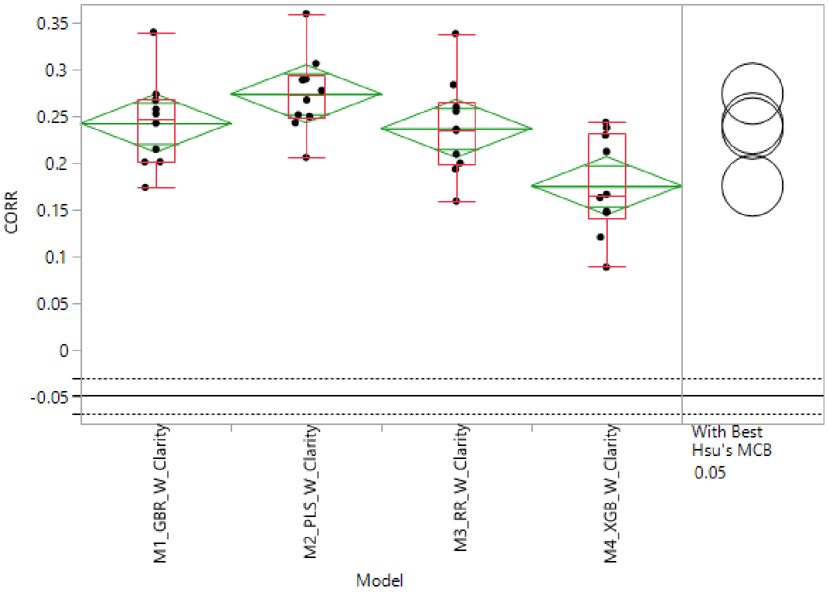


Figure 72. Whisker and box plot of correlation values for barley wort clarity (W_Clarity) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

Wort Color

Lighter wort colors, which are indicated by lower values, are generally desired for pilsner style beers. The models for GBR and RR had mean RSME values below the threshold (Figure 73). The mean correlation values for both of the models was about 0.32 (Figure 74).

In the analyses to determine the minimum number of markers to use for predicting wort color, the RSME values were below the threshold for 200 or more markers for the GBR model and for 100 or more markers for the RR model (Figure 75). No further improvements in RMSE or correlation values were observed when 500 or more makers were used (Figure 75 and 76). Given the RSME and correlation values are similar for both models, I chose the GBR model with a minimum of 500 markers as the model to use for genomic selection.

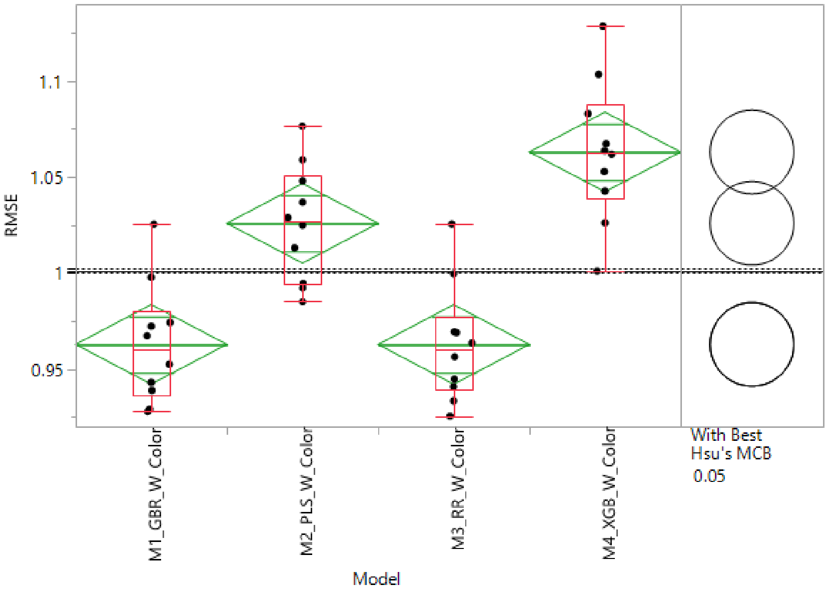


Figure 73. Whisker and box plot of root mean square error (RMSE) values for wort color for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

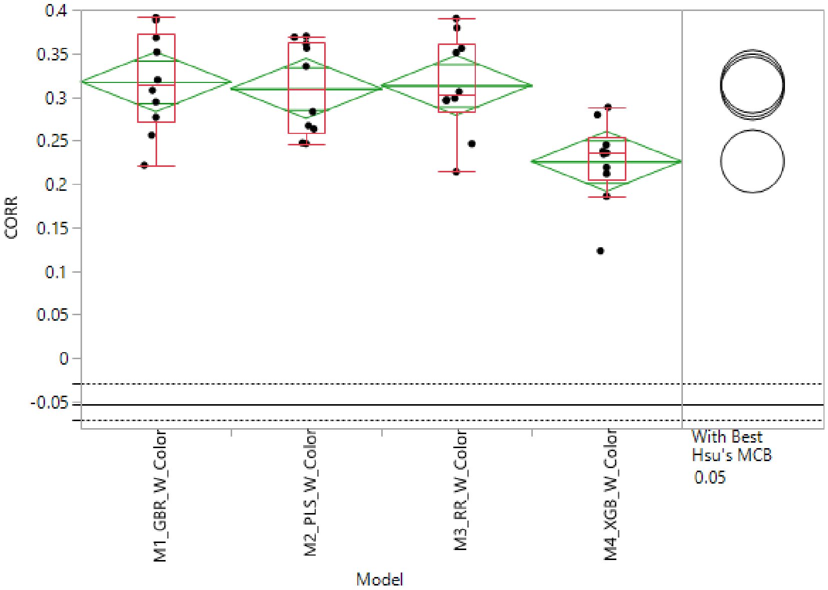


Figure 74. Whisker and box plot of correlation values for barley wort color (W_Color) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

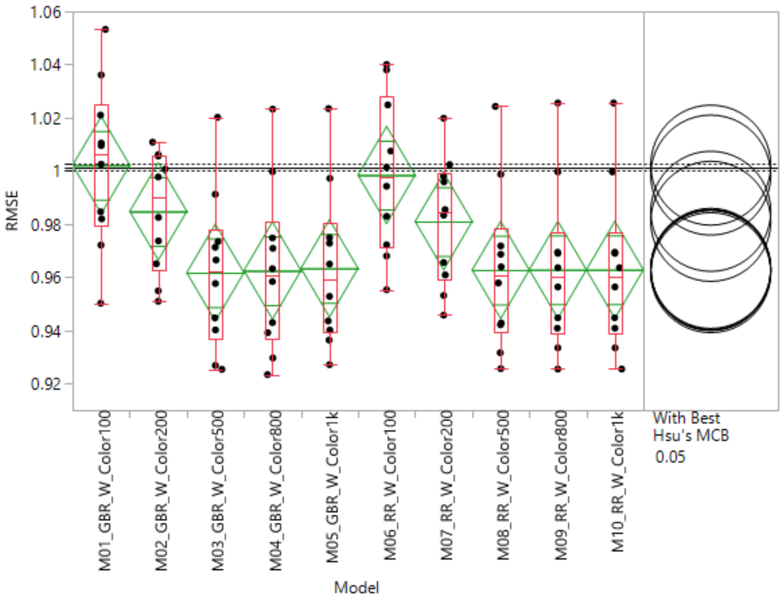


Figure 75. Whisker and box plot of root mean square error (RMSE) values for wort color (W_Color) for two different models (M1_GBR=Bayesian B and M2_RR=ridge regression), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

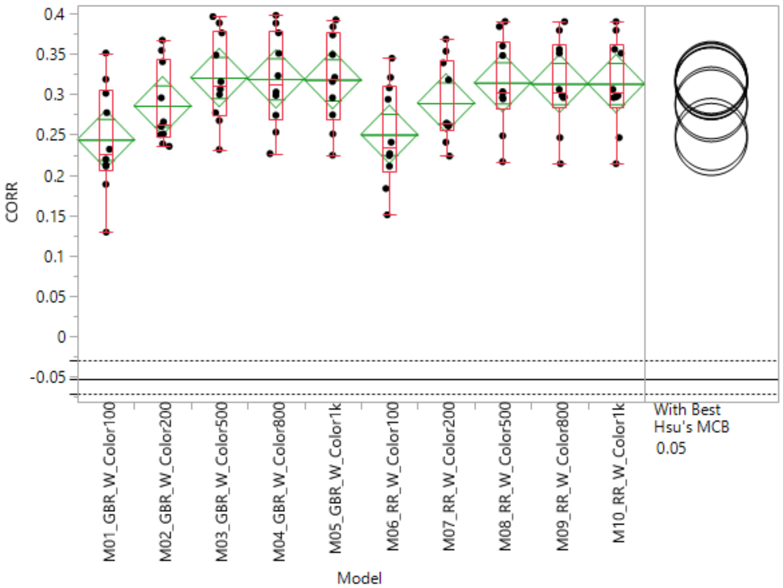


Figure 76. Whisker and box plot of correlation values for wort color (W_Color) for two different models (M1_GBR=Bayesian B and M2_RR=ridge regression), each tested using 100, 200, 500, 800, or 1000 SNP markers. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

Wort Protein

Wort protein is another trait where desired values differ based on the type of beer produced. Wort protein values between 4.8-5.6% are desired for adjunct beers and values less than 5.3% are desired for all malt beers. None of the models for wort protein had mean RMSE values (Figure 77) below the threshold and the correlation values (Figure 78) were all below 0.20; thus, based on the TP and phenotypic values I used in my analyses, wort protein is not a candidate for genomic selection at this time.

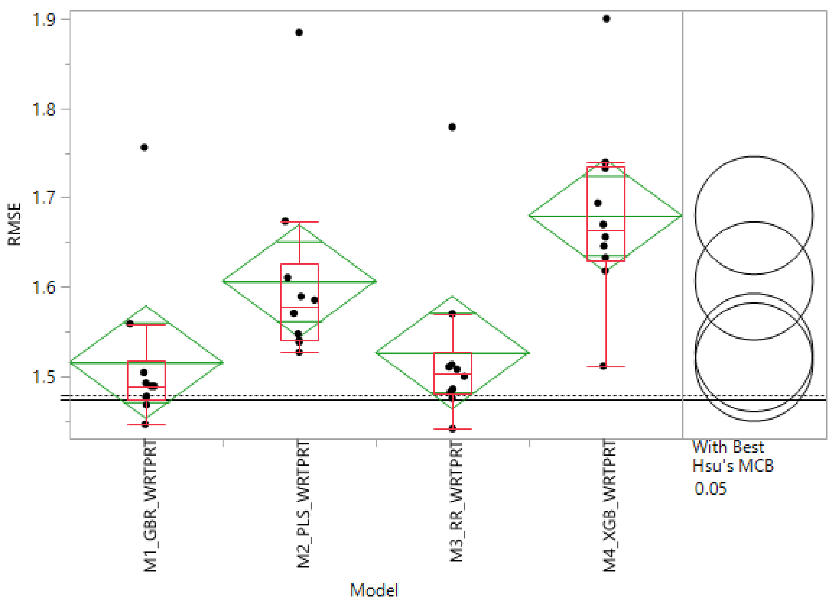


Figure 77. Whisker and box plot of root mean square error (RMSE) values for wort protein for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

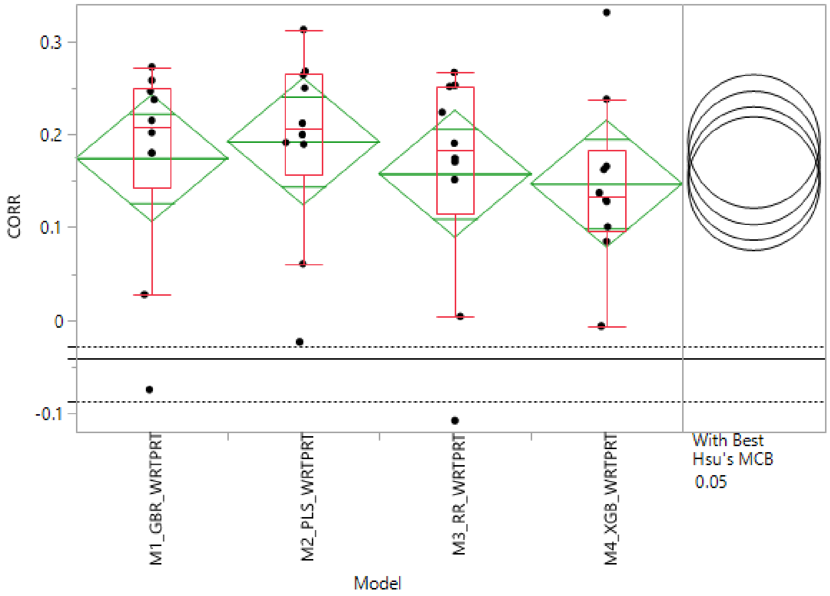


Figure 78. Whisker and box plot of correlation values for barley wort protein (WRTPRT) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

Disease Traits

DON

The levels of DON accumulated on barley is a complex trait that is important in malting barley quality. Barley with greater than 1.0 µg g^{-1} DON is either discounted or rejected at the point of sale. Mean RMSE values were above the threshold for all four models (Figure 79). Additionally, the greatest correlation value of 0.22 was observed for GBR and RR, which suggests that genomic selection for DON may not be effective using any of the models developed from the phenotype data for DON used in my research (Figure 80). The unacceptably high RSME values and lower correlation values for DON may have occurred due to the nature of how the phenotypic values for the values were calculated. The lines in the combined TP were never grown together in a single experiment, but across several years where the checks Conlon and Pinnacle always appeared. Another cause for the high RSME and low correlation values may be due to the high variability for the level of FHB infection in disease nurseries. Disease levels tend to be low around the margins of the nursery and increases towards the center of the nursery. To determine if the unbalanced data or field variability may be a cause of the high RSME and lower correlation values, the entire combined TP should be phenotyped using trials grown at multiple locations across years with an experimental design that accounts for phenotypic variability. One such design would be a randomized complete block with repeated checks arranged in a diagonal arrangement across the field. This design allows for the data to be analyzed using a spatial analysis. DON data collected in these new experiments should then be used for predictive modeling analyses to see if more favorable RMSE and correlation values are obtained as compared to the ones I obtained in my research.

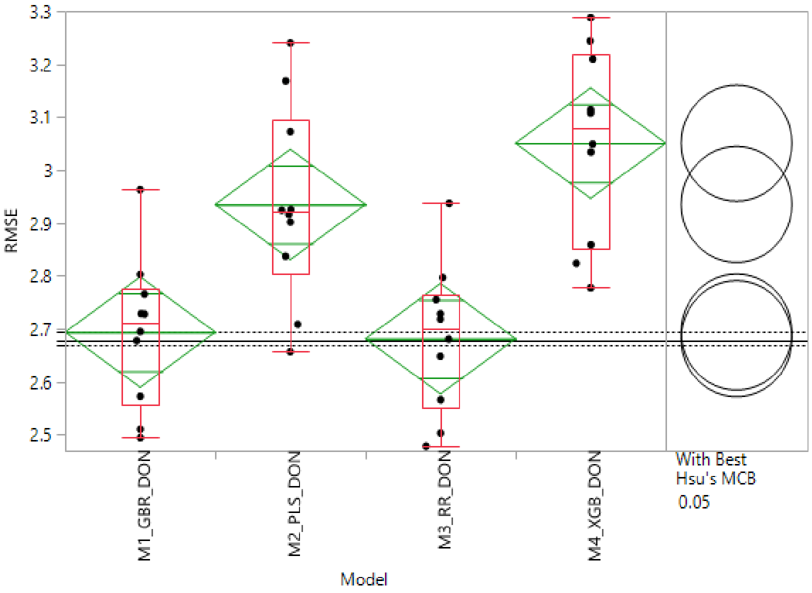


Figure 79. Whisker and box plot of root mean square error (RMSE) values for deoxynivalenol (DON) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

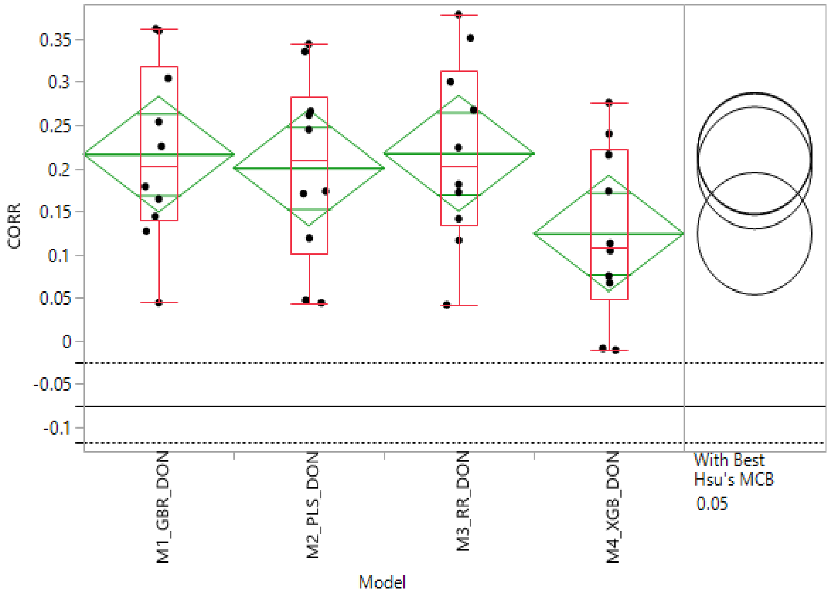


Figure 80. Whisker and box plot of correlation values for deoxynivalenol (DON) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

Foliar Disease

The mean RMSE values for foliar disease were all above the threshold for all models (Figure 81) and the mean correlation values were all below 0.2 (Figure 82). This trait is a general measurement of the foliar disease level on plants in a plot using a 1 to 9 scale. Since it’s not a specific measure of damage from a specific pathogen, the presence of multiple diseases might have an impact on the variation in the data and thus the predictability of the trait. PLS and XGBoost had the highest correlations of around 0.18 (Figure 82); yet, these are unacceptably low. Thus, results from this study cannot be used to develop genomic selection models for foliar disease.

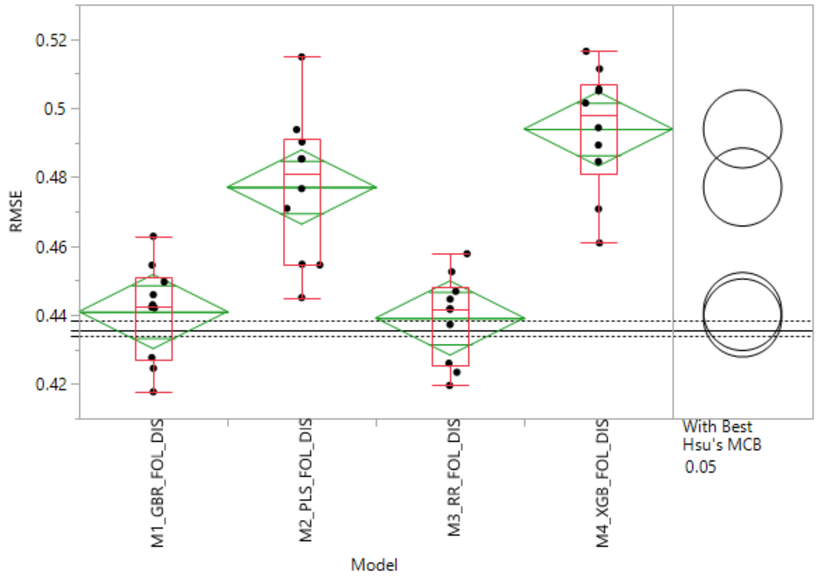


Figure 81. Whisker and box plot of root mean square error (RMSE) values for foliar disease for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

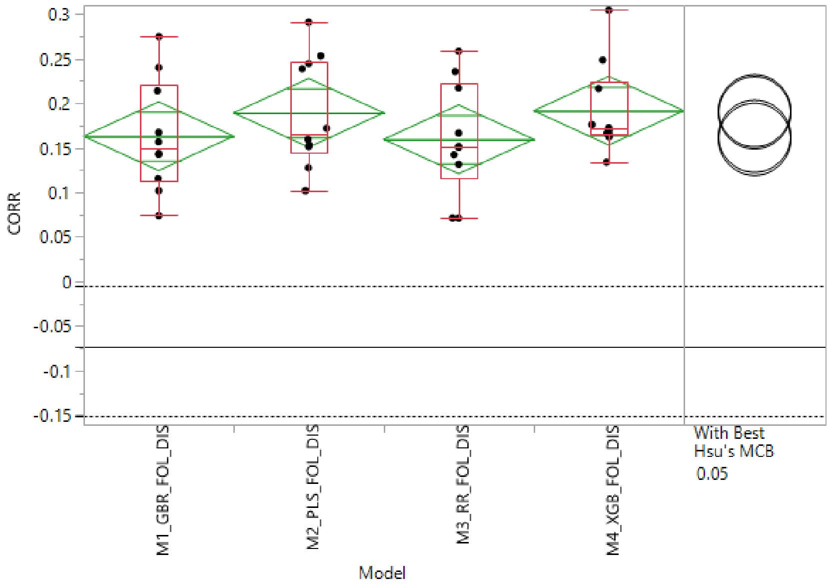


Figure 82. Whisker and box plot of correlation values for foliar disease (FOL_DIS) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

Net Blotch

Mean RMSE values for all models (Figure 83) were above the threshold and correlation values were also low, ranging from 0.20 – 0.25 (Figure 84). Thus, this is not a trait for genomic selection at this time. The unbalanced nature of the data may be a cause for the high RSME and poor correlation values. All of the lines in the combined TP should be phenotyped together for NB resistance at the same time in a single experiment.

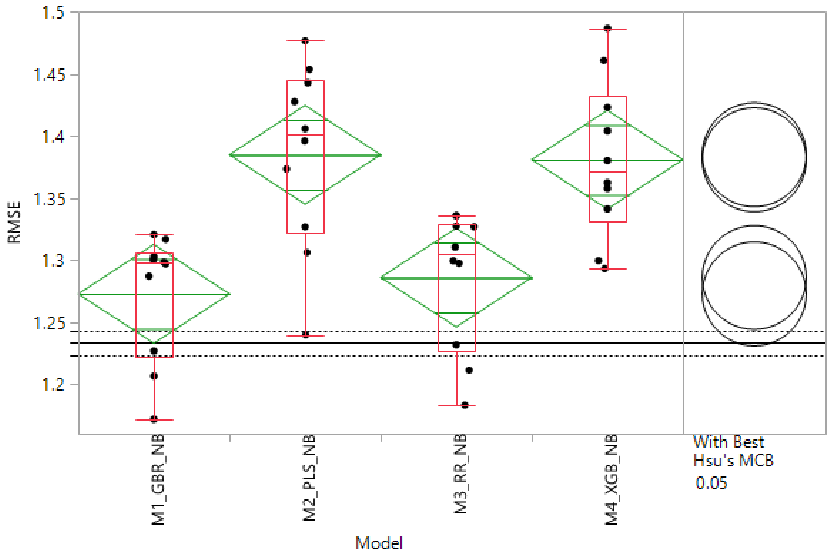


Figure 83. Whisker and box plot of root mean square error (RMSE) values for net blotch (NB) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

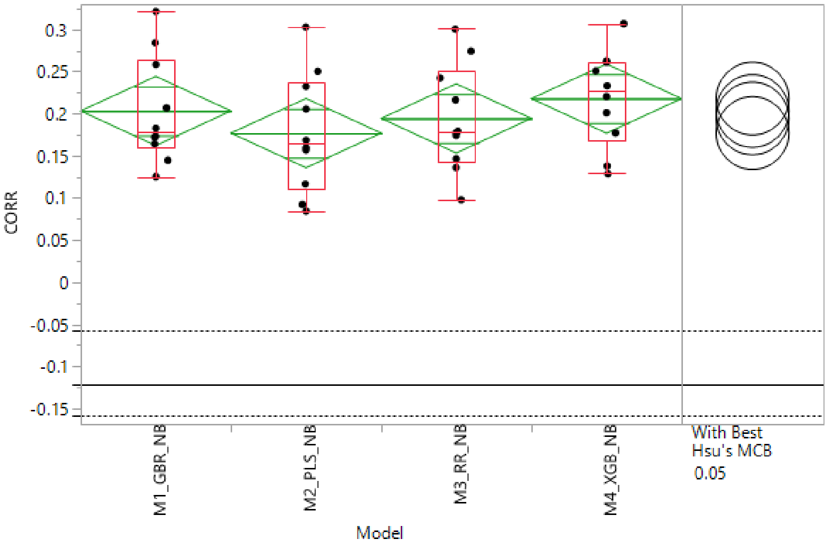


Figure 84. Whisker and box plot of correlation values for net blotch (NB) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

Spot Blotch

Given that all models fall had mean RMSE values (Figure 85) above the threshold and low correlations (Figure 86), genomic selection is not expected to be reliable for predicting spot blotch resistance. The poor values for RSME and correlation for SB could be due to the same reasons as described for NB. Thus, all of the lines in the combined TP should be phenotyped together for SB resistance at the same time in a single experiment.

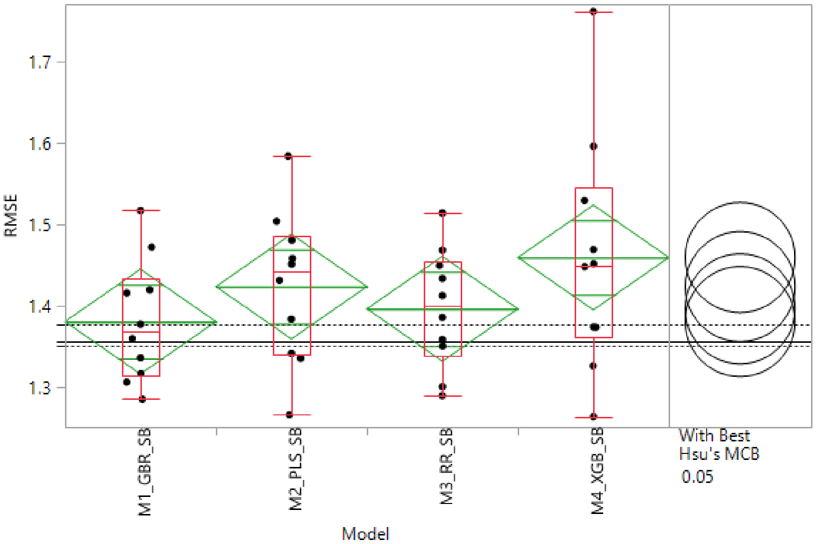


Figure 85. Whisker and box plot of root mean square error (RMSE) values for spot blotch (SB) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which RMSE values should be below. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

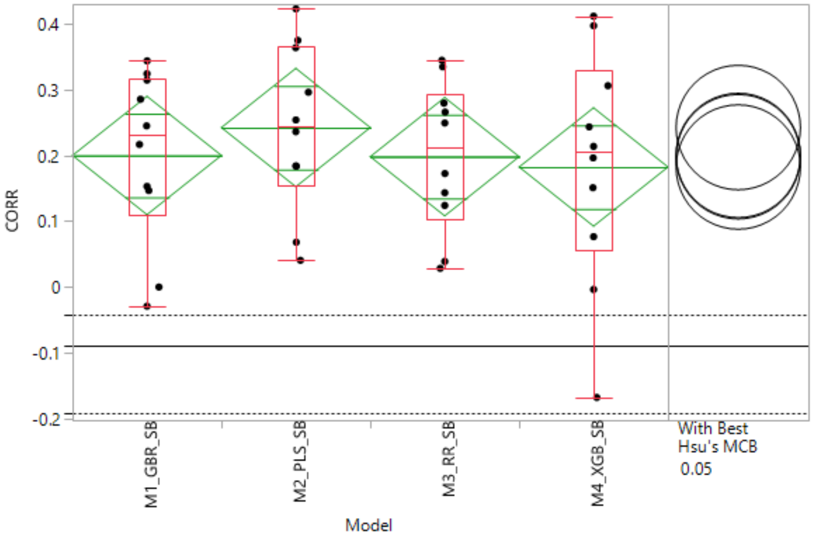


Figure 86. Whisker and box plot of correlation values for spot blotch (SB) for four different models. M1_GBR=Bayesian B, M2_PLS=partial least squares, M3_RR=ridge regression, and M4_XGB=XG Boost. The dark dashed line in the plot represents the threshold for which correlation values should be below above. The circles on the right represent the results from Hsu's multiple comparison method that is designed to identify factor levels that are the best, insignificantly different from the best, and those that are significantly different from the best.

Summary of Cross Validation Analyses

Table 2 contains the mean RMSE and correlation values found throughout the previously described steps in model comparisons. The bold RMSE values in the table are those where mean RMSE values were below the thresholds. From the initial 24 traits analyzed with four models each, 18 had mean RMSE values that fell below the threshold value, but I decided that only 13 were candidates for genomic selection due to the variability within said models. Figure 87 illustrates one factor that may play a role in predictability within each trait, observations per trait. Some traits do not contain the same number of observations as others. For example, net blotch only has 200 observations within our selected TP, and as seen previously, does not have a successful model for prediction purposes when compared to another trait (such as DP that has 700 observations and a successful model for prediction purposes). This does not mean that the amount of observation is completely responsible for predictions since there are many key players (e.g., genetics of the trait and the error within each experiment that can impact results). As mentioned previously, studies have determined that those traits that are better for prediction are generally those that also have higher heritability. As seen during these analyses, the highest heritability values were found for ß-glucan, barley color, height and yield within this population and consequently are also traits that have been found to have the highest correlation values when compared to all traits.

Forest max predictor reduction was used to determine the minimum number of markers that should be used as predictors. The number of SNP markers chosen for each model were 100, 200, 500, 800, and 1000. The purpose of selecting the minimal number of markers to include on the new SNP chip for effectively predicting each trait was to reduce costs of designing the new chip. The cost of including a SNP on the new is between $9-10 per marker.

Table 2. Mean root mean square errors (RMSE) and correlation values obtained from the cross validation analyses of four models for genomic selection for agronomic, barley and malt quality, and disease resistance traits.

Traits	RMSE				Correlation values			
	GBR†	PLS	RR	XGB	GBR	PLS	RR	XGB
				Agronomic Traits				
Barley color	**6.17**	**6.25**	**6.15**	**7.13**	0.54	0.55	0.55	0.47
Heading date	**2.32**	**2.47**	**2.31**	2.77	0.42	0.39	0.42	0.34
Height	**1.67**	**1.7**	**1.67**	2.98	0.47	0.49	0.48	0.29
1000-kernel weight	**10.41**	10.86	**10.38**	11.12	0.32	0.34	0.33	0.31
Moisture	0.37	0.4	0.37	0.6	0.21	0.24	0.22	0.06
Lodging	0.18	0.19	0.18	0.21	0.07	0.1	0.07	0.01
Stem breakage	**0.26**	**0.26**	**0.26**	0.3	0.48	0.51	0.47	0.4
Yield	**5.44**	**5.56**	**5.44**	6.73	0.52	0.52	0.52	0.47
				Malt Quality Traits				
A-amylase	**10.06**	**10.41**	**10.11**	11.83	0.45	0.45	0.43	0.32
ß-glucan	**82.67**	**85.17**	**88.09**	**89.7**	0.75	0.73	0.72	0.71
Diastatic power	**17.87**	**18.72**	**17.94**	20.42	0.36	0.36	0.35	0.3
Free amino nitrogen	32.21	34.81	32.43	37.62	0.25	0.22	0.22	0.14
Malt extract	**8.26**	8.76	**8.26**	9.82	0.28	0.3	0.27	0.22
Plump kernels	**8.93**	9.36	**8.92**	10.68	0.27	0.29	0.27	0.2
Protein	**1.83**	1.9	**1.84**	2.12	0.3	0.33	0.3	0.23
S/T	**11.95**	12.36	**11.95**	12.8	0.33	0.35	0.33	0.31
Test weight	**11.33**	12.1	**11.3**	12.37	0.29	0.3	0.28	0.29
Wort clarity	**0.98**	1.04	**0.98**	1.08	0.24	0.27	0.24	0.18
Wort color	**0.96**	1.03	**0.96**	1.06	0.32	0.31	0.31	0.23
Wort protein	**1.25**	1.32	**1.25**	1.43	0.27	0.29	0.27	0.2
				Disease Traits				
Deoxynivalenol	**2.63**	2.99	**2.62**	2.97	0.19	0.15	0.19	0.11
Foliar disease	0.44	0.48	0.44	0.49	0.16	0.19	0.16	0.19
Net blotch	1.27	1.38	1.29	1.38	0.2	0.18	0.19	0.22
Spot blotch	1.38	1.42	1.4	1.46	0.2	0.24	0.2	0.18

†GBR = Genomic Bayesian Regression, PLS = Partial least squares, RR = Ridge regression, and XGB = XG Boost.

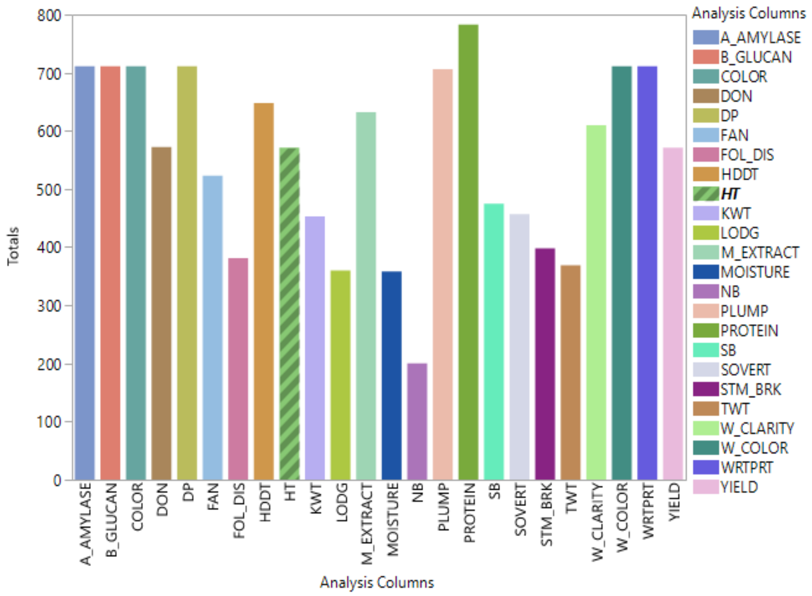


Figure 87. Number of observations used for predicting the 24 traits.

Table 3 summarizes the best models for each trait. The selection criterion for each model was dependent on the best combination of RMSE and correlation values. Even if not ideal, many of the selected traits have correlation values that are not as high as wanted. A good target for correlation between the observed and predicted models is debatable and dependent on the importance of the trait and the breeding programs economic capacity.

Table 3. Selected models, minimum number of markers, root mean square errors (RSME), and correlations for traits suggested for genomic selection on the NDSU barley breeding program.

Trait	Model†	Forest	RMSE	Correlation
		Agronomic Traits		
Barley color	GBR	500	6.17	0.54
Heading date	RR	500	2.31	0.42
Height	RR	500	1.68	0.48
1000-kernel weight	RR	500	10.38	0.33
Stem breakage	PLS	500	0.26	0.51
Yield	RR	500	5.44	0.52
		Malt Traits		
α -amylase	GBR	200	10.10	0.44
ß-Glucan	GBR	500	82.75	0.75
Protein	GBR	500	1.84	0.30
Wort Color	GBR	500	0.96	0.32
Diastatic power	GBR	500	17.88	0.36
Malt extract	GBR	500	8.26	0.28
S/T	RR	500	11.95	0.33

†GBR = Genomic Bayesian Regression and RR = Ridge regression.

SNP Chip Markers

A major goal of this research was to identify traits that are candidates for genomic selection, which model is best for predicting these traits, and which markers should be used for predicting these traits. This information is necessary to design a new SNP chip for the NDSU barley breeding program to use in selecting F_4 and F_5 lines to advance to their preliminary yield trials.

Table 4 summarizes the traits that were selected as candidates for genomic selection, the best model for predicting the trait, and the correlation between the observed and predicted values during the cross-validation model comparison using all markers and the recommended minimum number of markers. The criterion I used to determine which markers to include on the chip was based on the frequency that the markers were included in models during the multiple cross validations. JMP Genomics uses hierarchical clustering analysis to group the prevalence of occurrence of each individual marker across the iterations of modeling methods, levels within these methods, and the overall frequency. Thus, the markers that occur with the highest frequency are likely to be the best predictors for each trait. Now that the number of markers necessary to predict our selected trait has been identified, I can identify the top performing markers by their frequency and run the analyses using these markers for each trait. In these analyses using only the highest frequency markers, the correlation values obtained were higher than those obtained when all markers were used.

It is likely that the reason higher correlation values were obtained in the cases where high frequency markers were used is due to a biased effect size. It is possible that when using all markers, the model may be unable to establish an effect size of zero for those markers that do not control the trait while also estimating the effect size for significant markers without creating bias resulting in a biased effect size for all markers, both true and false. Consequently, this will decrease the predictability of the fitted model. Having said this, there will be less bias in the effect size when running cross validation with the selected markers. This is due to the fact that only the markers that have a strong effect will be selected, including true markers and some false markers since the sample size is not infinite. Less bias in the effect size is more than likely the reason that there is an increase in correlation values for each trait when using only their respective significant markers (L. Silva, personal communication, 17 Mar. 2020).

Table 4. Correlation values for each trait using all markers vs. the minimum number of markers to use frequent markers.

Selected models						
			All Markers		Highest Frequency Markers†	
Trait	Model‡	Forest	RMSE	Correlation	RMSE	Correlation
Agronomic Traits						
Barley color	GBR	500	6.17	0.54	5.33	0.69
Heading date	RR	500	2.31	0.42	2.06	0.58
Height	RR	500	1.67	0.48	1.45	0.64
1000-kernel weight	RR	500	10.38	0.33	9.13	0.53
Stem breakage	PLS	500	0.261	0.51	0.22	0.68
Yield	RR	800	5.44	0.52	4.70	0.67
Malt Traits						
α -amylase	GBR	200	10.10	0.44	8.65	0.63
ß-Glucan	GBR	500	82.75	0.75	69.77	0.83
Protein	GBR	500	1.84	0.30	1.63	0.51
Wort Color	GBR	500	0.96	0.32	0.87	0.49
Diastatic power	GBR	500	17.88	0.36	15.66	0.56
Malt extract	GBR	500	8.26	0.28	7.34	0.50
S/T	RR	500	11.95	0.33	10.40	0.545

†Markers selected were those most frequently used in the validation iterations.
‡ GBR = Genomic Bayesian Regression, RR = Ridge regression, and PLS = Partial Least Square.

Figures 88 and 89 summarize the number of markers from each chromosome that the analyses suggest should be included on the new SNP chip for each trait. These numbers are much less than the number of significant markers that were detected during the GWAS analyses (Figure 11). The use of less markers to make the genomic selection predictions will most definitely benefit the program in terms of economic input for section. As stated earlier, the estimated cost of constructing the new SNP chip is between $9-10 per SNP and it is thought that the chip will be useful for about three years. After this time, the training population will need to be updated and new genomic selection models will need to be developed as was done in my research.

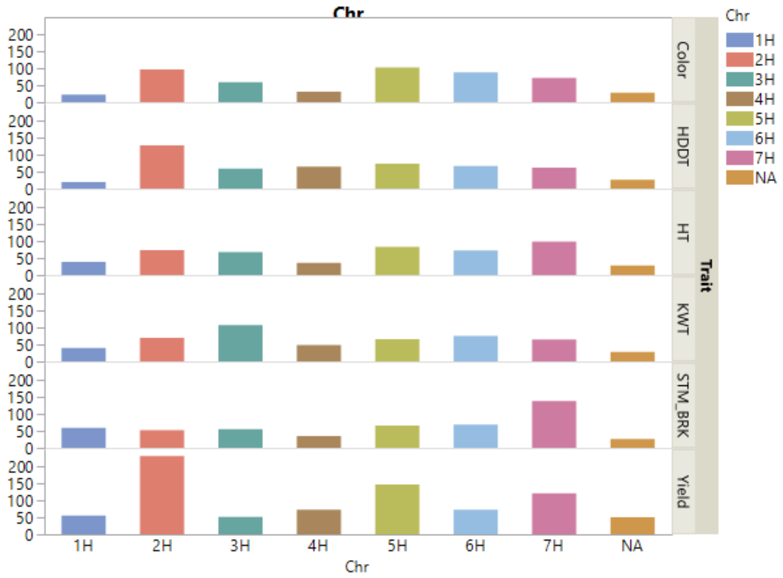


Figure 88. Candidate markers per chromosome for agronomic traits

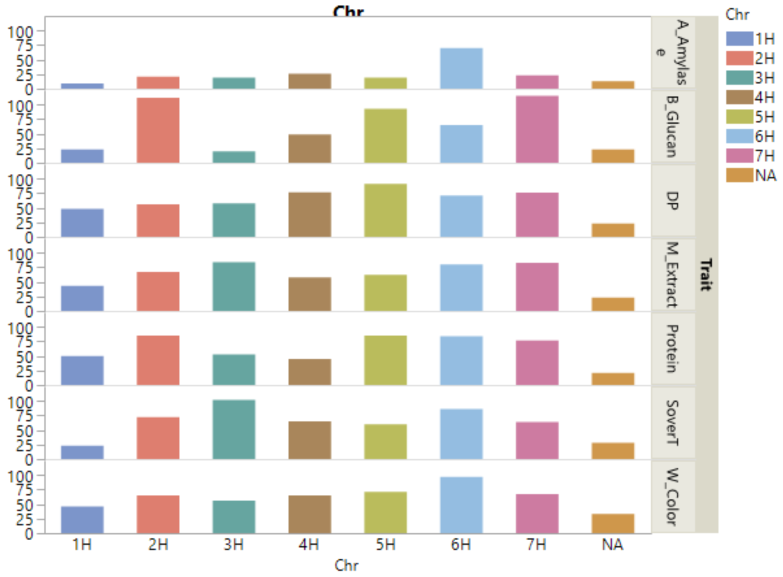


Figure 89. Candidate markers per chromosome for malt quality traits

What would be helpful in keeping the costs of constructing the new chip would be if the SNPs were predictors for multiple traits. A series of Venn diagrams were created with the intent of providing an illustration of the relationship between traits and the number of predictive markers. There was no single SNP that was predictive for KWT, HT, HDDT, Yield, and STM_BRK (Figure 90), while there were three SNPs that were predictive for the malt quality traits (DP, B_GLUCAN, A_Amylase, Protein, and M_Extract. These diagrams represent how some SNPs are predictive for multiple traits. For example, Figure 80 depicts 46 common markers that are predictors for HDDT and KWT.

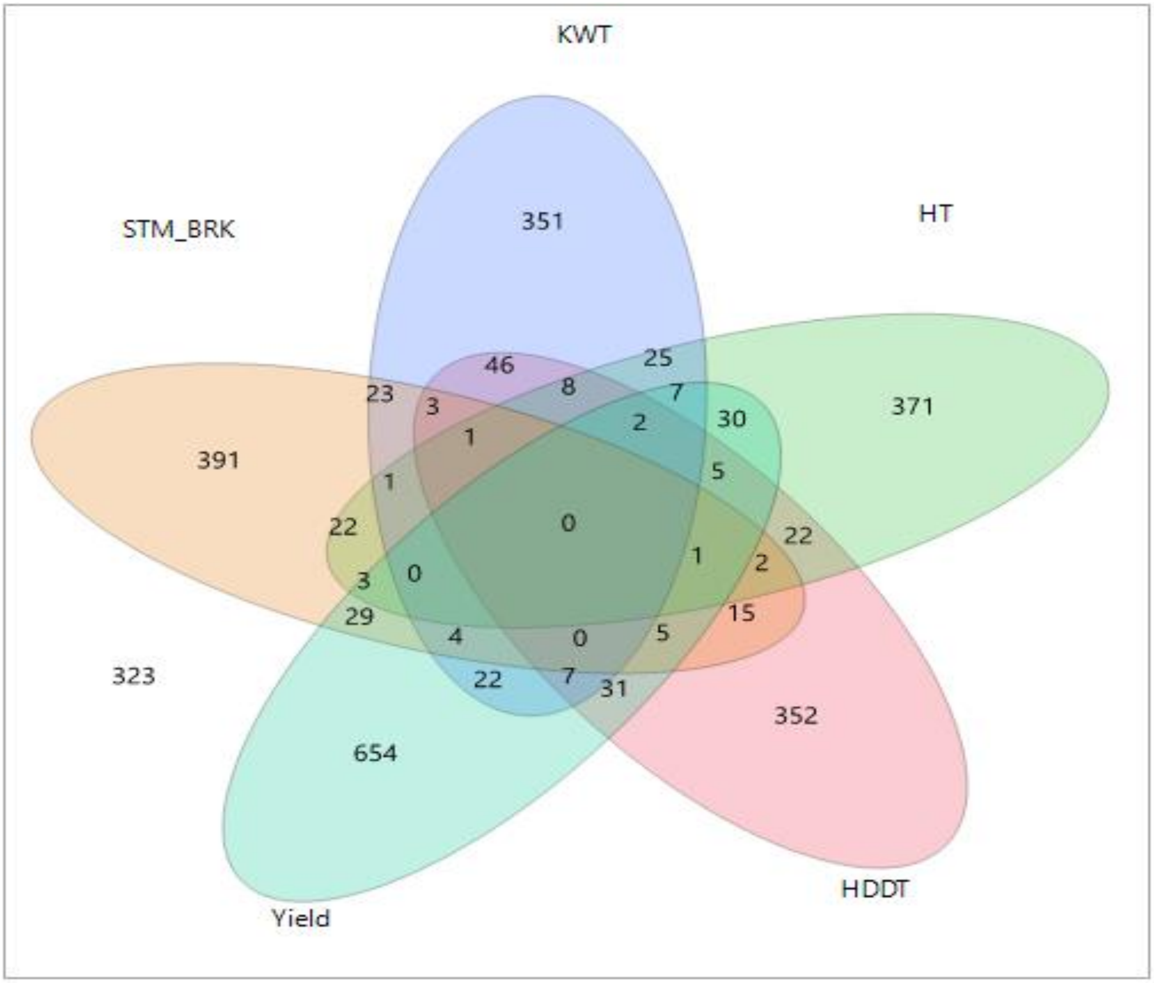


Figure 90. Venn diagram showing the number of SNPs selected for selecting agronomic traits.

Malt extract and DP in Figure 91 have 36 shared predictors. Diastatic power being a measurement of the total activity of malt enzymes that hydrolyze starch to fermentable sugars whereas the malt extract is the brewer’s yield. These diagrams reinforce that not only can we use markers to predict specific traits one at a time, be we can make predictions for multiple traits simultaneously with shared markers between traits.

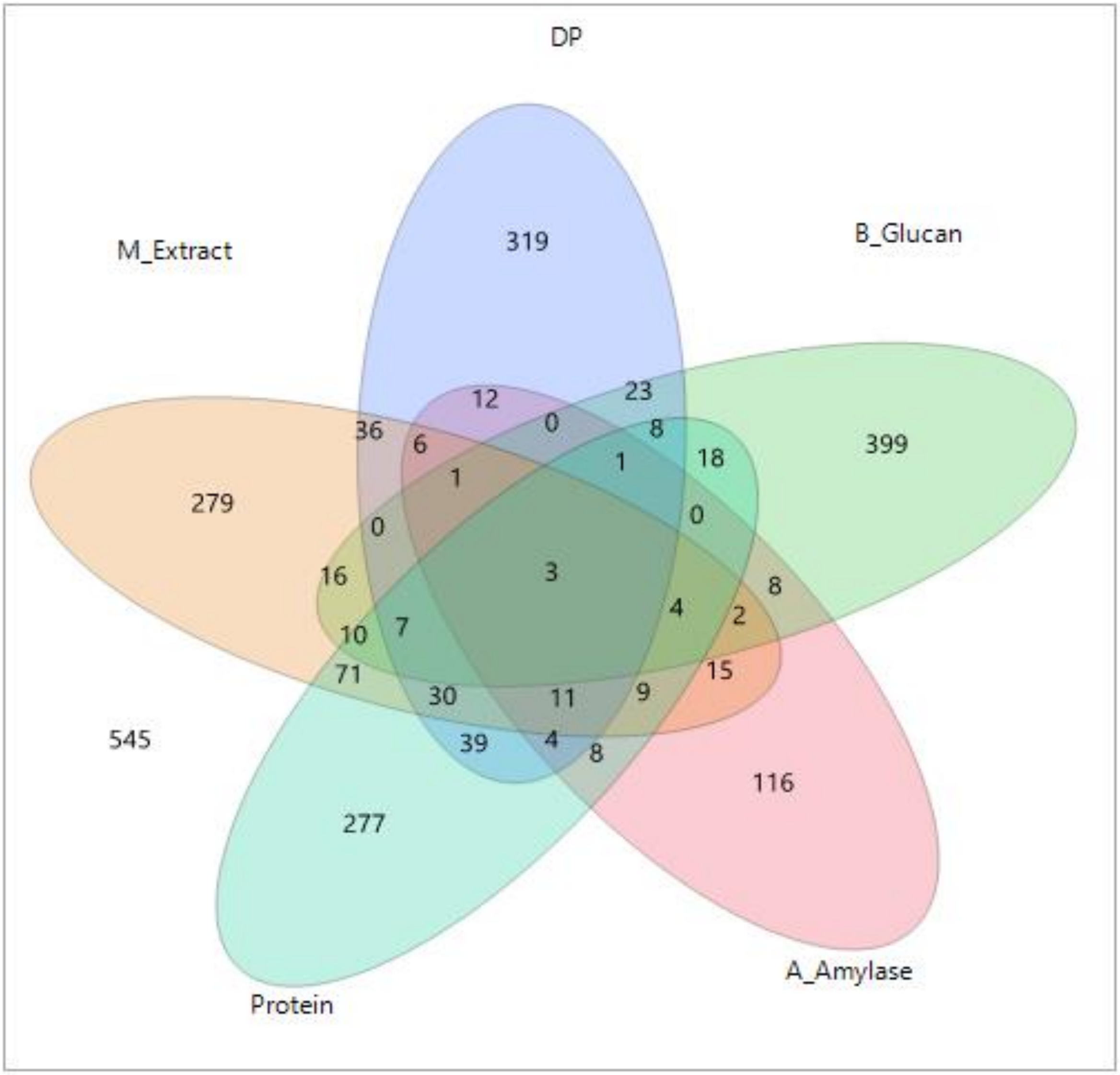


Figure 91. Venn diagram showing the number of SNPs selected for selecting barley and malt quality traits

CONCLUSION

The purpose of this experiment was to identify SNP markers to include on a new SNP chip for use by the NDSU Barley Breeding Program for genomic selection of multiple traits associated with agronomic performance, barley and malt quality, and disease resistance. The first step in this process was to identify the best of three populations to use as the training population for the genomic selection models. I determined that the combined TP, which included parents used in the last nine years by the NDSU Barley-Breeding Program and the original TP, was the best due to the lower genetic relationship between lines in the program as compared to the original population used previously and the amount of data available by using the combination of the populations. The broader genetic background found in the combined TP will be better at covering a more diverse breeding program.

Next, four different models were compared for their predictive modeling ability for the 24 traits that the NDSU barley breeding program regularly collects data. The models were GBR, RR, PLS, and XGBoost. For each trait, two models were selected as candidates for further analyses based on their mean RSME and correlations between observed and predicted values obtained in the cross-validation model comparisons. Once models were selected, I ran analyses to determine the final model and the minimum number of markers that were needed to predict each trait. Finally, I chose the markers to include on the new chip. The markers were chosen based on the overall frequencies in which they appeared in the cross validation. These markers were retested to predict traits using only the high frequency markers for each trait.

Table 5. Total number of significant markers in each chromosome for new SNP chip

Chromosome	Markers
1H	334
2H	710
3H	492
4H	427
5H	670
6H	586
7H	654
NA	212

The total number of SNP markers to be on the new SNP chip is 4,085. Table 5. summarizes the number of SNPs for each chromosome and Appendix B provides a list of the SNPs, their chromosome, and position. The final step that needs to be done in the next 2-3 years is to determine the efficacy of the new SNP chip in predicting performance for lines that are not part of the training population. Genomic selection for a trait will be deemed successful if the frequency of lines advanced to preliminary yield trials with the desired trait level is higher or equal than would have occurred with phenotypic selection alone.

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APPENDIX A. GENOTYPES USED IN COMBINED POPULATION

Genotype	Pedigree	Years
2ND20798	ND16461-1/ND17266	2007
2ND21089-3	ND18172/ND18076 raw	2011 2012 2013
2ND21867	ND18172/ND19130	2007 2008 2009
2ND22182	ND18413/ND19134//ND19164	2007 2008
2ND22927	Rawson/ND19931	2007 2008
2ND23146	ND18187//ND18370/ND19119-1	2011 2012 2013
2ND24175	Rawson//ND18365/ND20033	2007
2ND24186	ND19130/ND19119-5	2011 2012 2013
2ND24205	ND19852-1/ND20790	2011 2012 2013
2ND24238	ND19854//ND20028/Rawson	2007 2008 2009 2010
2ND24253	ND19855/Rawson	2007
2ND24259	ND19869-1//ND17274/ND19119	2011 2012 2013
2ND24263	ND19869/3/ND18998//ND16092/ND17268	2007 2008 2009 2010
2ND24341	ND19845/5/18427/3/M//16723/4/19088	2011 2012 2013
2ND24365	ND18172-1/ND19974//ND20040-1	2011 2012 2013
2ND24379	ND20824//ND20028/ND19119-1	2011 2012 2013
2ND24383	ND17274/ND19119//ND19854	2007
2ND24385	ND17274/ND19119//ND19854	2007 2011 2012 2013
2ND24388	ND17274/ND19119//ND19854	2007 2008 2009 2010 2011 2012 2013
2ND24393	ND17274/ND19119//ND19854	2007 2008 2011 2012 2013
2ND24424	MUNDA 5/ND19119-1//ND21099	2011 2012 2013
2ND24434	Shenmai 3/ND19119-1//ND21099	2011 2012 2013
2ND24510	ND19119-5*2/ZAU 7	2011 2012 2013
2ND24519	ND19922/ND19130	2011 2012 2013
2ND24527	ND20135-2/ND20794	2007
2ND25253	Rawson sib/ND22087	2007 2008
2ND25265	2ND20801/2ND22122	2007 2008
2ND25270	2ND20802/3/ND19922//ND19929/2ND20177	2007 2008
2ND25272	ND20802/3/ND19922//ND19929/ND20177	2007 2008 2009 2010 2011
2ND25275	ND20802/3/ND19922//ND19929/ND2017	2007 2008
2ND25483	Pinnacle/2ND22180	2007 2008
2ND25484	Pinnacle/2ND22180	2007 2008
2ND26306	ND22996//RAWSON/ND22162	2007 2011 2012 2013
2ND26319	ND21957-2/ND23024	2007 2011 2012 2013
2ND26321	ND21957-2/ND23024	2007 2011 2012 2013
2ND26322	ND21957-2/ND23024	2007 2011 2012 2013
2ND26324	ND21957-2/ND23024	2007 2011 2012 2013
2ND26325	ND21957-2/ND23024	2007 2011 2012 2013
2ND26328	ND22032-2/ND21972	2007 2008 2009 2010
2ND26330	ND22032-2/ND21972	2007 2011 2012 2013

Genotype	Pedigree	Years
2ND26333	ND22032-2/ND21972	2007 2008 2009 2010 2011 2012 2013
2ND26334	ND22032-2/ND21972	2007 2011 2012 2013
2ND26341	C2-00-303-18/ND21089-3	2007 2011 2012 2013
2ND26342	C2-00-303-18/ND21089-3	2007 2011 2012 2013
2ND26346	C2-00-303-18/ND21089-3	2007 2011 2012 2013
2ND26348	ND19854-2/ND22947	2007 2008 2011 2012 2013
2ND26350	ND19854-2/ND22947	2007 2011 2012 2013
2ND26351	ND19854-2/ND22947	2007 2008 2011 2012 2013
2ND26352	SHN105/RAWSON	2007 2011 2012 2013
2ND26361	SHN105/RAWSON	2007 2011 2012 2013
2ND26369	ND23013/RAWSON	2007 2011 2012 2013
2ND26373	ND23013/ND21865-6	2007 2011 2012 2013
2ND26388	ND21089-2//RAWSON/ND22998	2007 2011 2012 2013
2ND26508	ND21089-6/ND23124	2007 2008 2009
2ND26512	ND21089-6/ND23124	2007 2008 2009
2ND26627	ND21871/ND22895	2007 2008
2ND26635	ND22023-2/ND23146	2007 2008 2009
2ND27343	ND24289/ND22996//CONLON	2008 2011 2012 2013
2ND27344	ND24289/ND22996//CONLON	2008 2011 2012 2013
2ND27347	ND23164/ND23146//ND24383	2008 2011 2012 2013
2ND27348	ND23164/ND23146//ND24383	2008 2009 2011 2012 2013
2ND27353	ND23164/ND23146//ND24383	2008 2011 2012 2013
2ND27360	ND23164/ND23146//ND24383	2008 2011 2012 2013
2ND27362	ND22895/ND24490//ND24365	2008 2011 2012 2013
2ND27368	ND24519//ND24289/ND23203	2008 2009 2010 2011 2012 2013
2ND27373	ND24519/ND24383	2008 2011 2012 2013
2ND27374	ND24519/ND24383	2008 2009 2010 2011 2012 2013
2ND27375	ND24519/ND24383	2008 2009 2011 2012 2013
2ND27377	ND24519/ND24383	2008 2011 2012 2013
2ND27378	ND24519/ND24383	2008 2011 2012 2013
2ND27379	ND24519/ND24383	2008 2011 2012 2013
2ND27380	ND24519/ND24383	2008 2011 2012 2013
2ND27390	ND24519/ND24260	2008 2011 2012 2013
2ND27392	ND24519/CONLON	2008 2011 2012 2013
2ND27394	ND24519/CONLON	2008 2011 2012 2013
2ND27395	ND24383/ND24260	2008 2009 2011 2012 2013
2ND27396	ND24383/ND24260	2008 2011 2012 2013
2ND27397	ND24383/ND24260	2008 2009 2011 2012 2013
2ND27403	ND24383/ND24260	2008 2011 2012 2013
2ND27404	ND24383/ND24260	2008 2011 2012 2013
2ND27408	ND24365/ND24519	2008 2011 2012 2013
2ND27416	ND24260//ND23250/ND21089-2	2008 2011 2012 2013

Genotype	Pedigree	Years
2ND27419	ND24260//ND23250/ND21089-2	2008 2011 2012 2013
2ND27440	ND24190/ND22895	2008 2009 2010 2011 2012
2ND27480	ND22996//ND22895/ND24490	2008 2009 2010
2ND27518	ND19922//ND19974/ND19119/3/ND23146	2008 2009 2010 2011 2012 2013
2ND27560	SHN105/ND22947//ND23164	2008 2009 2010
2ND27625	ND24253/ND24519	2008 2009 2010 2011 2012 2013
2ND27628	ND24365/ND24519	2008 2009 2011 2012 2013
2ND27633	ND24519/ND24379	2008 2009 2010 2011 2012 2013
2ND27667	2ND24175/TR05285	2009 2011 2012 2013
2ND27669	2ND24175/TR05285	2009 2011 2012 2013
2ND27670	2ND24175/TR05285	2009 2011 2012 2013
2ND27671	2ND24175/TR05285	2009 2011 2012 2013
2ND27672	2ND24175/TR05285	2009 2011 2012 2013
2ND27673	2ND24175/TR05285	2009 2011 2012 2013
2ND27674	2ND24175/TR05285	2009 2011 2012 2013
2ND27675	2ND24175/TR05285	2009 2011 2012 2013
2ND27676	2ND24175/TR05285	2009 2010 2011 2012 2013
2ND27677	2ND24175/TR05285	2009 2011 2012 2013
2ND27678	2ND24175/TR05285	2009 2010 2011 2012 2013
2ND27681	2ND24266/TR05285	2009 2011 2012 2013
2ND27692	2ND24341/TR05286	2009 2011 2012 2013
2ND27699	2ND24383/TR05285	2009 2010 2011 2012 2013
2ND27702	2ND24383/TR05285	2009 2011 2012 2013
2ND27705	2ND24393/TR05285	2009 2010 2011 2012 2013 2014 2015
2ND27732	TR05286/2ND22927	2009 2010 2011
2ND27767	2ND24383/JB MARY	2009 2010 2011
2ND27830	Pinnacle/2ND24266	2009 2010 2011
2ND27855	Pinnacle/JB MARY	2009 2010 2011
2ND28046	2ND21867/2ND24253	2009 2010 2011
2ND28065	2ND21867/2ND24238	2009 2010 2011 2012 2013 2014 2015 2016 2017 2018
2ND28071	2ND21867/2ND24383	2009 2010 2011 2012 2013
2ND28074	2ND21867/2ND24383	2009 2010 2011
2ND28086	2ND23146/2ND24238	2009 2010 2011
2ND28131	2ND24238/2ND24341	2009 2010 2011 2012 2013
2ND28133	2ND24238/2ND24341	2009 2010 2011
2ND29817	2ND22927/2ND24263	2010 2011 2012 2013
2ND29835	2ND22927/2ND24263	2010 2011 2012
2ND29888	2ND24238/2ND25484	2010 2011 2012
2ND29977	2ND24238/2ND24263	2010 2011 2012
2ND29990	2ND24238/2ND25265	2010 2011 2012 2013
2ND30002	2ND24388/2ND24527	2010 2011 2012 2013
2ND30612	2ND24263/2ND26635	2011 2012 2013

Genotype	Pedigree	Years
2ND30635	2ND25253/Posada	2011 2012
2ND30639	2ND25253/Posada	2011 2012 2013 2014 2015
2ND30658	2ND25253/Posada	2011 2012 2013
2ND30680	2ND25265/2ND25275	2011 2012 2013
2ND30682	2ND25265/2ND25275	2011 2012 2013
2ND30724	2ND25265/2ND26328	2011 2012 2013 2014 2015
2ND30749	2ND25265/2ND26333	2011 2012 2013 2014 2015
2ND30765	2ND25265/2ND26512	2011 2012 2013
2ND30815	2ND25265/2ND26627	2011 2012 2013
2ND30837	2ND25265/Grace	2011 2012 2013 2014 2015 2016
2ND30879	2ND25270/2ND25275	2011 2012 2013 2014 2015
2ND31732	2ND25272/Grace	2012 2013 2014
2ND31815	2ND24263/Grace	2012 2013 2014 2015
2ND31885	2ND24388/2ND25276	2012 2013 2014
2ND31899	2ND24388/2ND26328	2012 2013 2014
2ND31914	2ND252762/Lilly	2012 2013 2014 2015 2016
2ND32008	2ND25272/2ND26512	2012 2013 2014
2ND32014	2ND25272/Lilly	2012 2013 2014
2ND32184	2ND25275/Grace	2012 2013 2014 2015 2016 2017 2018
2ND32205	CDC Bold/2ND25265	2012 2013 2014
2ND32210	CDC Bold/2ND25275	2012 2013 2014
2ND32311	2ND27705/2ND25276	2012 2013 2014 2015
2ND32322	2ND27705/2ND25276	2012 2013 2014 2015 2016
2ND32342	2ND27705/2ND26328	2012 2013 2014 2015
2ND32462	2ND27705/2ND27518	2012 2013 2014 2015
2ND32529	2ND27705/2ND27560	2012 2013 2014 2015 2016 2017 2018
2ND32657	2ND28086/2ND27705	2012 2013 2014 2015 2016 2017 2018
2ND32658	2ND28086/2ND27705	2012 2013 2014 2015 2016
2ND32667	2ND28086/2ND27705	2012 2013 2014 2015
2ND32746	2ND24388/2ND28065	2012 2013 2014 2015
2ND32784	2ND25276/2ND28065	2012 2013 2014
2ND32802	2ND26328/2ND28065	2012 2013 2014
2ND32820	2ND27480/2ND28065	2012 2013 2014
2ND32824	2ND27480/2ND28065	2012 2013 2014 2015
2ND32829	2ND27480/2ND28065	2012 2013 2014 2015 2016 2017 2018
2ND32831	2ND27480/2ND28065	2012 2013 2014 2015
2ND32833	2ND27480/2ND28065	2012 2013 2014 2015
2ND32834	2ND27480/2ND28065	2012 2013 2014 2015
2ND32838	2ND27480/2ND28065	2012 2013 2014 2015
2ND32854	(04/506/42/5)/2ND27480	2012 2013 2014 2015
2ND33669	2ND28065/2ND27767	2014 2015 2016
2ND33672	2ND28065/2ND27767	2014 2015 2016

Genotype	Pedigree	Years
2ND33685	2ND28065/2ND27767	2014 2015 2016
2ND33686	2ND28065/2ND27767	2014 2015 2016
2ND33690	2ND28065/2ND27767	2014 2015 2016
2ND33699	2ND28065/2ND27767	2014 2015 2016
2ND33710	2ND28065/2ND27767	2014 2015 2016 2017 2018
2ND33757	2ND28065/2ND28086	2014 2015 2016 2017 2018
2ND33760	2ND28065/2ND28086	2014 2015 2016 2017 2018
2ND33821	2ND28131/2ND28046	2014 2015 2016 2017 2018
2ND33996	2ND28133/2ND27767	2014 2015 2016
2ND34783	2ND28065/2ND29835	2015 2016
2ND34784	2ND28065/2ND29835	2015 2016
CONLON	BOWMAN*2/DWS1008//ND10232	2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018
PINNACLE	ND18172/ND19130	2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018

APPENDIX B. ALL MARKERS FOR NEW SNP CHIP IN THE NDSU BARLEY BREEDING PROGRAM

Marker	Chromosome	Position (cM)	Position (BP)
SCRI_RS_120059	1H	1.36	1025718
SCRI_RS_60145	1H	5.68	4184290
BOPA1_10922_503	1H	21.99	N/A
BOPA1_6792_1945	1H	26.05	N/A
BOPA1_4226_570	1H	26.32	N/A
SCRI_RS_171221	1H	27.29	17332852
SCRI_RS_183171	1H	45.01	37378707
BOPA1_8613_278	1H	50	N/A
SCRI_RS_149726	1H	50	305524938
BOPA2_12_30478	1H	50.99	N/A
BOPA2_12_30672	1H	50.99	N/A
BOPA2_12_30786	1H	50.99	N/A
SCRI_RS_148600	1H	50.99	380771324
SCRI_RS_198546	1H	51.19	383207519
SCRI_RS_207081	1H	54.5	415035061
BOPA1_3675_2615	1H	64.44	N/A
BOPA1_6142_1544	1H	71.77	N/A
BOPA1_4665_882	1H	72.86	N/A
SCRI_RS_121048	1H	89.04	508312976
BOPA1_3201_603	1H	89.34	N/A
SCRI_RS_17486	1H	89.34	0
SCRI_RS_194371	1H	96.25	513076586
SCRI_RS_171501	1H	101.05	519278467
BOPA1_5336_400	1H	108.4	N/A
BOPA2_12_30532	1H	109.53	N/A
SCRI_RS_224392	1H	122.4	533870871
SCRI_RS_170110	1H	126.9	537711544
SCRI_RS_147611	1H	128.4	539381333
SCRI_RS_165588	1H	128.92	539695184
BOPA2_12_30649	1H	131.66	N/A
BOPA1_3639_969	1H	142.16	N/A
BOPA1_ConsensusGBS0554_4	1H	142.16	N/A
BOPA2_12_11496	1H	142.16	N/A
BOPA1_3263_2865	1H	142.74	N/A
BOPA1_4057_2114	1H	142.74	N/A
JHI_Hv50k_2016_24	1H	N/A	44868
JHI_Hv50k_2016_273	1H	N/A	277479
JHI_Hv50k_2016_284	1H	N/A	278305
JHI_Hv50k_2016_392	1H	N/A	474959

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_721	1H	N/A	944856
JHI_Hv50k_2016_752	1H	N/A	946524
JHI_Hv50k_2016_2322	1H	N/A	2199759
JHI_Hv50k_2016_2693	1H	N/A	2304252
JHI_Hv50k_2016_3293	1H	N/A	3091960
JHI_Hv50k_2016_3888	1H	N/A	3700056
JHI_Hv50k_2016_3891	1H	N/A	3700190
JHI_Hv50k_2016_3897	1H	N/A	3700428
JHI_Hv50k_2016_4173	1H	N/A	3847831
JHI_Hv50k_2016_5029	1H	N/A	4328018
JHI_Hv50k_2016_5228	1H	N/A	4405609
JHI_Hv50k_2016_5337	1H	N/A	4626400
JHI_Hv50k_2016_6437	1H	N/A	5277337
JHI_Hv50k_2016_7035	1H	N/A	5768430
JHI_Hv50k_2016_7404	1H	N/A	6332460
JHI_Hv50k_2016_7618	1H	N/A	6573692
JHI_Hv50k_2016_7965	1H	N/A	7228236
JHI_Hv50k_2016_7983	1H	N/A	7424578
JHI_Hv50k_2016_7985	1H	N/A	7424687
JHI_Hv50k_2016_8173	1H	N/A	7686927
JHI_Hv50k_2016_8214	1H	N/A	7712530
JHI_Hv50k_2016_8493	1H	N/A	8059626
JHI_Hv50k_2016_8618	1H	N/A	8164440
JHI_Hv50k_2016_8793	1H	N/A	8352810
JHI_Hv50k_2016_9237	1H	N/A	8587066
JHI_Hv50k_2016_10260	1H	N/A	9847490
JHI_Hv50k_2016_10265	1H	N/A	9848504
JHI_Hv50k_2016_10642	1H	N/A	11164784
JHI_Hv50k_2016_10782	1H	N/A	11211578
JHI_Hv50k_2016_10800	1H	N/A	11212937
JHI_Hv50k_2016_11098	1H	N/A	11498533
JHI_Hv50k_2016_11229	1H	N/A	11665121
JHI_Hv50k_2016_11408	1H	N/A	11950782
JHI_Hv50k_2016_11753	1H	N/A	12480703
JHI_Hv50k_2016_12547	1H	N/A	13512960
JHI_Hv50k_2016_12594	1H	N/A	13514961
JHI_Hv50k_2016_12669	1H	N/A	13523367
JHI_Hv50k_2016_12682	1H	N/A	13577257
JHI_Hv50k_2016_12965	1H	N/A	13979013
JHI_Hv50k_2016_13282	1H	N/A	14600265
JHI_Hv50k_2016_13325	1H	N/A	14737572
JHI_Hv50k_2016_13782	1H	N/A	16614864

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_13805	1H	N/A	16617700
JHI_Hv50k_2016_14263	1H	N/A	17331521
JHI_Hv50k_2016_14342	1H	N/A	17569802
JHI_Hv50k_2016_14491	1H	N/A	17906562
JHI_Hv50k_2016_14681	1H	N/A	18357862
JHI_Hv50k_2016_15027	1H	N/A	18776441
JHI_Hv50k_2016_18138	1H	N/A	36948781
JHI_Hv50k_2016_18164	1H	N/A	37164706
JHI_Hv50k_2016_18382	1H	N/A	38769152
JHI_Hv50k_2016_19014	1H	N/A	59788441
JHI_Hv50k_2016_21018	1H	N/A	239155791
JHI_Hv50k_2016_21079	1H	N/A	270047714
JHI_Hv50k_2016_21166	1H	N/A	273343057
JHI_Hv50k_2016_22058	1H	N/A	290624056
JHI_Hv50k_2016_22324	1H	N/A	297936968
JHI_Hv50k_2016_23021	1H	N/A	313061576
JHI_Hv50k_2016_23706	1H	N/A	328729616
JHI_Hv50k_2016_26048	1H	N/A	355820267
JHI_Hv50k_2016_26103	1H	N/A	356632379
JHI_Hv50k_2016_27713	1H	N/A	380287505
JHI_Hv50k_2016_27737	1H	N/A	380767247
JHI_Hv50k_2016_27738	1H	N/A	380767406
JHI_Hv50k_2016_27761	1H	N/A	380773532
JHI_Hv50k_2016_27787	1H	N/A	380927946
JHI_Hv50k_2016_27805	1H	N/A	381206778
JHI_Hv50k_2016_27837	1H	N/A	381320833
JHI_Hv50k_2016_27873	1H	N/A	382646302
JHI_Hv50k_2016_28014	1H	N/A	386191079
JHI_Hv50k_2016_30124	1H	N/A	415043149
JHI_Hv50k_2016_30879	1H	N/A	420008547
JHI_Hv50k_2016_31007	1H	N/A	420580355
JHI_Hv50k_2016_31053	1H	N/A	421688736
JHI_Hv50k_2016_31277	1H	N/A	423328374
JHI_Hv50k_2016_31307	1H	N/A	423403343
JHI_Hv50k_2016_31323	1H	N/A	423924422
JHI_Hv50k_2016_31390	1H	N/A	425655548
JHI_Hv50k_2016_31529	1H	N/A	427022223
JHI_Hv50k_2016_32880	1H	N/A	435651052
JHI_Hv50k_2016_33015	1H	N/A	437446680
JHI_Hv50k_2016_33099	1H	N/A	439176975
JHI_Hv50k_2016_33180	1H	N/A	443261926
JHI_Hv50k_2016_33191	1H	N/A	443279736

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_33402	1H	N/A	444533520
JHI_Hv50k_2016_34151	1H	N/A	450208875
JHI_Hv50k_2016_34338	1H	N/A	451730670
JHI_Hv50k_2016_34353	1H	N/A	452223955
JHI_Hv50k_2016_34364	1H	N/A	452493890
JHI_Hv50k_2016_34823	1H	N/A	454532385
JHI_Hv50k_2016_34951	1H	N/A	455156994
JHI_Hv50k_2016_35137	1H	N/A	456203868
JHI_Hv50k_2016_35187	1H	N/A	456559903
JHI_Hv50k_2016_35205	1H	N/A	456592676
JHI_Hv50k_2016_35242	1H	N/A	456852870
JHI_Hv50k_2016_35307	1H	N/A	457845196
JHI_Hv50k_2016_35395	1H	N/A	458198186
JHI_Hv50k_2016_37164	1H	N/A	476740800
JHI_Hv50k_2016_37244	1H	N/A	477605084
JHI_Hv50k_2016_37341	1H	N/A	478254975
JHI_Hv50k_2016_37481	1H	N/A	479077672
JHI_Hv50k_2016_37617	1H	N/A	482740363
JHI_Hv50k_2016_37618	1H	N/A	482741972
JHI_Hv50k_2016_37626	1H	N/A	485705493
JHI_Hv50k_2016_37630	1H	N/A	486184675
JHI_Hv50k_2016_37681	1H	N/A	488845426
JHI_Hv50k_2016_37682	1H	N/A	488845731
JHI_Hv50k_2016_37717	1H	N/A	489138267
JHI_Hv50k_2016_37726	1H	N/A	489144764
JHI_Hv50k_2016_37731	1H	N/A	489146584
JHI_Hv50k_2016_37837	1H	N/A	492697044
JHI_Hv50k_2016_37914	1H	N/A	493988581
JHI_Hv50k_2016_37947	1H	N/A	494247879
JHI_Hv50k_2016_38321	1H	N/A	497144520
JHI_Hv50k_2016_38355	1H	N/A	497470173
JHI_Hv50k_2016_38445	1H	N/A	498028284
JHI_Hv50k_2016_38510	1H	N/A	498204293
JHI_Hv50k_2016_38598	1H	N/A	498570769
JHI_Hv50k_2016_38685	1H	N/A	498707118
JHI_Hv50k_2016_38788	1H	N/A	498980603
JHI_Hv50k_2016_38903	1H	N/A	501010068
JHI_Hv50k_2016_38961	1H	N/A	501363354
JHI_Hv50k_2016_38977	1H	N/A	501616750
JHI_Hv50k_2016_39014	1H	N/A	501990344
JHI_Hv50k_2016_39015	1H	N/A	501990685
JHI_Hv50k_2016_39035	1H	N/A	502238041

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_39043	1H	N/A	502239345
JHI_Hv50k_2016_39146	1H	N/A	503311689
JHI_Hv50k_2016_39220	1H	N/A	503412950
JHI_Hv50k_2016_39288	1H	N/A	503508107
JHI_Hv50k_2016_39362	1H	N/A	503658177
JHI_Hv50k_2016_39364	1H	N/A	503658518
JHI_Hv50k_2016_39423	1H	N/A	503857529
JHI_Hv50k_2016_39438	1H	N/A	504071938
JHI_Hv50k_2016_39462	1H	N/A	504079622
JHI_Hv50k_2016_39526	1H	N/A	504438999
JHI_Hv50k_2016_39666	1H	N/A	504916893
JHI_Hv50k_2016_39694	1H	N/A	504931156
JHI_Hv50k_2016_39710	1H	N/A	505148485
JHI_Hv50k_2016_39821	1H	N/A	505769216
JHI_Hv50k_2016_39860	1H	N/A	506256782
JHI_Hv50k_2016_39884	1H	N/A	506349638
JHI_Hv50k_2016_40174	1H	N/A	507640941
JHI_Hv50k_2016_40175	1H	N/A	507641100
JHI_Hv50k_2016_40213	1H	N/A	507687209
JHI_Hv50k_2016_40367	1H	N/A	507976562
JHI_Hv50k_2016_40412	1H	N/A	508029936
JHI_Hv50k_2016_40640	1H	N/A	508773904
JHI_Hv50k_2016_40970	1H	N/A	509574872
JHI_Hv50k_2016_41028	1H	N/A	509580576
JHI_Hv50k_2016_41035	1H	N/A	509585037
JHI_Hv50k_2016_41065	1H	N/A	509763470
JHI_Hv50k_2016_41168	1H	N/A	510050357
JHI_Hv50k_2016_41171	1H	N/A	510050650
JHI_Hv50k_2016_41432	1H	N/A	511072802
JHI_Hv50k_2016_41445	1H	N/A	511076710
JHI_Hv50k_2016_41684	1H	N/A	511568434
JHI_Hv50k_2016_41900	1H	N/A	512560611
JHI_Hv50k_2016_42315	1H	N/A	513257265
JHI_Hv50k_2016_42352	1H	N/A	513276451
JHI_Hv50k_2016_42551	1H	N/A	514098322
JHI_Hv50k_2016_42553	1H	N/A	514098702
JHI_Hv50k_2016_42866	1H	N/A	515144517
JHI_Hv50k_2016_43206	1H	N/A	516132372
JHI_Hv50k_2016_43633	1H	N/A	517062174
JHI_Hv50k_2016_44458	1H	N/A	518984802
JHI_Hv50k_2016_44526	1H	N/A	519005491
JHI_Hv50k_2016_44643	1H	N/A	519178487

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_44760	1H	N/A	519295390
JHI_Hv50k_2016_44780	1H	N/A	519347869
JHI_Hv50k_2016_45022	1H	N/A	519774271
JHI_Hv50k_2016_45837	1H	N/A	522836612
JHI_Hv50k_2016_46103	1H	N/A	523092455
JHI_Hv50k_2016_46229	1H	N/A	523376160
JHI_Hv50k_2016_46264	1H	N/A	523730536
JHI_Hv50k_2016_46302	1H	N/A	523884520
JHI_Hv50k_2016_46375	1H	N/A	523963926
JHI_Hv50k_2016_46632	1H	N/A	524505027
JHI_Hv50k_2016_46786	1H	N/A	524654451
JHI_Hv50k_2016_47368	1H	N/A	526672388
JHI_Hv50k_2016_47371	1H	N/A	526673015
JHI_Hv50k_2016_47395	1H	N/A	526677841
JHI_Hv50k_2016_47402	1H	N/A	526678767
JHI_Hv50k_2016_47405	1H	N/A	526679248
JHI_Hv50k_2016_47462	1H	N/A	526701480
JHI_Hv50k_2016_47470	1H	N/A	526702588
JHI_Hv50k_2016_47517	1H	N/A	526711095
JHI_Hv50k_2016_47545	1H	N/A	526788238
JHI_Hv50k_2016_48112	1H	N/A	528172048
JHI_Hv50k_2016_48696	1H	N/A	529762084
JHI_Hv50k_2016_48737	1H	N/A	529827330
JHI_Hv50k_2016_48738	1H	N/A	529827450
JHI_Hv50k_2016_49181	1H	N/A	532368222
JHI_Hv50k_2016_50252	1H	N/A	535618266
JHI_Hv50k_2016_50304	1H	N/A	536108741
JHI_Hv50k_2016_50343	1H	N/A	536151709
JHI_Hv50k_2016_50481	1H	N/A	536425459
JHI_Hv50k_2016_50801	1H	N/A	536739230
JHI_Hv50k_2016_50842	1H	N/A	536784046
JHI_Hv50k_2016_50909	1H	N/A	536888527
JHI_Hv50k_2016_50947	1H	N/A	536947347
JHI_Hv50k_2016_50954	1H	N/A	537067636
JHI_Hv50k_2016_50981	1H	N/A	537081214
JHI_Hv50k_2016_51025	1H	N/A	537119089
JHI_Hv50k_2016_51026	1H	N/A	537119168
JHI_Hv50k_2016_51031	1H	N/A	537119868
JHI_Hv50k_2016_51034	1H	N/A	537120468
JHI_Hv50k_2016_51200	1H	N/A	537429320
JHI_Hv50k_2016_51452	1H	N/A	538416630
JHI_Hv50k_2016_51471	1H	N/A	538422783

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_51525	1H	N/A	538483574
JHI_Hv50k_2016_51563	1H	N/A	538504338
JHI_Hv50k_2016_51564	1H	N/A	538504510
JHI_Hv50k_2016_51636	1H	N/A	538584087
JHI_Hv50k_2016_51996	1H	N/A	539129894
JHI_Hv50k_2016_52080	1H	N/A	539694057
JHI_Hv50k_2016_52082	1H	N/A	539694343
JHI_Hv50k_2016_52144	1H	N/A	539807741
JHI_Hv50k_2016_52420	1H	N/A	540811743
JHI_Hv50k_2016_52435	1H	N/A	540819675
JHI_Hv50k_2016_52477	1H	N/A	540987717
JHI_Hv50k_2016_52551	1H	N/A	541120200
JHI_Hv50k_2016_52552	1H	N/A	541120861
JHI_Hv50k_2016_52599	1H	N/A	541488307
JHI_Hv50k_2016_52736	1H	N/A	542206974
JHI_Hv50k_2016_52789	1H	N/A	542282338
JHI_Hv50k_2016_52932	1H	N/A	543063317
JHI_Hv50k_2016_52977	1H	N/A	543219660
JHI_Hv50k_2016_53127	1H	N/A	543803299
JHI_Hv50k_2016_53167	1H	N/A	543859509
JHI_Hv50k_2016_53186	1H	N/A	543861247
JHI_Hv50k_2016_53264	1H	N/A	544041223
JHI_Hv50k_2016_53353	1H	N/A	544586520
JHI_Hv50k_2016_53397	1H	N/A	544735435
JHI_Hv50k_2016_53913	1H	N/A	547222981
JHI_Hv50k_2016_53930	1H	N/A	547238351
JHI_Hv50k_2016_53963	1H	N/A	547251582
JHI_Hv50k_2016_54260	1H	N/A	548077112
JHI_Hv50k_2016_54263	1H	N/A	548124464
JHI_Hv50k_2016_54355	1H	N/A	548352460
JHI_Hv50k_2016_54358	1H	N/A	548352814
JHI_Hv50k_2016_54460	1H	N/A	548699914
JHI_Hv50k_2016_54461	1H	N/A	548700188
JHI_Hv50k_2016_54484	1H	N/A	548713535
JHI_Hv50k_2016_54505	1H	N/A	548750511
JHI_Hv50k_2016_54529	1H	N/A	548766363
JHI_Hv50k_2016_54613	1H	N/A	548905154
JHI_Hv50k_2016_54620	1H	N/A	548928574
JHI_Hv50k_2016_54621	1H	N/A	548929174
JHI_Hv50k_2016_54625	1H	N/A	548932430
JHI_Hv50k_2016_54678	1H	N/A	549112412
JHI_Hv50k_2016_54761	1H	N/A	549184293

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_54763	1H	N/A	549184584
JHI_Hv50k_2016_54829	1H	N/A	549325370
JHI_Hv50k_2016_54830	1H	N/A	549325459
JHI_Hv50k_2016_54850	1H	N/A	549328687
JHI_Hv50k_2016_54852	1H	N/A	549329337
JHI_Hv50k_2016_54855	1H	N/A	549329409
JHI_Hv50k_2016_54862	1H	N/A	549329797
JHI_Hv50k_2016_54979	1H	N/A	549860989
JHI_Hv50k_2016_55006	1H	N/A	550179166
JHI_Hv50k_2016_55085	1H	N/A	550269211
JHI_Hv50k_2016_55121	1H	N/A	550308263
JHI_Hv50k_2016_55188	1H	N/A	550385170
JHI_Hv50k_2016_55342	1H	N/A	550659770
JHI_Hv50k_2016_55370	1H	N/A	550797770
JHI_Hv50k_2016_55395	1H	N/A	550804619
JHI_Hv50k_2016_55454	1H	N/A	551198989
JHI_Hv50k_2016_55455	1H	N/A	551199001
JHI_Hv50k_2016_55533	1H	N/A	551349826
JHI_Hv50k_2016_55570	1H	N/A	551382516
JHI_Hv50k_2016_55968	1H	N/A	553203810
JHI_Hv50k_2016_55969	1H	N/A	553203955
JHI_Hv50k_2016_56077	1H	N/A	553651520
JHI_Hv50k_2016_56198	1H	N/A	553912749
JHI_Hv50k_2016_56290	1H	N/A	554062393
JHI_Hv50k_2016_56331	1H	N/A	554075428
JHI_Hv50k_2016_56413	1H	N/A	554147665
JHI_Hv50k_2016_56431	1H	N/A	554149527
JHI_Hv50k_2016_56490	1H	N/A	554283108
JHI_Hv50k_2016_56682	1H	N/A	554564536
JHI_Hv50k_2016_56683	1H	N/A	554564583
JHI_Hv50k_2016_56732	1H	N/A	554614193
JHI_Hv50k_2016_56816	1H	N/A	554834199
JHI_Hv50k_2016_56967	1H	N/A	555427160
JHI_Hv50k_2016_57024	1H	N/A	555605132
JHI_Hv50k_2016_57152	1H	N/A	555721039
JHI_Hv50k_2016_57256	1H	N/A	556178374
JHI_Hv50k_2016_57290	1H	N/A	556374393
JHI_Hv50k_2016_57491	1H	N/A	556673062
JHI_Hv50k_2016_57497	1H	N/A	556675842
JHI_Hv50k_2016_57547	1H	N/A	556785446
JHI_Hv50k_2016_57728	1H	N/A	556926579
JHI_Hv50k_2016_57831	1H	N/A	557109167

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_57945	1H	N/A	557543558
SCRI_RS_165171	2H	7.99	133816
SCRI_RS_136200	2H	8.29	205010
SCRI_RS_173486	2H	8.29	212492
SCRI_RS_10642	2H	9.79	441233
SCRI_RS_141564	2H	23.56	1215631
BOPA2_12_10777	2H	30.36	1549666
SCRI_RS_210172	2H	31.74	1564888
SCRI_RS_188893	2H	35.04	1766828
SCRI_RS_186448	2H	40.17	2245844
SCRI_RS_115905	2H	41.67	2377500
SCRI_RS_115892	2H	41.77	2763227
SCRI_RS_207244	2H	52.96	2956832
SCRI_RS_78277	2H	52.96	2960326
BOPA1_2964_382	2H	53.26	2967178
SCRI_RS_137093	2H	53.26	3273755
BOPA2_12_30703	2H	63.08	3690178
BOPA1_4065_397	2H	65	3990934
SCRI_RS_182050	2H	65.1	3994132
BOPA1_5113_624	2H	66.11	4549372
BOPA2_12_31288	2H	68.3	6192657
BOPA1_5254_1845	2H	68.7	6193254
SCRI_RS_106444	2H	68.7	6223904
SCRI_RS_131936	2H	68.7	6224431
SCRI_RS_136233	2H	68.7	6225259
SCRI_RS_164343	2H	68.7	6427378
SCRI_RS_186840	2H	68.7	6428257
SCRI_RS_220718	2H	68.7	6432544
BOPA1_3212_2979	2H	68.8	6755738
BOPA1_411_495	2H	68.8	6755829
BOPA1_ABC01644_1_3_379	2H	68.8	6961963
BOPA1_ABC06091_1_1_187	2H	68.8	7046402
BOPA2_12_30828	2H	68.8	7273288
SCRI_RS_135633	2H	68.8	7352365
SCRI_RS_167882	2H	68.8	7489621
SCRI_RS_192676	2H	68.8	7490280
BOPA1_1062_478	2H	69	8035960
BOPA1_2802_685	2H	69	8042647
BOPA1_2998_508	2H	69	8172965
BOPA2_12_10099	2H	69	8470574
BOPA2_12_10474	2H	69	8470764
BOPA2_12_30561	2H	69	8955426

Marker	Chromosome	Position (cM)	Position (BP)
BOPA2_12_30582	2H	69	8994156
SCRI_RS_135468	2H	69	9181416
SCRI_RS_160277	2H	69	9611800
SCRI_RS_170235	2H	69	9612171
SCRI_RS_173145	2H	69	9612335
SCRI_RS_176173	2H	69	9641921
SCRI_RS_182959	2H	69	9658643
SCRI_RS_194604	2H	69	9845349
SCRI_RS_219740	2H	69	10053727
SCRI_RS_220670	2H	69	10054562
SCRI_RS_236995	2H	69	10361143
SCRI_RS_240011	2H	69	10362006
SCRI_RS_55840	2H	69	10388420
SCRI_RS_87934	2H	69	10499572
BOPA1_7489_442	2H	69.55	11186021
BOPA2_12_11278	2H	69.55	11191240
BOPA2_12_30108	2H	69.55	11291582
BOPA2_12_30724	2H	69.55	11315131
SCRI_RS_136740	2H	69.55	11390698
SCRI_RS_153880	2H	69.55	11397291
SCRI_RS_167594	2H	69.55	11633933
SCRI_RS_171203	2H	69.55	11639882
SCRI_RS_195208	2H	69.55	12012221
SCRI_RS_196026	2H	69.55	12012851
SCRI_RS_208320	2H	69.55	12014836
SCRI_RS_231725	2H	69.55	12200019
BOPA1_6510_1430	2H	69.88	12351439
SCRI_RS_153531	2H	72.64	12698266
BOPA2_12_31021	2H	76.26	12864480
BOPA1_7187_382	2H	76.3	12868227
BOPA1_7660_476	2H	76.3	12868404
BOPA1_4037_916	2H	77.34	12950821
BOPA2_12_31383	2H	77.34	12995170
SCRI_RS_156871	2H	77.34	13005058
SCRI_RS_9469	2H	77.54	13109164
BOPA1_2809_271	2H	77.68	13109325
SCRI_RS_133539	2H	85.19	14054382
SCRI_RS_2961	2H	87.34	14266765
BOPA1_6117_1507	2H	88.04	14594798
SCRI_RS_171038	2H	91.69	15377658
BOPA1_6752_1013	2H	93.83	15539994
BOPA1_6024_1095	2H	93.93	16409825

Marker	Chromosome	Position (cM)	Position (BP)
SCRI_RS_219074	2H	95.24	16422753
BOPA1_2020_539	2H	99.04	16650044
SCRI_RS_157140	2H	99.04	16709939
SCRI_RS_2911	2H	99.04	16748926
SCRI_RS_165795	2H	99.24	16749051
SCRI_RS_172220	2H	102.38	16813092
BOPA1_5347_585	2H	106.9	16965052
BOPA1_3206_670	2H	107.47	17271661
BOPA2_12_30480	2H	108.14	17542569
BOPA1_8523_316	2H	110.49	17790711
BOPA1_7487_390	2H	125.56	18296352
BOPA1_868_675	2H	125.76	18297459
BOPA1_ABC05640_1_1_248	2H	125.76	18515806
SCRI_RS_190073	2H	125.76	18519602
SCRI_RS_222093	2H	125.76	18519653
SCRI_RS_156220	2H	127.36	18658962
SCRI_RS_154176	2H	133.16	18679787
SCRI_RS_12444	2H	134.66	18759723
SCRI_RS_149429	2H	135.36	18811200
BOPA1_5541_418	2H	136.06	19008576
BOPA2_12_30152	2H	138.13	19468650
SCRI_RS_159243	2H	138.13	19618409
SCRI_RS_205807	2H	138.13	19618508
BOPA1_4218_1230	2H	142.03	19824395
BOPA1_8817_798	2H	143.07	19900675
BOPA1_9291_1322	2H	143.07	19901760
BOPA2_12_20183	2H	143.1	19959481
SCRI_RS_238605	2H	148.3	20580400
SCRI_RS_204022	2H	150.2	21397578
SCRI_RS_230951	2H	157.42	22221728
BOPA1_4879_1560	2H	160.69	22375016
SCRI_RS_205658	2H	160.69	22446535
SCRI_RS_161636	2H	162.76	22770248
BOPA1_2052_792	2H	163.46	22770395
SCRI_RS_134343	2H	168.73	23304373
BOPA1_1283_332	2H	171.55	23431465
BOPA2_12_31527	2H	171.85	23432118
BOPA1_3450_692	2H	175.48	24559665
BOPA1_9910_427	2H	175.48	24565145
JHI_Hv50k_2016_58540	2H	N/A	26301027
JHI_Hv50k_2016_58568	2H	N/A	26302933
JHI_Hv50k_2016_58577	2H	N/A	26303593

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_58608	2H	N/A	26589581
JHI_Hv50k_2016_58666	2H	N/A	26934749
JHI_Hv50k_2016_58973	2H	N/A	27043220
JHI_Hv50k_2016_59024	2H	N/A	27043413
JHI_Hv50k_2016_59032	2H	N/A	27174235
JHI_Hv50k_2016_59344	2H	N/A	27512682
JHI_Hv50k_2016_59964	2H	N/A	28769684
JHI_Hv50k_2016_60178	2H	N/A	28949582
JHI_Hv50k_2016_60227	2H	N/A	29040103
JHI_Hv50k_2016_60329	2H	N/A	29201894
JHI_Hv50k_2016_60646	2H	N/A	29669343
JHI_Hv50k_2016_60694	2H	N/A	29669609
JHI_Hv50k_2016_60708	2H	N/A	29918572
JHI_Hv50k_2016_60770	2H	N/A	30188357
JHI_Hv50k_2016_61157	2H	N/A	31153517
JHI_Hv50k_2016_61289	2H	N/A	31212881
JHI_Hv50k_2016_61321	2H	N/A	31563084
JHI_Hv50k_2016_61823	2H	N/A	32081674
JHI_Hv50k_2016_62144	2H	N/A	33900600
JHI_Hv50k_2016_62154	2H	N/A	33900891
JHI_Hv50k_2016_62805	2H	N/A	35715124
JHI_Hv50k_2016_62968	2H	N/A	35771387
JHI_Hv50k_2016_63100	2H	N/A	37030503
JHI_Hv50k_2016_63101	2H	N/A	37204390
JHI_Hv50k_2016_63210	2H	N/A	37726739
JHI_Hv50k_2016_63322	2H	N/A	37966041
JHI_Hv50k_2016_63369	2H	N/A	38084142
JHI_Hv50k_2016_63733	2H	N/A	38248974
JHI_Hv50k_2016_63977	2H	N/A	38384093
JHI_Hv50k_2016_63979	2H	N/A	38600629
JHI_Hv50k_2016_64055	2H	N/A	38600698
JHI_Hv50k_2016_64151	2H	N/A	38839083
JHI_Hv50k_2016_64531	2H	N/A	39896757
JHI_Hv50k_2016_64584	2H	N/A	39902482
JHI_Hv50k_2016_64592	2H	N/A	39979539
JHI_Hv50k_2016_64656	2H	N/A	40287059
JHI_Hv50k_2016_64670	2H	N/A	40851553
JHI_Hv50k_2016_65186	2H	N/A	44648329
JHI_Hv50k_2016_65312	2H	N/A	44786265
JHI_Hv50k_2016_65392	2H	N/A	44861965
JHI_Hv50k_2016_65426	2H	N/A	45103314
JHI_Hv50k_2016_65427	2H	N/A	45103718

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_67577	2H	N/A	48452862
JHI_Hv50k_2016_68102	2H	N/A	50530026
JHI_Hv50k_2016_68256	2H	N/A	50937741
JHI_Hv50k_2016_68480	2H	N/A	51928516
JHI_Hv50k_2016_68514	2H	N/A	51932747
JHI_Hv50k_2016_68734	2H	N/A	52794715
JHI_Hv50k_2016_68843	2H	N/A	53704078
JHI_Hv50k_2016_68866	2H	N/A	53708928
JHI_Hv50k_2016_68901	2H	N/A	53903306
JHI_Hv50k_2016_68911	2H	N/A	53908188
JHI_Hv50k_2016_68928	2H	N/A	54582922
JHI_Hv50k_2016_68940	2H	N/A	54787893
JHI_Hv50k_2016_69230	2H	N/A	57276616
JHI_Hv50k_2016_69235	2H	N/A	57276880
JHI_Hv50k_2016_69616	2H	N/A	58536665
JHI_Hv50k_2016_69628	2H	N/A	58545016
JHI_Hv50k_2016_69929	2H	N/A	62038309
JHI_Hv50k_2016_70074	2H	N/A	65089245
JHI_Hv50k_2016_70091	2H	N/A	65412470
JHI_Hv50k_2016_70544	2H	N/A	66380571
JHI_Hv50k_2016_70617	2H	N/A	67516405
JHI_Hv50k_2016_70646	2H	N/A	67705049
JHI_Hv50k_2016_70745	2H	N/A	68011794
JHI_Hv50k_2016_70765	2H	N/A	68014106
JHI_Hv50k_2016_70801	2H	N/A	68481553
JHI_Hv50k_2016_70833	2H	N/A	68631940
JHI_Hv50k_2016_70945	2H	N/A	69925476
JHI_Hv50k_2016_71066	2H	N/A	72243329
JHI_Hv50k_2016_71113	2H	N/A	72279054
JHI_Hv50k_2016_71121	2H	N/A	72729981
JHI_Hv50k_2016_71139	2H	N/A	73401463
JHI_Hv50k_2016_71918	2H	N/A	75980517
JHI_Hv50k_2016_72354	2H	N/A	78373556
JHI_Hv50k_2016_72708	2H	N/A	79860409
JHI_Hv50k_2016_72712	2H	N/A	80109528
JHI_Hv50k_2016_72715	2H	N/A	80390188
JHI_Hv50k_2016_72718	2H	N/A	80842053
JHI_Hv50k_2016_72853	2H	N/A	81229274
JHI_Hv50k_2016_72946	2H	N/A	82495191
JHI_Hv50k_2016_72949	2H	N/A	82524951
JHI_Hv50k_2016_73026	2H	N/A	83157027
JHI_Hv50k_2016_73140	2H	N/A	83430590

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_74875	2H	N/A	100641956
JHI_Hv50k_2016_74914	2H	N/A	100644454
JHI_Hv50k_2016_74920	2H	N/A	101120783
JHI_Hv50k_2016_75013	2H	N/A	101445958
JHI_Hv50k_2016_75090	2H	N/A	102391719
JHI_Hv50k_2016_75091	2H	N/A	102391829
JHI_Hv50k_2016_75178	2H	N/A	102395346
JHI_Hv50k_2016_75197	2H	N/A	102398281
JHI_Hv50k_2016_75198	2H	N/A	102511236
JHI_Hv50k_2016_75251	2H	N/A	103694991
JHI_Hv50k_2016_75253	2H	N/A	104089257
JHI_Hv50k_2016_75255	2H	N/A	104089718
JHI_Hv50k_2016_75278	2H	N/A	105046329
JHI_Hv50k_2016_75316	2H	N/A	105468151
JHI_Hv50k_2016_75493	2H	N/A	107982415
JHI_Hv50k_2016_75502	2H	N/A	107982432
JHI_Hv50k_2016_75908	2H	N/A	110812545
JHI_Hv50k_2016_75915	2H	N/A	111449554
JHI_Hv50k_2016_75950	2H	N/A	111802892
JHI_Hv50k_2016_75954	2H	N/A	112363303
JHI_Hv50k_2016_76081	2H	N/A	113048065
JHI_Hv50k_2016_77176	2H	N/A	123602929
JHI_Hv50k_2016_77416	2H	N/A	128351383
JHI_Hv50k_2016_77474	2H	N/A	129647065
JHI_Hv50k_2016_77519	2H	N/A	129961258
JHI_Hv50k_2016_77812	2H	N/A	147159492
JHI_Hv50k_2016_77884	2H	N/A	150100384
JHI_Hv50k_2016_77964	2H	N/A	158745630
JHI_Hv50k_2016_78157	2H	N/A	163001614
JHI_Hv50k_2016_78199	2H	N/A	167096509
JHI_Hv50k_2016_78221	2H	N/A	167687200
JHI_Hv50k_2016_78264	2H	N/A	168144872
JHI_Hv50k_2016_78345	2H	N/A	172220450
JHI_Hv50k_2016_78593	2H	N/A	177377775
JHI_Hv50k_2016_78627	2H	N/A	179219322
JHI_Hv50k_2016_78835	2H	N/A	185900649
JHI_Hv50k_2016_79131	2H	N/A	196202069
JHI_Hv50k_2016_79228	2H	N/A	197579359
JHI_Hv50k_2016_79235	2H	N/A	197904020
JHI_Hv50k_2016_79451	2H	N/A	214721799
JHI_Hv50k_2016_80540	2H	N/A	397766385
JHI_Hv50k_2016_80701	2H	N/A	405153153

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_80839	2H	N/A	432600983
JHI_Hv50k_2016_81017	2H	N/A	443116026
JHI_Hv50k_2016_81375	2H	N/A	463681631
JHI_Hv50k_2016_81420	2H	N/A	464533269
JHI_Hv50k_2016_81426	2H	N/A	464802619
JHI_Hv50k_2016_83843	2H	N/A	549097403
JHI_Hv50k_2016_83876	2H	N/A	549644400
JHI_Hv50k_2016_84334	2H	N/A	567328834
JHI_Hv50k_2016_84359	2H	N/A	570839933
JHI_Hv50k_2016_84372	2H	N/A	570928925
JHI_Hv50k_2016_85001	2H	N/A	585986296
JHI_Hv50k_2016_85799	2H	N/A	611113648
JHI_Hv50k_2016_85965	2H	N/A	611855771
JHI_Hv50k_2016_86080	2H	N/A	612016780
JHI_Hv50k_2016_86571	2H	N/A	614343724
JHI_Hv50k_2016_87405	2H	N/A	619596637
JHI_Hv50k_2016_87501	2H	N/A	620112577
JHI_Hv50k_2016_87510	2H	N/A	620115148
JHI_Hv50k_2016_87514	2H	N/A	620115236
JHI_Hv50k_2016_87585	2H	N/A	620615023
JHI_Hv50k_2016_87608	2H	N/A	620784840
JHI_Hv50k_2016_87610	2H	N/A	620785633
JHI_Hv50k_2016_87627	2H	N/A	620805246
JHI_Hv50k_2016_87770	2H	N/A	621068730
JHI_Hv50k_2016_87809	2H	N/A	621071980
JHI_Hv50k_2016_87838	2H	N/A	621116571
JHI_Hv50k_2016_87850	2H	N/A	621116966
JHI_Hv50k_2016_87899	2H	N/A	621298533
JHI_Hv50k_2016_87973	2H	N/A	621473379
JHI_Hv50k_2016_87976	2H	N/A	621781761
JHI_Hv50k_2016_88014	2H	N/A	621793627
JHI_Hv50k_2016_88019	2H	N/A	621793862
JHI_Hv50k_2016_88059	2H	N/A	622757766
JHI_Hv50k_2016_88665	2H	N/A	624657512
JHI_Hv50k_2016_89612	2H	N/A	628422355
JHI_Hv50k_2016_90179	2H	N/A	631095446
JHI_Hv50k_2016_90243	2H	N/A	631136794
JHI_Hv50k_2016_90347	2H	N/A	632310865
JHI_Hv50k_2016_90385	2H	N/A	632316539
JHI_Hv50k_2016_90572	2H	N/A	632678632
JHI_Hv50k_2016_90623	2H	N/A	633738901
JHI_Hv50k_2016_90638	2H	N/A	633763055

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_90688	2H	N/A	634090673
JHI_Hv50k_2016_90856	2H	N/A	635549634
JHI_Hv50k_2016_90865	2H	N/A	635651686
JHI_Hv50k_2016_90954	2H	N/A	635860279
JHI_Hv50k_2016_90971	2H	N/A	635867055
JHI_Hv50k_2016_90993	2H	N/A	635867081
JHI_Hv50k_2016_91056	2H	N/A	636432184
JHI_Hv50k_2016_91125	2H	N/A	636549434
JHI_Hv50k_2016_91201	2H	N/A	638240562
JHI_Hv50k_2016_91660	2H	N/A	638687907
JHI_Hv50k_2016_91952	2H	N/A	638690416
JHI_Hv50k_2016_92462	2H	N/A	640058219
JHI_Hv50k_2016_92557	2H	N/A	640340121
JHI_Hv50k_2016_92907	2H	N/A	641328020
JHI_Hv50k_2016_92911	2H	N/A	641328977
JHI_Hv50k_2016_93108	2H	N/A	642176084
JHI_Hv50k_2016_93785	2H	N/A	645215930
JHI_Hv50k_2016_95083	2H	N/A	649447490
JHI_Hv50k_2016_95813	2H	N/A	649648905
JHI_Hv50k_2016_96175	2H	N/A	649826144
JHI_Hv50k_2016_97345	2H	N/A	651465209
JHI_Hv50k_2016_98660	2H	N/A	655112752
JHI_Hv50k_2016_98851	2H	N/A	655401659
JHI_Hv50k_2016_98853	2H	N/A	655480078
JHI_Hv50k_2016_98889	2H	N/A	655481375
JHI_Hv50k_2016_98931	2H	N/A	655481954
JHI_Hv50k_2016_99332	2H	N/A	656413721
JHI_Hv50k_2016_99374	2H	N/A	656596131
JHI_Hv50k_2016_99486	2H	N/A	657354011
JHI_Hv50k_2016_99495	2H	N/A	657354366
JHI_Hv50k_2016_99929	2H	N/A	657753145
JHI_Hv50k_2016_100077	2H	N/A	658901951
JHI_Hv50k_2016_100667	2H	N/A	663679067
JHI_Hv50k_2016_100960	2H	N/A	669741446
JHI_Hv50k_2016_101012	2H	N/A	670616035
JHI_Hv50k_2016_101096	2H	N/A	671202036
JHI_Hv50k_2016_101233	2H	N/A	672370933
JHI_Hv50k_2016_101262	2H	N/A	672582732
JHI_Hv50k_2016_101297	2H	N/A	672931114
JHI_Hv50k_2016_101424	2H	N/A	673850109
JHI_Hv50k_2016_101459	2H	N/A	673852868
JHI_Hv50k_2016_101515	2H	N/A	674145076

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_101516	2H	N/A	674148296
JHI_Hv50k_2016_101549	2H	N/A	674150766
JHI_Hv50k_2016_101585	2H	N/A	674156009
JHI_Hv50k_2016_101631	2H	N/A	674255908
JHI_Hv50k_2016_101735	2H	N/A	674965396
JHI_Hv50k_2016_101742	2H	N/A	674966614
JHI_Hv50k_2016_101910	2H	N/A	676535301
JHI_Hv50k_2016_101914	2H	N/A	676535432
JHI_Hv50k_2016_102062	2H	N/A	676766638
JHI_Hv50k_2016_102138	2H	N/A	676852798
JHI_Hv50k_2016_102158	2H	N/A	676985724
JHI_Hv50k_2016_102223	2H	N/A	677079528
JHI_Hv50k_2016_102254	2H	N/A	677132462
JHI_Hv50k_2016_102255	2H	N/A	677132643
JHI_Hv50k_2016_102268	2H	N/A	677197708
JHI_Hv50k_2016_102289	2H	N/A	677257391
JHI_Hv50k_2016_102606	2H	N/A	677541154
JHI_Hv50k_2016_102625	2H	N/A	677541234
JHI_Hv50k_2016_102739	2H	N/A	678192246
JHI_Hv50k_2016_102748	2H	N/A	678192979
JHI_Hv50k_2016_103007	2H	N/A	679906317
JHI_Hv50k_2016_103135	2H	N/A	681290440
JHI_Hv50k_2016_104046	2H	N/A	685908201
JHI_Hv50k_2016_104839	2H	N/A	687827381
JHI_Hv50k_2016_105493	2H	N/A	688787136
JHI_Hv50k_2016_105615	2H	N/A	689293132
JHI_Hv50k_2016_106126	2H	N/A	690777651
JHI_Hv50k_2016_106155	2H	N/A	690974068
JHI_Hv50k_2016_106893	2H	N/A	692407406
JHI_Hv50k_2016_107445	2H	N/A	693683494
JHI_Hv50k_2016_107681	2H	N/A	694019755
JHI_Hv50k_2016_108145	2H	N/A	694517288
JHI_Hv50k_2016_108296	2H	N/A	695304821
JHI_Hv50k_2016_108325	2H	N/A	695392182
JHI_Hv50k_2016_108465	2H	N/A	695639360
JHI_Hv50k_2016_108466	2H	N/A	695778792
JHI_Hv50k_2016_108518	2H	N/A	695881923
JHI_Hv50k_2016_108868	2H	N/A	695915844
JHI_Hv50k_2016_108926	2H	N/A	696116916
JHI_Hv50k_2016_109299	2H	N/A	696780914
JHI_Hv50k_2016_109411	2H	N/A	697191257
JHI_Hv50k_2016_109418	2H	N/A	697192263

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_109430	2H	N/A	697520666
JHI_Hv50k_2016_109494	2H	N/A	698220223
JHI_Hv50k_2016_109499	2H	N/A	698220684
JHI_Hv50k_2016_109641	2H	N/A	698668470
JHI_Hv50k_2016_109666	2H	N/A	698876917
JHI_Hv50k_2016_109698	2H	N/A	698915052
JHI_Hv50k_2016_109711	2H	N/A	699045160
JHI_Hv50k_2016_109824	2H	N/A	699224738
JHI_Hv50k_2016_109837	2H	N/A	699312607
JHI_Hv50k_2016_109843	2H	N/A	699312820
JHI_Hv50k_2016_109861	2H	N/A	699323903
JHI_Hv50k_2016_109902	2H	N/A	699324511
JHI_Hv50k_2016_109909	2H	N/A	699436220
JHI_Hv50k_2016_109912	2H	N/A	699436638
JHI_Hv50k_2016_109914	2H	N/A	699438244
JHI_Hv50k_2016_109934	2H	N/A	699445006
JHI_Hv50k_2016_110014	2H	N/A	699804411
JHI_Hv50k_2016_110124	2H	N/A	700120815
JHI_Hv50k_2016_110146	2H	N/A	700120890
JHI_Hv50k_2016_110190	2H	N/A	700121605
JHI_Hv50k_2016_110594	2H	N/A	700560336
JHI_Hv50k_2016_110773	2H	N/A	701025110
JHI_Hv50k_2016_111050	2H	N/A	702956693
JHI_Hv50k_2016_111072	2H	N/A	703319885
JHI_Hv50k_2016_111150	2H	N/A	703356864
JHI_Hv50k_2016_111156	2H	N/A	703472827
JHI_Hv50k_2016_111157	2H	N/A	703645495
JHI_Hv50k_2016_111369	2H	N/A	703980010
JHI_Hv50k_2016_111436	2H	N/A	704121722
JHI_Hv50k_2016_111657	2H	N/A	704392546
JHI_Hv50k_2016_112097	2H	N/A	705593048
JHI_Hv50k_2016_112182	2H	N/A	706345003
JHI_Hv50k_2016_112768	2H	N/A	707154844
JHI_Hv50k_2016_112813	2H	N/A	707380176
JHI_Hv50k_2016_112814	2H	N/A	707380483
JHI_Hv50k_2016_113288	2H	N/A	708254136
JHI_Hv50k_2016_113385	2H	N/A	708562737
JHI_Hv50k_2016_113410	2H	N/A	708564600
JHI_Hv50k_2016_113411	2H	N/A	708564863
JHI_Hv50k_2016_113444	2H	N/A	708638025
JHI_Hv50k_2016_113490	2H	N/A	708848376
JHI_Hv50k_2016_113491	2H	N/A	708848558

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_113514	2H	N/A	708860425
JHI_Hv50k_2016_113518	2H	N/A	708863067
JHI_Hv50k_2016_113525	2H	N/A	708863235
JHI_Hv50k_2016_113528	2H	N/A	708968651
JHI_Hv50k_2016_113569	2H	N/A	708994395
JHI_Hv50k_2016_113577	2H	N/A	708994486
JHI_Hv50k_2016_113582	2H	N/A	708994595
JHI_Hv50k_2016_113598	2H	N/A	709122025
JHI_Hv50k_2016_113633	2H	N/A	709326820
JHI_Hv50k_2016_113642	2H	N/A	709348203
JHI_Hv50k_2016_113715	2H	N/A	709593946
JHI_Hv50k_2016_113753	2H	N/A	709630820
JHI_Hv50k_2016_113836	2H	N/A	710148532
JHI_Hv50k_2016_113855	2H	N/A	710162911
JHI_Hv50k_2016_113866	2H	N/A	710163569
JHI_Hv50k_2016_113871	2H	N/A	710164460
JHI_Hv50k_2016_113950	2H	N/A	710748144
JHI_Hv50k_2016_113997	2H	N/A	710843638
JHI_Hv50k_2016_114023	2H	N/A	710858744
JHI_Hv50k_2016_114071	2H	N/A	710952994
JHI_Hv50k_2016_114428	2H	N/A	712676153
JHI_Hv50k_2016_114491	2H	N/A	712797520
JHI_Hv50k_2016_114548	2H	N/A	713101192
JHI_Hv50k_2016_114549	2H	N/A	713111720
JHI_Hv50k_2016_114596	2H	N/A	713241243
JHI_Hv50k_2016_114620	2H	N/A	713711618
JHI_Hv50k_2016_114706	2H	N/A	713744262
JHI_Hv50k_2016_114762	2H	N/A	713820081
JHI_Hv50k_2016_114817	2H	N/A	714102734
JHI_Hv50k_2016_114948	2H	N/A	715380972
JHI_Hv50k_2016_114965	2H	N/A	715587188
JHI_Hv50k_2016_115172	2H	N/A	716364517
JHI_Hv50k_2016_115174	2H	N/A	716364887
JHI_Hv50k_2016_115176	2H	N/A	716369087
JHI_Hv50k_2016_115191	2H	N/A	716478426
JHI_Hv50k_2016_115200	2H	N/A	716480377
JHI_Hv50k_2016_115210	2H	N/A	716482621
JHI_Hv50k_2016_115245	2H	N/A	716589500
JHI_Hv50k_2016_115450	2H	N/A	717373251
JHI_Hv50k_2016_115451	2H	N/A	717608710
JHI_Hv50k_2016_115461	2H	N/A	717611197
JHI_Hv50k_2016_115468	2H	N/A	717611446

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_115492	2H	N/A	717873016
JHI_Hv50k_2016_115517	2H	N/A	717878163
JHI_Hv50k_2016_115825	2H	N/A	720093215
JHI_Hv50k_2016_116779	2H	N/A	724913360
JHI_Hv50k_2016_116859	2H	N/A	724986617
JHI_Hv50k_2016_116864	2H	N/A	725103565
JHI_Hv50k_2016_116946	2H	N/A	725230278
JHI_Hv50k_2016_117112	2H	N/A	725658581
JHI_Hv50k_2016_117210	2H	N/A	726012437
JHI_Hv50k_2016_117256	2H	N/A	726021847
JHI_Hv50k_2016_117431	2H	N/A	726970655
JHI_Hv50k_2016_117448	2H	N/A	727209488
JHI_Hv50k_2016_117509	2H	N/A	727355157
JHI_Hv50k_2016_117529	2H	N/A	727484106
JHI_Hv50k_2016_117560	2H	N/A	727485379
JHI_Hv50k_2016_117563	2H	N/A	727570672
JHI_Hv50k_2016_117674	2H	N/A	727650304
JHI_Hv50k_2016_117675	2H	N/A	727652449
JHI_Hv50k_2016_117736	2H	N/A	728043143
JHI_Hv50k_2016_117807	2H	N/A	728045350
JHI_Hv50k_2016_117874	2H	N/A	728159388
JHI_Hv50k_2016_117898	2H	N/A	728240963
JHI_Hv50k_2016_117939	2H	N/A	728298636
JHI_Hv50k_2016_118118	2H	N/A	729222272
JHI_Hv50k_2016_118163	2H	N/A	729222603
JHI_Hv50k_2016_118203	2H	N/A	729223358
JHI_Hv50k_2016_118223	2H	N/A	729223571
JHI_Hv50k_2016_118273	2H	N/A	729229245
JHI_Hv50k_2016_118293	2H	N/A	729235967
JHI_Hv50k_2016_118422	2H	N/A	729295251
JHI_Hv50k_2016_118494	2H	N/A	729506693
JHI_Hv50k_2016_118780	2H	N/A	730029104
JHI_Hv50k_2016_118807	2H	N/A	730029515
JHI_Hv50k_2016_118995	2H	N/A	731272759
JHI_Hv50k_2016_119027	2H	N/A	731305353
JHI_Hv50k_2016_119167	2H	N/A	732424023
JHI_Hv50k_2016_119199	2H	N/A	732543479
JHI_Hv50k_2016_119243	2H	N/A	732618705
JHI_Hv50k_2016_119256	2H	N/A	732633801
JHI_Hv50k_2016_119334	2H	N/A	732702705
JHI_Hv50k_2016_119408	2H	N/A	732706943
JHI_Hv50k_2016_119419	2H	N/A	732708605

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_119518	2H	N/A	733399294
JHI_Hv50k_2016_119586	2H	N/A	733462774
JHI_Hv50k_2016_119653	2H	N/A	733462948
JHI_Hv50k_2016_120115	2H	N/A	733688511
JHI_Hv50k_2016_120125	2H	N/A	733688790
JHI_Hv50k_2016_120244	2H	N/A	733925058
JHI_Hv50k_2016_120332	2H	N/A	734189807
JHI_Hv50k_2016_120481	2H	N/A	734431895
JHI_Hv50k_2016_120520	2H	N/A	734501016
JHI_Hv50k_2016_120563	2H	N/A	734856781
JHI_Hv50k_2016_120639	2H	N/A	734859614
JHI_Hv50k_2016_120660	2H	N/A	735081153
JHI_Hv50k_2016_120717	2H	N/A	735115161
JHI_Hv50k_2016_120806	2H	N/A	735300130
JHI_Hv50k_2016_120824	2H	N/A	735302807
JHI_Hv50k_2016_120825	2H	N/A	735309362
JHI_Hv50k_2016_120907	2H	N/A	735390224
JHI_Hv50k_2016_120980	2H	N/A	736214477
JHI_Hv50k_2016_121126	2H	N/A	736298543
JHI_Hv50k_2016_121151	2H	N/A	736751512
JHI_Hv50k_2016_121350	2H	N/A	737639643
JHI_Hv50k_2016_121464	2H	N/A	738013879
JHI_Hv50k_2016_121708	2H	N/A	738342065
JHI_Hv50k_2016_121813	2H	N/A	738614758
JHI_Hv50k_2016_122089	2H	N/A	739146287
JHI_Hv50k_2016_122286	2H	N/A	739332214
JHI_Hv50k_2016_122516	2H	N/A	740414463
JHI_Hv50k_2016_122743	2H	N/A	740991508
JHI_Hv50k_2016_123653	2H	N/A	742067073
JHI_Hv50k_2016_123879	2H	N/A	742103920
JHI_Hv50k_2016_124110	2H	N/A	742203037
JHI_Hv50k_2016_124427	2H	N/A	743138631
JHI_Hv50k_2016_124437	2H	N/A	743139400
JHI_Hv50k_2016_124450	2H	N/A	743140689
JHI_Hv50k_2016_124462	2H	N/A	743142768
JHI_Hv50k_2016_124463	2H	N/A	743143121
JHI_Hv50k_2016_124472	2H	N/A	743143663
JHI_Hv50k_2016_124927	2H	N/A	743455786
JHI_Hv50k_2016_124972	2H	N/A	743753531
JHI_Hv50k_2016_124974	2H	N/A	743758316
JHI_Hv50k_2016_125290	2H	N/A	744583482
JHI_Hv50k_2016_125328	2H	N/A	744774301

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_125349	2H	N/A	744775750
JHI_Hv50k_2016_125359	2H	N/A	744825209
JHI_Hv50k_2016_125427	2H	N/A	744833374
JHI_Hv50k_2016_125449	2H	N/A	744898426
JHI_Hv50k_2016_125451	2H	N/A	744898525
JHI_Hv50k_2016_125681	2H	N/A	744900332
JHI_Hv50k_2016_125747	2H	N/A	745070219
JHI_Hv50k_2016_125778	2H	N/A	745271769
JHI_Hv50k_2016_125845	2H	N/A	745320358
JHI_Hv50k_2016_125904	2H	N/A	745320843
JHI_Hv50k_2016_126153	2H	N/A	745360336
JHI_Hv50k_2016_126452	2H	N/A	746482987
JHI_Hv50k_2016_127497	2H	N/A	749604221
JHI_Hv50k_2016_127506	2H	N/A	749741637
JHI_Hv50k_2016_128077	2H	N/A	750812375
JHI_Hv50k_2016_128314	2H	N/A	751207045
JHI_Hv50k_2016_128362	2H	N/A	751639819
JHI_Hv50k_2016_128451	2H	N/A	751898115
JHI_Hv50k_2016_128509	2H	N/A	751961010
JHI_Hv50k_2016_128530	2H	N/A	752027338
JHI_Hv50k_2016_128726	2H	N/A	753016178
JHI_Hv50k_2016_128784	2H	N/A	753099360
JHI_Hv50k_2016_129614	2H	N/A	754503668
JHI_Hv50k_2016_129807	2H	N/A	754624512
JHI_Hv50k_2016_130223	2H	N/A	755181466
JHI_Hv50k_2016_131503	2H	N/A	758556234
JHI_Hv50k_2016_132251	2H	N/A	760184175
JHI_Hv50k_2016_132258	2H	N/A	760725412
JHI_Hv50k_2016_132262	2H	N/A	760725754
JHI_Hv50k_2016_132415	2H	N/A	761107172
JHI_Hv50k_2016_132416	2H	N/A	761107447
JHI_Hv50k_2016_132762	2H	N/A	762708157
JHI_Hv50k_2016_132930	2H	N/A	764283631
JHI_Hv50k_2016_132982	2H	N/A	764420583
JHI_Hv50k_2016_132988	2H	N/A	764424264
JHI_Hv50k_2016_133067	2H	N/A	765158629
JHI_Hv50k_2016_133076	2H	N/A	765606488
JHI_Hv50k_2016_133378	2H	N/A	766100032
JHI_Hv50k_2016_133445	2H	N/A	766143832
JHI_Hv50k_2016_133476	2H	N/A	766144463
JHI_Hv50k_2016_133490	2H	N/A	766316093
JHI_Hv50k_2016_133534	2H	N/A	767018019

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_133699	2H	N/A	767300010
JHI_Hv50k_2016_133856	2H	N/A	767354172
JHI_Hv50k_2016_133873	2H	N/A	767604185
JHI_Hv50k_2016_134208	2H	N/A	254221
JHI_Hv50k_2016_134209	2H	N/A	257509
JHI_Hv50k_2016_134751	2H	N/A	586783
JHI_Hv50k_2016_134862	2H	N/A	643774
JHI_Hv50k_2016_134947	2H	N/A	1004506
JHI_Hv50k_2016_135055	2H	N/A	1115868
JHI_Hv50k_2016_135056	2H	N/A	1116868
JHI_Hv50k_2016_135143	2H	N/A	1118782
JHI_Hv50k_2016_135188	2H	N/A	1118987
JHI_Hv50k_2016_135357	2H	N/A	1122983
JHI_Hv50k_2016_135438	2H	N/A	1124681
JHI_Hv50k_2016_135561	2H	N/A	1125596
JHI_Hv50k_2016_135562	2H	N/A	1125712
JHI_Hv50k_2016_135637	2H	N/A	1130006
JHI_Hv50k_2016_135671	2H	N/A	1130836
JHI_Hv50k_2016_135693	2H	N/A	1134689
JHI_Hv50k_2016_136007	2H	N/A	1147676
JHI_Hv50k_2016_136058	2H	N/A	1148868
JHI_Hv50k_2016_136071	2H	N/A	1149313
JHI_Hv50k_2016_136164	2H	N/A	1159397
JHI_Hv50k_2016_136225	2H	N/A	1324984
JHI_Hv50k_2016_136275	2H	N/A	1473134
JHI_Hv50k_2016_136561	2H	N/A	1671086
JHI_Hv50k_2016_136577	2H	N/A	1671472
JHI_Hv50k_2016_136634	2H	N/A	1710755
JHI_Hv50k_2016_136636	2H	N/A	1717537
JHI_Hv50k_2016_137127	2H	N/A	1948339
JHI_Hv50k_2016_137347	2H	N/A	2016614
JHI_Hv50k_2016_137369	2H	N/A	2375123
JHI_Hv50k_2016_137428	2H	N/A	2701269
JHI_Hv50k_2016_137433	2H	N/A	2703071
JHI_Hv50k_2016_137586	2H	N/A	2816784
JHI_Hv50k_2016_137596	2H	N/A	2871874
JHI_Hv50k_2016_137991	2H	N/A	3693226
JHI_Hv50k_2016_138310	2H	N/A	4058298
JHI_Hv50k_2016_138375	2H	N/A	4183579
JHI_Hv50k_2016_138459	2H	N/A	4569804
JHI_Hv50k_2016_138652	2H	N/A	6528475
JHI_Hv50k_2016_138670	2H	N/A	6810389

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_138719	2H	N/A	6812281
JHI_Hv50k_2016_138729	2H	N/A	6812369
JHI_Hv50k_2016_138858	2H	N/A	6984695
JHI_Hv50k_2016_138894	2H	N/A	6985185
JHI_Hv50k_2016_138932	2H	N/A	7057912
JHI_Hv50k_2016_139076	2H	N/A	7211550
JHI_Hv50k_2016_139244	2H	N/A	7596796
JHI_Hv50k_2016_139283	2H	N/A	7596959
JHI_Hv50k_2016_139334	2H	N/A	7739991
JHI_Hv50k_2016_139335	2H	N/A	7767001
JHI_Hv50k_2016_139338	2H	N/A	7775424
JHI_Hv50k_2016_139339	2H	N/A	7775598
JHI_Hv50k_2016_139341	2H	N/A	7778965
JHI_Hv50k_2016_139507	2H	N/A	8183470
JHI_Hv50k_2016_139525	2H	N/A	8644805
JHI_Hv50k_2016_139631	2H	N/A	8743770
JHI_Hv50k_2016_139657	2H	N/A	8743824
JHI_Hv50k_2016_139740	2H	N/A	8787233
JHI_Hv50k_2016_139857	2H	N/A	9114716
JHI_Hv50k_2016_140235	2H	N/A	9233421
JHI_Hv50k_2016_140239	2H	N/A	9233492
JHI_Hv50k_2016_140451	2H	N/A	9234218
JHI_Hv50k_2016_140485	2H	N/A	9234523
JHI_Hv50k_2016_140582	2H	N/A	10544517
JHI_Hv50k_2016_140717	2H	N/A	10851274
JHI_Hv50k_2016_141465	2H	N/A	11516678
JHI_Hv50k_2016_141568	2H	N/A	11700217
JHI_Hv50k_2016_141703	2H	N/A	11727043
JHI_Hv50k_2016_141906	2H	N/A	12125574
JHI_Hv50k_2016_141922	2H	N/A	12240757
JHI_Hv50k_2016_141981	2H	N/A	13053070
JHI_Hv50k_2016_142033	2H	N/A	13078256
JHI_Hv50k_2016_142048	2H	N/A	13092889
JHI_Hv50k_2016_142123	2H	N/A	13429662
JHI_Hv50k_2016_142124	2H	N/A	13431406
JHI_Hv50k_2016_142161	2H	N/A	13432212
JHI_Hv50k_2016_142225	2H	N/A	13454829
JHI_Hv50k_2016_142226	2H	N/A	13455985
JHI_Hv50k_2016_142305	2H	N/A	13619398
JHI_Hv50k_2016_142355	2H	N/A	13621178
JHI_Hv50k_2016_142360	2H	N/A	13622780
JHI_Hv50k_2016_142430	2H	N/A	14012118

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_142528	2H	N/A	14026597
JHI_Hv50k_2016_142540	2H	N/A	14110599
JHI_Hv50k_2016_142592	2H	N/A	14177483
JHI_Hv50k_2016_142596	2H	N/A	14203953
JHI_Hv50k_2016_142604	2H	N/A	14333181
JHI_Hv50k_2016_142605	2H	N/A	14333381
JHI_Hv50k_2016_142624	2H	N/A	14731388
JHI_Hv50k_2016_142708	2H	N/A	14949518
JHI_Hv50k_2016_142802	2H	N/A	15202656
JHI_Hv50k_2016_142804	2H	N/A	15215565
JHI_Hv50k_2016_142905	2H	N/A	15300370
JHI_Hv50k_2016_143398	2H	N/A	15708313
JHI_Hv50k_2016_143440	2H	N/A	15721046
JHI_Hv50k_2016_143482	2H	N/A	15721542
JHI_Hv50k_2016_143489	2H	N/A	16009110
JHI_Hv50k_2016_143636	2H	N/A	16092005
JHI_Hv50k_2016_143696	2H	N/A	16388052
JHI_Hv50k_2016_143733	2H	N/A	16388136
JHI_Hv50k_2016_143888	2H	N/A	16490657
JHI_Hv50k_2016_143890	2H	N/A	16497809
JHI_Hv50k_2016_144078	2H	N/A	17165109
JHI_Hv50k_2016_144336	2H	N/A	17263562
JHI_Hv50k_2016_144340	2H	N/A	17264293
JHI_Hv50k_2016_144861	2H	N/A	17407196
JHI_Hv50k_2016_144957	2H	N/A	17408296
JHI_Hv50k_2016_145116	2H	N/A	17460109
JHI_Hv50k_2016_145133	2H	N/A	17555874
JHI_Hv50k_2016_145709	2H	N/A	17888920
JHI_Hv50k_2016_146031	2H	N/A	17965564
JHI_Hv50k_2016_147392	2H	N/A	19637230
JHI_Hv50k_2016_147903	2H	N/A	20122784
JHI_Hv50k_2016_147952	2H	N/A	20537486
JHI_Hv50k_2016_148086	2H	N/A	21019901
JHI_Hv50k_2016_148090	2H	N/A	21038617
JHI_Hv50k_2016_148100	2H	N/A	21180590
JHI_Hv50k_2016_148159	2H	N/A	21663984
JHI_Hv50k_2016_148211	2H	N/A	22513996
JHI_Hv50k_2016_148233	2H	N/A	22514114
JHI_Hv50k_2016_148247	2H	N/A	22515912
BOPA2_12_31428	3H	0	22602806
SCRI_RS_148646	3H	3.79	22620381
SCRI_RS_174383	3H	3.79	22620454

Marker	Chromosome	Position (cM)	Position (BP)
SCRI_RS_190002	3H	3.79	22621886
SCRI_RS_216164	3H	3.79	22622558
SCRI_RS_1804	3H	3.89	22622622
BOPA2_12_10103	3H	5.39	23090548
SCRI_RS_173491	3H	5.69	23097169
BOPA1_13924_403	3H	5.91	23158274
BOPA1_ConsensusGBS0194_1	3H	6.11	23185882
BOPA1_4593_2007	3H	43.79	24615852
SCRI_RS_119697	3H	44.12	24869215
SCRI_RS_136959	3H	44.42	24939838
BOPA2_12_10968	3H	44.82	24940657
SCRI_RS_151299	3H	44.92	25088482
SCRI_RS_115969	3H	45.02	25097256
SCRI_RS_133685	3H	45.91	25115774
SCRI_RS_185596	3H	55.57	26611274
BOPA2_12_31122	3H	55.67	26613514
SCRI_RS_189045	3H	56.27	26625827
BOPA1_7728_341	3H	58.31	27688886
BOPA2_12_31368	3H	58.31	28089950
SCRI_RS_142442	3H	58.31	29398256
BOPA2_12_31393	3H	59.56	32575037
BOPA1_10126_999	3H	59.86	32577119
SCRI_RS_168665	3H	61.99	32611132
BOPA1_2338_1572	3H	62.97	32636741
BOPA1_ABC08184_2_1_35	3H	62.97	32637324
SCRI_RS_151680	3H	62.97	32663134
SCRI_RS_152371	3H	64.17	32814127
SCRI_RS_1799	3H	64.37	33112981
SCRI_RS_200042	3H	64.37	33148571
BOPA2_12_30788	3H	65.44	34061526
BOPA1_2677_501	3H	67.19	36038114
SCRI_RS_162931	3H	67.39	36380089
SCRI_RS_237939	3H	67.39	36381736
SCRI_RS_13778	3H	68.09	36391095
SCRI_RS_194602	3H	68.09	36391518
BOPA1_4150_398	3H	68.29	36391650
BOPA1_4618_1559	3H	68.29	36402952
BOPA2_12_10609	3H	68.29	36403081
BOPA2_12_30743	3H	68.29	36647973
SCRI_RS_104564	3H	68.39	36648230
SCRI_RS_155609	3H	68.39	36651096
SCRI_RS_160216	3H	68.84	36652844

Marker	Chromosome	Position (cM)	Position (BP)
BOPA1_1639_613	3H	70.87	36766055
BOPA2_12_30170	3H	71.84	36787911
SCRI_RS_208373	3H	71.84	37637652
SCRI_RS_137852	3H	72.81	37827910
SCRI_RS_227898	3H	72.81	37938567
BOPA2_12_30677	3H	72.91	37940795
SCRI_RS_190676	3H	73.21	38314110
SCRI_RS_219894	3H	73.21	38391566
SCRI_RS_238157	3H	73.21	38393085
BOPA1_42_512	3H	76.76	39198626
SCRI_RS_116760	3H	81.21	39774829
BOPA2_12_10134	3H	81.31	40023910
SCRI_RS_156111	3H	81.71	40051823
BOPA1_963_386	3H	82.19	40555520
SCRI_RS_227472	3H	87.77	40817294
BOPA2_12_30250	3H	88.17	40941721
BOPA1_6302_250	3H	92.18	41441460
SCRI_RS_170206	3H	93.43	41661708
SCRI_RS_133339	3H	99.56	42860412
SCRI_RS_7396	3H	99.56	42860865
BOPA2_12_30927	3H	105.89	44046171
SCRI_RS_151711	3H	107.46	44250870
SCRI_RS_193132	3H	107.46	44325440
SCRI_RS_153915	3H	107.66	44327854
SCRI_RS_14857	3H	108.04	44458033
BOPA1_76_1059	3H	111.7	44459457
SCRI_RS_151733	3H	126.41	49677487
SCRI_RS_208297	3H	126.41	50398280
SCRI_RS_175038	3H	129.13	51060753
SCRI_RS_183550	3H	133.78	54500081
BOPA1_5520_925	3H	137.14	67427303
SCRI_RS_189186	3H	138.32	72344688
SCRI_RS_179447	3H	140.42	75106483
SCRI_RS_194527	3H	153.59	139193210
SCRI_RS_230717	3H	153.89	139613321
JHI_Hv50k_2016_148459	3H	N/A	149257373
JHI_Hv50k_2016_148460	3H	N/A	149466673
JHI_Hv50k_2016_148529	3H	N/A	161084961
JHI_Hv50k_2016_148531	3H	N/A	162895245
JHI_Hv50k_2016_148537	3H	N/A	163293693
JHI_Hv50k_2016_148548	3H	N/A	163386856
JHI_Hv50k_2016_148570	3H	N/A	163428827

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_148590	3H	N/A	163940290
JHI_Hv50k_2016_148640	3H	N/A	164561418
JHI_Hv50k_2016_148674	3H	N/A	165033159
JHI_Hv50k_2016_148745	3H	N/A	167105550
JHI_Hv50k_2016_148750	3H	N/A	169956751
JHI_Hv50k_2016_148809	3H	N/A	170155350
JHI_Hv50k_2016_148933	3H	N/A	176202147
JHI_Hv50k_2016_148944	3H	N/A	180392187
JHI_Hv50k_2016_148950	3H	N/A	182279209
JHI_Hv50k_2016_148980	3H	N/A	185397067
JHI_Hv50k_2016_148996	3H	N/A	190502360
JHI_Hv50k_2016_149021	3H	N/A	195720902
JHI_Hv50k_2016_149026	3H	N/A	196391413
JHI_Hv50k_2016_149027	3H	N/A	196464855
JHI_Hv50k_2016_149070	3H	N/A	203953584
JHI_Hv50k_2016_149079	3H	N/A	207316584
JHI_Hv50k_2016_149081	3H	N/A	207319474
JHI_Hv50k_2016_149087	3H	N/A	208353985
JHI_Hv50k_2016_149125	3H	N/A	211532602
JHI_Hv50k_2016_149133	3H	N/A	212192392
JHI_Hv50k_2016_149225	3H	N/A	213675892
JHI_Hv50k_2016_149269	3H	N/A	214377353
JHI_Hv50k_2016_149285	3H	N/A	215662543
JHI_Hv50k_2016_149450	3H	N/A	218870534
JHI_Hv50k_2016_149455	3H	N/A	219521780
JHI_Hv50k_2016_149459	3H	N/A	219522142
JHI_Hv50k_2016_149544	3H	N/A	221289238
JHI_Hv50k_2016_149558	3H	N/A	222490827
JHI_Hv50k_2016_149689	3H	N/A	233583596
JHI_Hv50k_2016_149691	3H	N/A	233879554
JHI_Hv50k_2016_150426	3H	N/A	261022647
JHI_Hv50k_2016_150427	3H	N/A	261024890
JHI_Hv50k_2016_151060	3H	N/A	283319420
JHI_Hv50k_2016_151156	3H	N/A	285998983
JHI_Hv50k_2016_151291	3H	N/A	292097971
JHI_Hv50k_2016_152033	3H	N/A	329257951
JHI_Hv50k_2016_152075	3H	N/A	330288834
JHI_Hv50k_2016_152104	3H	N/A	333547646
JHI_Hv50k_2016_152481	3H	N/A	351335033
JHI_Hv50k_2016_152539	3H	N/A	354287037
JHI_Hv50k_2016_152915	3H	N/A	362273268
JHI_Hv50k_2016_152968	3H	N/A	362408150

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_153517	3H	N/A	381158849
JHI_Hv50k_2016_156390	3H	N/A	476386324
JHI_Hv50k_2016_156392	3H	N/A	476719372
JHI_Hv50k_2016_158178	3H	N/A	493843952
JHI_Hv50k_2016_158664	3H	N/A	497615398
JHI_Hv50k_2016_159306	3H	N/A	503233899
JHI_Hv50k_2016_159492	3H	N/A	505517786
JHI_Hv50k_2016_159556	3H	N/A	505521312
JHI_Hv50k_2016_159689	3H	N/A	507024435
JHI_Hv50k_2016_159773	3H	N/A	507319913
JHI_Hv50k_2016_159965	3H	N/A	509127078
JHI_Hv50k_2016_160066	3H	N/A	510246993
JHI_Hv50k_2016_160142	3H	N/A	510839598
JHI_Hv50k_2016_160250	3H	N/A	512189057
JHI_Hv50k_2016_160328	3H	N/A	513769745
JHI_Hv50k_2016_160329	3H	N/A	513770581
JHI_Hv50k_2016_160331	3H	N/A	513771919
JHI_Hv50k_2016_160352	3H	N/A	514125642
JHI_Hv50k_2016_160470	3H	N/A	517014259
JHI_Hv50k_2016_161758	3H	N/A	535467403
JHI_Hv50k_2016_161806	3H	N/A	535790398
JHI_Hv50k_2016_162026	3H	N/A	536961931
JHI_Hv50k_2016_162411	3H	N/A	540509224
JHI_Hv50k_2016_162483	3H	N/A	540780617
JHI_Hv50k_2016_162668	3H	N/A	540867256
JHI_Hv50k_2016_162712	3H	N/A	542299569
JHI_Hv50k_2016_162717	3H	N/A	542640804
JHI_Hv50k_2016_162768	3H	N/A	544014334
JHI_Hv50k_2016_162805	3H	N/A	544040144
JHI_Hv50k_2016_162960	3H	N/A	545999523
JHI_Hv50k_2016_163538	3H	N/A	552234467
JHI_Hv50k_2016_163546	3H	N/A	552638132
JHI_Hv50k_2016_163619	3H	N/A	553192276
JHI_Hv50k_2016_163732	3H	N/A	555558633
JHI_Hv50k_2016_163734	3H	N/A	555558740
JHI_Hv50k_2016_163759	3H	N/A	556007747
JHI_Hv50k_2016_163867	3H	N/A	557360000
JHI_Hv50k_2016_163880	3H	N/A	557367812
JHI_Hv50k_2016_164079	3H	N/A	557952236
JHI_Hv50k_2016_164149	3H	N/A	558789682
JHI_Hv50k_2016_164162	3H	N/A	559146951
JHI_Hv50k_2016_164264	3H	N/A	560246485

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_164669	3H	N/A	566624840
JHI_Hv50k_2016_164943	3H	N/A	567955226
JHI_Hv50k_2016_165309	3H	N/A	568146251
JHI_Hv50k_2016_165924	3H	N/A	568712220
JHI_Hv50k_2016_166635	3H	N/A	570852138
JHI_Hv50k_2016_167092	3H	N/A	571322478
JHI_Hv50k_2016_167135	3H	N/A	571377308
JHI_Hv50k_2016_172337	3H	N/A	586904201
JHI_Hv50k_2016_178277	3H	N/A	596133885
JHI_Hv50k_2016_179736	3H	N/A	599980572
JHI_Hv50k_2016_179926	3H	N/A	600362794
JHI_Hv50k_2016_179962	3H	N/A	600367354
JHI_Hv50k_2016_180173	3H	N/A	600889826
JHI_Hv50k_2016_180310	3H	N/A	601016754
JHI_Hv50k_2016_180630	3H	N/A	602735994
JHI_Hv50k_2016_180822	3H	N/A	602896037
JHI_Hv50k_2016_180989	3H	N/A	603292544
JHI_Hv50k_2016_181001	3H	N/A	603627172
JHI_Hv50k_2016_181037	3H	N/A	603818920
JHI_Hv50k_2016_181066	3H	N/A	603819327
JHI_Hv50k_2016_181207	3H	N/A	604286426
JHI_Hv50k_2016_181460	3H	N/A	604675189
JHI_Hv50k_2016_181515	3H	N/A	604675367
JHI_Hv50k_2016_181519	3H	N/A	604675429
JHI_Hv50k_2016_181528	3H	N/A	604766631
JHI_Hv50k_2016_181622	3H	N/A	605213263
JHI_Hv50k_2016_181655	3H	N/A	605215866
JHI_Hv50k_2016_181725	3H	N/A	605272027
JHI_Hv50k_2016_181844	3H	N/A	605824250
JHI_Hv50k_2016_182218	3H	N/A	606997436
JHI_Hv50k_2016_182237	3H	N/A	606998641
JHI_Hv50k_2016_182240	3H	N/A	606999257
JHI_Hv50k_2016_182278	3H	N/A	607099455
JHI_Hv50k_2016_182481	3H	N/A	607296984
JHI_Hv50k_2016_182496	3H	N/A	607298325
JHI_Hv50k_2016_182600	3H	N/A	607679754
JHI_Hv50k_2016_182741	3H	N/A	608260768
JHI_Hv50k_2016_182801	3H	N/A	608426950
JHI_Hv50k_2016_182810	3H	N/A	608629181
JHI_Hv50k_2016_182817	3H	N/A	608631111
JHI_Hv50k_2016_182827	3H	N/A	608658392
JHI_Hv50k_2016_182848	3H	N/A	608821623

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_182867	3H	N/A	608893241
JHI_Hv50k_2016_182998	3H	N/A	610514517
JHI_Hv50k_2016_183028	3H	N/A	610519888
JHI_Hv50k_2016_183041	3H	N/A	610608496
JHI_Hv50k_2016_183100	3H	N/A	611134550
JHI_Hv50k_2016_184503	3H	N/A	616467022
JHI_Hv50k_2016_184618	3H	N/A	617339425
JHI_Hv50k_2016_184627	3H	N/A	617340110
JHI_Hv50k_2016_184654	3H	N/A	617523665
JHI_Hv50k_2016_184663	3H	N/A	617523850
JHI_Hv50k_2016_184790	3H	N/A	619132496
JHI_Hv50k_2016_184851	3H	N/A	619133915
JHI_Hv50k_2016_184865	3H	N/A	619313749
JHI_Hv50k_2016_184869	3H	N/A	619314552
JHI_Hv50k_2016_184908	3H	N/A	619314808
JHI_Hv50k_2016_184992	3H	N/A	619335789
JHI_Hv50k_2016_184995	3H	N/A	619335958
JHI_Hv50k_2016_185121	3H	N/A	619840923
JHI_Hv50k_2016_185504	3H	N/A	620758058
JHI_Hv50k_2016_185538	3H	N/A	621113789
JHI_Hv50k_2016_185725	3H	N/A	621229878
JHI_Hv50k_2016_185997	3H	N/A	621794235
JHI_Hv50k_2016_186051	3H	N/A	621960983
JHI_Hv50k_2016_186225	3H	N/A	622532147
JHI_Hv50k_2016_186240	3H	N/A	622532194
JHI_Hv50k_2016_186447	3H	N/A	622809773
JHI_Hv50k_2016_186800	3H	N/A	624103478
JHI_Hv50k_2016_186836	3H	N/A	624110902
JHI_Hv50k_2016_186837	3H	N/A	624125218
JHI_Hv50k_2016_186913	3H	N/A	624447968
JHI_Hv50k_2016_186961	3H	N/A	624933503
JHI_Hv50k_2016_186962	3H	N/A	624933627
JHI_Hv50k_2016_186966	3H	N/A	624933683
JHI_Hv50k_2016_187031	3H	N/A	625619288
JHI_Hv50k_2016_187117	3H	N/A	626222953
JHI_Hv50k_2016_187129	3H	N/A	626444286
JHI_Hv50k_2016_187210	3H	N/A	626507231
JHI_Hv50k_2016_188022	3H	N/A	628715835
JHI_Hv50k_2016_188075	3H	N/A	628818553
JHI_Hv50k_2016_188134	3H	N/A	629325970
JHI_Hv50k_2016_188412	3H	N/A	630644104
JHI_Hv50k_2016_188666	3H	N/A	630867186

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_189021	3H	N/A	632913362
JHI_Hv50k_2016_189047	3H	N/A	633067775
JHI_Hv50k_2016_189406	3H	N/A	634075081
JHI_Hv50k_2016_190151	3H	N/A	635076762
JHI_Hv50k_2016_190152	3H	N/A	635081185
JHI_Hv50k_2016_190194	3H	N/A	635114418
JHI_Hv50k_2016_190340	3H	N/A	635160509
JHI_Hv50k_2016_190349	3H	N/A	635266070
JHI_Hv50k_2016_190374	3H	N/A	635416060
JHI_Hv50k_2016_190426	3H	N/A	637659177
JHI_Hv50k_2016_190544	3H	N/A	637928325
JHI_Hv50k_2016_190592	3H	N/A	637930873
JHI_Hv50k_2016_190597	3H	N/A	637931032
JHI_Hv50k_2016_190601	3H	N/A	638067169
JHI_Hv50k_2016_190668	3H	N/A	638431989
JHI_Hv50k_2016_190711	3H	N/A	638433283
JHI_Hv50k_2016_190756	3H	N/A	638533817
JHI_Hv50k_2016_190757	3H	N/A	638547478
JHI_Hv50k_2016_190771	3H	N/A	638548567
JHI_Hv50k_2016_190842	3H	N/A	638580317
JHI_Hv50k_2016_190876	3H	N/A	638623773
JHI_Hv50k_2016_190980	3H	N/A	638970063
JHI_Hv50k_2016_190997	3H	N/A	638970342
JHI_Hv50k_2016_191062	3H	N/A	639082709
JHI_Hv50k_2016_191065	3H	N/A	639083568
JHI_Hv50k_2016_191098	3H	N/A	639084856
JHI_Hv50k_2016_191123	3H	N/A	639084967
JHI_Hv50k_2016_191253	3H	N/A	639130354
JHI_Hv50k_2016_191674	3H	N/A	639954242
JHI_Hv50k_2016_191859	3H	N/A	640197783
JHI_Hv50k_2016_191953	3H	N/A	640357048
JHI_Hv50k_2016_192081	3H	N/A	641887034
JHI_Hv50k_2016_192142	3H	N/A	641903839
JHI_Hv50k_2016_192191	3H	N/A	641906053
JHI_Hv50k_2016_192206	3H	N/A	641906252
JHI_Hv50k_2016_192282	3H	N/A	642583918
JHI_Hv50k_2016_192492	3H	N/A	642827763
JHI_Hv50k_2016_192532	3H	N/A	643167221
JHI_Hv50k_2016_192781	3H	N/A	644500480
JHI_Hv50k_2016_192892	3H	N/A	644883747
JHI_Hv50k_2016_193069	3H	N/A	645477479
JHI_Hv50k_2016_193149	3H	N/A	645654047

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_193186	3H	N/A	645671189
JHI_Hv50k_2016_193219	3H	N/A	646162962
JHI_Hv50k_2016_193279	3H	N/A	646242290
JHI_Hv50k_2016_193407	3H	N/A	647244878
JHI_Hv50k_2016_193476	3H	N/A	647457653
JHI_Hv50k_2016_193482	3H	N/A	647457862
JHI_Hv50k_2016_193498	3H	N/A	647577796
JHI_Hv50k_2016_193499	3H	N/A	647749627
JHI_Hv50k_2016_193551	3H	N/A	647753624
JHI_Hv50k_2016_193742	3H	N/A	648367180
JHI_Hv50k_2016_193773	3H	N/A	648391590
JHI_Hv50k_2016_193869	3H	N/A	648655490
JHI_Hv50k_2016_193928	3H	N/A	648673163
JHI_Hv50k_2016_193954	3H	N/A	648700927
JHI_Hv50k_2016_193972	3H	N/A	648703314
JHI_Hv50k_2016_194133	3H	N/A	649225193
JHI_Hv50k_2016_194259	3H	N/A	649839893
JHI_Hv50k_2016_194260	3H	N/A	649839955
JHI_Hv50k_2016_194267	3H	N/A	650047111
JHI_Hv50k_2016_194354	3H	N/A	650222414
JHI_Hv50k_2016_194381	3H	N/A	650242525
JHI_Hv50k_2016_194477	3H	N/A	650248935
JHI_Hv50k_2016_194652	3H	N/A	650698904
JHI_Hv50k_2016_194746	3H	N/A	650929400
JHI_Hv50k_2016_194756	3H	N/A	651021974
JHI_Hv50k_2016_194878	3H	N/A	651808751
JHI_Hv50k_2016_194888	3H	N/A	651809193
JHI_Hv50k_2016_194908	3H	N/A	651951286
JHI_Hv50k_2016_194935	3H	N/A	652178219
JHI_Hv50k_2016_195051	3H	N/A	653295018
JHI_Hv50k_2016_195059	3H	N/A	653295101
JHI_Hv50k_2016_195178	3H	N/A	653582242
JHI_Hv50k_2016_195535	3H	N/A	654554426
JHI_Hv50k_2016_195729	3H	N/A	654775579
JHI_Hv50k_2016_195967	3H	N/A	654833917
JHI_Hv50k_2016_196156	3H	N/A	655175456
JHI_Hv50k_2016_196158	3H	N/A	655175726
JHI_Hv50k_2016_196181	3H	N/A	655181993
JHI_Hv50k_2016_196276	3H	N/A	655406422
JHI_Hv50k_2016_196280	3H	N/A	655406635
JHI_Hv50k_2016_196379	3H	N/A	655541514
JHI_Hv50k_2016_196481	3H	N/A	656944353

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_196729	3H	N/A	657529824
JHI_Hv50k_2016_197189	3H	N/A	658547708
JHI_Hv50k_2016_197213	3H	N/A	659170862
JHI_Hv50k_2016_197473	3H	N/A	660575911
JHI_Hv50k_2016_197945	3H	N/A	661656529
JHI_Hv50k_2016_198582	3H	N/A	663654527
JHI_Hv50k_2016_198617	3H	N/A	663654860
JHI_Hv50k_2016_198732	3H	N/A	664525245
JHI_Hv50k_2016_198913	3H	N/A	664905444
JHI_Hv50k_2016_199513	3H	N/A	667567179
JHI_Hv50k_2016_199516	3H	N/A	667607429
JHI_Hv50k_2016_199520	3H	N/A	667624891
JHI_Hv50k_2016_199537	3H	N/A	667628646
JHI_Hv50k_2016_199632	3H	N/A	667804452
JHI_Hv50k_2016_199873	3H	N/A	668440529
JHI_Hv50k_2016_199971	3H	N/A	670178228
JHI_Hv50k_2016_199974	3H	N/A	670203123
JHI_Hv50k_2016_199976	3H	N/A	670212402
JHI_Hv50k_2016_200058	3H	N/A	670444443
JHI_Hv50k_2016_200334	3H	N/A	672398547
JHI_Hv50k_2016_200738	3H	N/A	673093268
JHI_Hv50k_2016_200741	3H	N/A	673097825
JHI_Hv50k_2016_200791	3H	N/A	673166490
JHI_Hv50k_2016_200982	3H	N/A	673830152
JHI_Hv50k_2016_201103	3H	N/A	675017080
JHI_Hv50k_2016_201104	3H	N/A	675017170
JHI_Hv50k_2016_201150	3H	N/A	675211941
JHI_Hv50k_2016_201218	3H	N/A	676333310
JHI_Hv50k_2016_201224	3H	N/A	676499149
JHI_Hv50k_2016_201289	3H	N/A	676525757
JHI_Hv50k_2016_201300	3H	N/A	676625191
JHI_Hv50k_2016_201348	3H	N/A	676668169
JHI_Hv50k_2016_201366	3H	N/A	676737075
JHI_Hv50k_2016_201477	3H	N/A	677527399
JHI_Hv50k_2016_201497	3H	N/A	677528039
JHI_Hv50k_2016_201525	3H	N/A	677551638
JHI_Hv50k_2016_201527	3H	N/A	677551734
JHI_Hv50k_2016_201529	3H	N/A	677561548
JHI_Hv50k_2016_201579	3H	N/A	677587891
JHI_Hv50k_2016_201591	3H	N/A	677736142
JHI_Hv50k_2016_201597	3H	N/A	677738953
JHI_Hv50k_2016_201626	3H	N/A	677739948

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_201672	3H	N/A	677881066
JHI_Hv50k_2016_201691	3H	N/A	678513678
JHI_Hv50k_2016_201727	3H	N/A	679065865
JHI_Hv50k_2016_201739	3H	N/A	679073293
JHI_Hv50k_2016_201751	3H	N/A	679257982
JHI_Hv50k_2016_201777	3H	N/A	679264880
JHI_Hv50k_2016_201793	3H	N/A	679322449
JHI_Hv50k_2016_201819	3H	N/A	679322583
JHI_Hv50k_2016_201883	3H	N/A	679434978
JHI_Hv50k_2016_201891	3H	N/A	679435476
JHI_Hv50k_2016_201892	3H	N/A	679435638
JHI_Hv50k_2016_201893	3H	N/A	679435740
JHI_Hv50k_2016_202332	3H	N/A	682161520
JHI_Hv50k_2016_202342	3H	N/A	682162675
JHI_Hv50k_2016_202499	3H	N/A	682755597
JHI_Hv50k_2016_202818	3H	N/A	683722794
JHI_Hv50k_2016_203559	3H	N/A	686559433
JHI_Hv50k_2016_203610	3H	N/A	686560237
JHI_Hv50k_2016_203611	3H	N/A	686560255
JHI_Hv50k_2016_203686	3H	N/A	686744924
JHI_Hv50k_2016_203690	3H	N/A	686745811
JHI_Hv50k_2016_203817	3H	N/A	686752394
JHI_Hv50k_2016_203818	3H	N/A	686820524
JHI_Hv50k_2016_203892	3H	N/A	687071124
JHI_Hv50k_2016_203907	3H	N/A	687325378
JHI_Hv50k_2016_203908	3H	N/A	687384243
JHI_Hv50k_2016_203909	3H	N/A	687384367
JHI_Hv50k_2016_203934	3H	N/A	687384796
JHI_Hv50k_2016_203966	3H	N/A	687388496
JHI_Hv50k_2016_204049	3H	N/A	687493590
JHI_Hv50k_2016_204079	3H	N/A	687530000
JHI_Hv50k_2016_204080	3H	N/A	687530226
JHI_Hv50k_2016_204091	3H	N/A	687534097
JHI_Hv50k_2016_204104	3H	N/A	687542160
JHI_Hv50k_2016_204137	3H	N/A	687542428
JHI_Hv50k_2016_204185	3H	N/A	687543789
JHI_Hv50k_2016_204244	3H	N/A	687548867
JHI_Hv50k_2016_204966	3H	N/A	689738578
JHI_Hv50k_2016_205163	3H	N/A	689773550
JHI_Hv50k_2016_205179	3H	N/A	689859861
JHI_Hv50k_2016_205208	3H	N/A	689866076
JHI_Hv50k_2016_205288	3H	N/A	690412594

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_205354	3H	N/A	690855290
JHI_Hv50k_2016_205371	3H	N/A	690901818
JHI_Hv50k_2016_205593	3H	N/A	691933236
JHI_Hv50k_2016_205626	3H	N/A	691941853
JHI_Hv50k_2016_205631	3H	N/A	691941946
JHI_Hv50k_2016_205634	3H	N/A	691942321
JHI_Hv50k_2016_206189	3H	N/A	694366806
JHI_Hv50k_2016_206197	3H	N/A	694540248
JHI_Hv50k_2016_206599	3H	N/A	696631524
JHI_Hv50k_2016_207227	3H	N/A	381858
JHI_Hv50k_2016_207340	3H	N/A	1087336
JHI_Hv50k_2016_207416	3H	N/A	1091576
JHI_Hv50k_2016_207563	3H	N/A	1141207
JHI_Hv50k_2016_207656	3H	N/A	1291385
JHI_Hv50k_2016_208211	3H	N/A	2673395
JHI_Hv50k_2016_208411	3H	N/A	3150321
JHI_Hv50k_2016_210202	3H	N/A	6162138
JHI_Hv50k_2016_210587	3H	N/A	6534650
JHI_Hv50k_2016_212440	3H	N/A	9110986
JHI_Hv50k_2016_212637	3H	N/A	9454683
JHI_Hv50k_2016_212667	3H	N/A	9468741
JHI_Hv50k_2016_213406	3H	N/A	9777812
JHI_Hv50k_2016_213524	3H	N/A	9803732
JHI_Hv50k_2016_213616	3H	N/A	9847402
JHI_Hv50k_2016_213660	3H	N/A	9995877
JHI_Hv50k_2016_213929	3H	N/A	10034719
JHI_Hv50k_2016_213966	3H	N/A	10044080
JHI_Hv50k_2016_214131	3H	N/A	10112786
JHI_Hv50k_2016_214535	3H	N/A	10193493
JHI_Hv50k_2016_214536	3H	N/A	10194342
JHI_Hv50k_2016_214634	3H	N/A	10317635
JHI_Hv50k_2016_214758	3H	N/A	10319469
JHI_Hv50k_2016_215365	3H	N/A	10704112
JHI_Hv50k_2016_218514	3H	N/A	16119812
JHI_Hv50k_2016_218678	3H	N/A	16122801
JHI_Hv50k_2016_218716	3H	N/A	16122841
JHI_Hv50k_2016_218725	3H	N/A	16124056
JHI_Hv50k_2016_218766	3H	N/A	16146247
JHI_Hv50k_2016_218879	3H	N/A	16472930
JHI_Hv50k_2016_219014	3H	N/A	17358453
JHI_Hv50k_2016_219104	3H	N/A	17377068
JHI_Hv50k_2016_219199	3H	N/A	17377586

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_219392	3H	N/A	18335836
JHI_Hv50k_2016_221117	3H	N/A	21787259
JHI_Hv50k_2016_221119	3H	N/A	21787314
JHI_Hv50k_2016_221122	3H	N/A	21789561
JHI_Hv50k_2016_221386	3H	N/A	22230954
JHI_Hv50k_2016_221774	3H	N/A	22861735
JHI_Hv50k_2016_221810	3H	N/A	22881972
JHI_Hv50k_2016_221842	3H	N/A	22933686
JHI_Hv50k_2016_221951	3H	N/A	22936395
JHI_Hv50k_2016_222075	3H	N/A	23377452
JHI_Hv50k_2016_222101	3H	N/A	23377819
JHI_Hv50k_2016_222317	3H	N/A	23476670
JHI_Hv50k_2016_222321	3H	N/A	23477891
JHI_Hv50k_2016_222633	3H	N/A	25517437
JHI_Hv50k_2016_222689	3H	N/A	25919461
JHI_Hv50k_2016_222965	3H	N/A	26146490
JHI_Hv50k_2016_222976	3H	N/A	26149469
JHI_Hv50k_2016_223181	3H	N/A	26450400
JHI_Hv50k_2016_223816	3H	N/A	27583769
JHI_Hv50k_2016_223911	3H	N/A	27598386
JHI_Hv50k_2016_224340	3H	N/A	33957271
JHI_Hv50k_2016_224341	3H	N/A	33958911
JHI_Hv50k_2016_224353	3H	N/A	34410208
JHI_Hv50k_2016_225151	3H	N/A	43878283
JHI_Hv50k_2016_225209	3H	N/A	44463562
JHI_Hv50k_2016_225326	3H	N/A	45245669
JHI_Hv50k_2016_225369	3H	N/A	46141379
BOPA1_3026_1011	4H	4.11	52517143
BOPA2_12_30540	4H	16.13	54143270
BOPA1_2055_947	4H	24.23	54571987
SCRI_RS_150585	4H	24.23	54572285
SCRI_RS_154178	4H	24.23	54575225
SCRI_RS_162743	4H	26.34	55357489
SCRI_RS_98443	4H	27.64	56100557
SCRI_RS_157832	4H	34.14	57496192
SCRI_RS_209362	4H	38.79	58451737
BOPA2_12_10860	4H	42.69	58461622
SCRI_RS_145412	4H	42.89	58462384
SCRI_RS_161528	4H	42.89	58463507
SCRI_RS_6956	4H	42.89	58463577
SCRI_RS_75805	4H	44.79	58637588
SCRI_RS_116338	4H	46.37	59047719

Marker	Chromosome	Position (cM)	Position (BP)
SCRI_RS_220122	4H	46.57	59670760
BOPA2_12_20240	4H	46.87	59739857
BOPA1_ABC07631_1_1_83	4H	50.7	60772449
BOPA1_ABC24906_1_1_279	4H	52.97	62861390
BOPA1_4636_1380	4H	53.87	66685884
BOPA2_12_30777	4H	53.87	70812437
SCRI_RS_135637	4H	53.87	73217052
SCRI_RS_156596	4H	53.87	74476879
SCRI_RS_157396	4H	53.87	74624537
SCRI_RS_160373	4H	53.87	75124164
SCRI_RS_170494	4H	53.87	75132417
SCRI_RS_188187	4H	53.87	76591760
SCRI_RS_74014	4H	53.87	82508106
BOPA1_3917_1365	4H	54.95	93178859
SCRI_RS_195935	4H	55.59	97456502
SCRI_RS_206232	4H	55.59	97582575
BOPA1_2421_520	4H	55.65	98876867
BOPA1_1110_715	4H	57.44	103852876
BOPA2_12_30755	4H	60.64	156517382
SCRI_RS_106799	4H	65.62	190298022
SCRI_RS_119486	4H	67.91	217194567
BOPA1_2196_195	4H	70.33	222450808
BOPA1_8463_466	4H	70.33	222687428
BOPA1_9149_1316	4H	70.33	223266790
BOPA2_12_31148	4H	72.7	233251112
SCRI_RS_200957	4H	73.91	239186827
BOPA1_ConsensusGBS0461_3	4H	74.05	240145458
BOPA2_12_31246	4H	78.11	261962922
BOPA1_4986_1214	4H	78.23	263031919
SCRI_RS_134956	4H	78.53	268039898
BOPA1_4039_1686	4H	83.34	287649928
SCRI_RS_210971	4H	83.34	287937638
BOPA2_12_10666	4H	96.99	347533198
SCRI_RS_209508	4H	98.65	349754154
BOPA2_12_30539	4H	98.78	350052818
BOPA2_12_30988	4H	99.68	352211044
BOPA2_12_30990	4H	99.68	352904766
BOPA1_6519_812	4H	102.18	374945515
BOPA2_12_31139	4H	102.38	383253274
BOPA1_10780_204	4H	104.15	393774050
BOPA2_12_20237	4H	111.29	396810771
BOPA2_12_11233	4H	111.43	400961933

Marker	Chromosome	Position (cM)	Position (BP)
BOPA1_5154_117	4H	117.13	409476902
JHI_Hv50k_2016_227371	4H	N/A	478353175
JHI_Hv50k_2016_227740	4H	N/A	490026527
JHI_Hv50k_2016_227753	4H	N/A	490917748
JHI_Hv50k_2016_227761	4H	N/A	491273012
JHI_Hv50k_2016_227763	4H	N/A	491397583
JHI_Hv50k_2016_227770	4H	N/A	491740664
JHI_Hv50k_2016_227897	4H	N/A	499430502
JHI_Hv50k_2016_227900	4H	N/A	499430802
JHI_Hv50k_2016_227950	4H	N/A	503615305
JHI_Hv50k_2016_227994	4H	N/A	504587654
JHI_Hv50k_2016_227996	4H	N/A	504733411
JHI_Hv50k_2016_228008	4H	N/A	505329517
JHI_Hv50k_2016_228046	4H	N/A	507100104
JHI_Hv50k_2016_228055	4H	N/A	508041134
JHI_Hv50k_2016_228525	4H	N/A	526356273
JHI_Hv50k_2016_228627	4H	N/A	531431235
JHI_Hv50k_2016_228896	4H	N/A	537436601
JHI_Hv50k_2016_228918	4H	N/A	538724180
JHI_Hv50k_2016_229073	4H	N/A	543437967
JHI_Hv50k_2016_229091	4H	N/A	544330222
JHI_Hv50k_2016_229411	4H	N/A	552174543
JHI_Hv50k_2016_229499	4H	N/A	554086713
JHI_Hv50k_2016_229699	4H	N/A	557870726
JHI_Hv50k_2016_229793	4H	N/A	559115605
JHI_Hv50k_2016_229940	4H	N/A	563087267
JHI_Hv50k_2016_230011	4H	N/A	564005905
JHI_Hv50k_2016_230076	4H	N/A	565281949
JHI_Hv50k_2016_230114	4H	N/A	565559261
JHI_Hv50k_2016_230239	4H	N/A	567865715
JHI_Hv50k_2016_230242	4H	N/A	567868718
JHI_Hv50k_2016_230361	4H	N/A	570200464
JHI_Hv50k_2016_230367	4H	N/A	570521388
JHI_Hv50k_2016_230368	4H	N/A	570521462
JHI_Hv50k_2016_230382	4H	N/A	570706000
JHI_Hv50k_2016_230383	4H	N/A	570707642
JHI_Hv50k_2016_230387	4H	N/A	570786203
JHI_Hv50k_2016_230409	4H	N/A	570786266
JHI_Hv50k_2016_230414	4H	N/A	570790524
JHI_Hv50k_2016_230419	4H	N/A	570855445
JHI_Hv50k_2016_230433	4H	N/A	570883721
JHI_Hv50k_2016_230444	4H	N/A	571398460

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_230449	4H	N/A	571398557
JHI_Hv50k_2016_230450	4H	N/A	571398928
JHI_Hv50k_2016_230451	4H	N/A	571399400
JHI_Hv50k_2016_230466	4H	N/A	571399842
JHI_Hv50k_2016_230806	4H	N/A	574823605
JHI_Hv50k_2016_230826	4H	N/A	574972120
JHI_Hv50k_2016_230833	4H	N/A	574975205
JHI_Hv50k_2016_230879	4H	N/A	576862188
JHI_Hv50k_2016_231145	4H	N/A	581070111
JHI_Hv50k_2016_231173	4H	N/A	581790179
JHI_Hv50k_2016_231218	4H	N/A	582603525
JHI_Hv50k_2016_231632	4H	N/A	584119032
JHI_Hv50k_2016_231679	4H	N/A	584932950
JHI_Hv50k_2016_231819	4H	N/A	586907735
JHI_Hv50k_2016_231859	4H	N/A	588345334
JHI_Hv50k_2016_232178	4H	N/A	595001571
JHI_Hv50k_2016_232180	4H	N/A	595002722
JHI_Hv50k_2016_232189	4H	N/A	595104971
JHI_Hv50k_2016_232220	4H	N/A	595769819
JHI_Hv50k_2016_232225	4H	N/A	595770432
JHI_Hv50k_2016_232276	4H	N/A	595815804
JHI_Hv50k_2016_232469	4H	N/A	595947767
JHI_Hv50k_2016_232504	4H	N/A	595963832
JHI_Hv50k_2016_232542	4H	N/A	595968931
JHI_Hv50k_2016_232625	4H	N/A	596523645
JHI_Hv50k_2016_232670	4H	N/A	596827354
JHI_Hv50k_2016_232679	4H	N/A	597094297
JHI_Hv50k_2016_232682	4H	N/A	597095579
JHI_Hv50k_2016_232707	4H	N/A	597426028
JHI_Hv50k_2016_232767	4H	N/A	598384572
JHI_Hv50k_2016_232769	4H	N/A	598384637
JHI_Hv50k_2016_232778	4H	N/A	598642678
JHI_Hv50k_2016_232779	4H	N/A	598643529
JHI_Hv50k_2016_232789	4H	N/A	598647927
JHI_Hv50k_2016_232799	4H	N/A	598648224
JHI_Hv50k_2016_232815	4H	N/A	598975547
JHI_Hv50k_2016_232816	4H	N/A	598975690
JHI_Hv50k_2016_232825	4H	N/A	598992196
JHI_Hv50k_2016_233000	4H	N/A	599238715
JHI_Hv50k_2016_233133	4H	N/A	599525639
JHI_Hv50k_2016_233193	4H	N/A	599681019
JHI_Hv50k_2016_233205	4H	N/A	599726845

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_233513	4H	N/A	600468334
JHI_Hv50k_2016_233560	4H	N/A	600635238
JHI_Hv50k_2016_233648	4H	N/A	600646758
JHI_Hv50k_2016_233781	4H	N/A	601128196
JHI_Hv50k_2016_233798	4H	N/A	601199692
JHI_Hv50k_2016_233879	4H	N/A	601567870
JHI_Hv50k_2016_233966	4H	N/A	601571298
JHI_Hv50k_2016_234121	4H	N/A	601707793
JHI_Hv50k_2016_234238	4H	N/A	601967486
JHI_Hv50k_2016_234333	4H	N/A	602072916
JHI_Hv50k_2016_234354	4H	N/A	602073093
JHI_Hv50k_2016_234356	4H	N/A	602073936
JHI_Hv50k_2016_234653	4H	N/A	604057523
JHI_Hv50k_2016_234799	4H	N/A	604403118
JHI_Hv50k_2016_235138	4H	N/A	604802318
JHI_Hv50k_2016_235425	4H	N/A	605244575
JHI_Hv50k_2016_235429	4H	N/A	605359375
JHI_Hv50k_2016_235646	4H	N/A	607739290
JHI_Hv50k_2016_235689	4H	N/A	607801267
JHI_Hv50k_2016_235864	4H	N/A	608057877
JHI_Hv50k_2016_236153	4H	N/A	608431314
JHI_Hv50k_2016_236181	4H	N/A	608733960
JHI_Hv50k_2016_236246	4H	N/A	608852900
JHI_Hv50k_2016_236633	4H	N/A	612086823
JHI_Hv50k_2016_236639	4H	N/A	612096829
JHI_Hv50k_2016_237614	4H	N/A	615742903
JHI_Hv50k_2016_238595	4H	N/A	618873578
JHI_Hv50k_2016_240101	4H	N/A	621711431
JHI_Hv50k_2016_241769	4H	N/A	627961920
JHI_Hv50k_2016_242788	4H	N/A	631729561
JHI_Hv50k_2016_242795	4H	N/A	632008758
JHI_Hv50k_2016_242908	4H	N/A	632281333
JHI_Hv50k_2016_242932	4H	N/A	632281534
JHI_Hv50k_2016_242966	4H	N/A	632282737
JHI_Hv50k_2016_243312	4H	N/A	632617624
JHI_Hv50k_2016_243454	4H	N/A	632760889
JHI_Hv50k_2016_243481	4H	N/A	632761013
JHI_Hv50k_2016_243491	4H	N/A	632999877
JHI_Hv50k_2016_243535	4H	N/A	633028810
JHI_Hv50k_2016_243625	4H	N/A	633041853
JHI_Hv50k_2016_243654	4H	N/A	633041934
JHI_Hv50k_2016_243692	4H	N/A	633171758

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_244022	4H	N/A	633359109
JHI_Hv50k_2016_244514	4H	N/A	634470445
JHI_Hv50k_2016_244552	4H	N/A	634680503
JHI_Hv50k_2016_245146	4H	N/A	634942310
JHI_Hv50k_2016_245362	4H	N/A	634965249
JHI_Hv50k_2016_246605	4H	N/A	636584133
JHI_Hv50k_2016_246735	4H	N/A	637360434
JHI_Hv50k_2016_246831	4H	N/A	637450761
JHI_Hv50k_2016_247444	4H	N/A	639213916
JHI_Hv50k_2016_247715	4H	N/A	639941872
JHI_Hv50k_2016_248233	4H	N/A	640516986
JHI_Hv50k_2016_249069	4H	N/A	640711411
JHI_Hv50k_2016_249100	4H	N/A	640720872
JHI_Hv50k_2016_249161	4H	N/A	640723224
JHI_Hv50k_2016_249490	4H	N/A	641157764
JHI_Hv50k_2016_249669	4H	N/A	641256179
JHI_Hv50k_2016_249684	4H	N/A	641276727
JHI_Hv50k_2016_249706	4H	N/A	641464303
JHI_Hv50k_2016_249748	4H	N/A	641771820
JHI_Hv50k_2016_249805	4H	N/A	641851631
JHI_Hv50k_2016_250700	4H	N/A	643513006
JHI_Hv50k_2016_251221	4H	N/A	644344147
JHI_Hv50k_2016_252060	4H	N/A	644851674
JHI_Hv50k_2016_252216	4H	N/A	645034013
JHI_Hv50k_2016_253909	4H	N/A	427419
JHI_Hv50k_2016_254062	4H	N/A	546242
JHI_Hv50k_2016_254066	4H	N/A	547268
JHI_Hv50k_2016_254513	4H	N/A	1316159
JHI_Hv50k_2016_254754	4H	N/A	1317431
JHI_Hv50k_2016_255055	4H	N/A	2260380
JHI_Hv50k_2016_255094	4H	N/A	2264999
JHI_Hv50k_2016_255177	4H	N/A	2454182
JHI_Hv50k_2016_255219	4H	N/A	2550223
JHI_Hv50k_2016_255357	4H	N/A	2755883
JHI_Hv50k_2016_255516	4H	N/A	2899818
JHI_Hv50k_2016_255754	4H	N/A	4057310
JHI_Hv50k_2016_255813	4H	N/A	4126901
JHI_Hv50k_2016_255869	4H	N/A	4133364
JHI_Hv50k_2016_255911	4H	N/A	4178204
JHI_Hv50k_2016_256226	4H	N/A	4930992
JHI_Hv50k_2016_256291	4H	N/A	5187130
JHI_Hv50k_2016_256470	4H	N/A	5701880

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_256698	4H	N/A	5795028
JHI_Hv50k_2016_256889	4H	N/A	5801095
JHI_Hv50k_2016_256891	4H	N/A	5801301
JHI_Hv50k_2016_257096	4H	N/A	6339127
JHI_Hv50k_2016_257103	4H	N/A	6354221
JHI_Hv50k_2016_257133	4H	N/A	6368318
JHI_Hv50k_2016_257188	4H	N/A	6398057
JHI_Hv50k_2016_257712	4H	N/A	6626906
JHI_Hv50k_2016_258194	4H	N/A	7556820
JHI_Hv50k_2016_258250	4H	N/A	7556965
JHI_Hv50k_2016_258610	4H	N/A	8794237
JHI_Hv50k_2016_258612	4H	N/A	8849138
JHI_Hv50k_2016_258621	4H	N/A	8875729
JHI_Hv50k_2016_258622	4H	N/A	8875987
JHI_Hv50k_2016_258623	4H	N/A	8876196
JHI_Hv50k_2016_258625	4H	N/A	8876346
JHI_Hv50k_2016_258626	4H	N/A	8876719
JHI_Hv50k_2016_258640	4H	N/A	9251495
JHI_Hv50k_2016_258656	4H	N/A	9253334
JHI_Hv50k_2016_258660	4H	N/A	9253442
JHI_Hv50k_2016_258664	4H	N/A	9253602
JHI_Hv50k_2016_258676	4H	N/A	9284135
JHI_Hv50k_2016_258689	4H	N/A	9494455
JHI_Hv50k_2016_258690	4H	N/A	9494831
JHI_Hv50k_2016_258691	4H	N/A	9497614
JHI_Hv50k_2016_258751	4H	N/A	9855689
JHI_Hv50k_2016_258889	4H	N/A	9868595
JHI_Hv50k_2016_258941	4H	N/A	9907958
JHI_Hv50k_2016_258991	4H	N/A	9929783
JHI_Hv50k_2016_259049	4H	N/A	9931274
JHI_Hv50k_2016_259052	4H	N/A	9931323
JHI_Hv50k_2016_259088	4H	N/A	9931435
JHI_Hv50k_2016_259092	4H	N/A	9931509
JHI_Hv50k_2016_259095	4H	N/A	9931607
JHI_Hv50k_2016_259104	4H	N/A	9931630
JHI_Hv50k_2016_259108	4H	N/A	9931906
JHI_Hv50k_2016_259133	4H	N/A	10173518
JHI_Hv50k_2016_259346	4H	N/A	10631653
JHI_Hv50k_2016_259362	4H	N/A	10632553
JHI_Hv50k_2016_259398	4H	N/A	10634247
JHI_Hv50k_2016_259556	4H	N/A	10956309
JHI_Hv50k_2016_259660	4H	N/A	11136356

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_259677	4H	N/A	11287957
JHI_Hv50k_2016_259749	4H	N/A	11395895
JHI_Hv50k_2016_259765	4H	N/A	11405748
JHI_Hv50k_2016_259937	4H	N/A	12037528
JHI_Hv50k_2016_260318	4H	N/A	12450758
JHI_Hv50k_2016_260363	4H	N/A	12611932
JHI_Hv50k_2016_260410	4H	N/A	12687207
JHI_Hv50k_2016_260411	4H	N/A	12688001
JHI_Hv50k_2016_260417	4H	N/A	12690379
JHI_Hv50k_2016_260435	4H	N/A	12720259
JHI_Hv50k_2016_260657	4H	N/A	13036128
JHI_Hv50k_2016_261020	4H	N/A	14109320
JHI_Hv50k_2016_261130	4H	N/A	15292712
JHI_Hv50k_2016_261184	4H	N/A	15598914
JHI_Hv50k_2016_261301	4H	N/A	15651965
JHI_Hv50k_2016_261412	4H	N/A	16127688
JHI_Hv50k_2016_261435	4H	N/A	16276890
JHI_Hv50k_2016_261458	4H	N/A	16278368
JHI_Hv50k_2016_261479	4H	N/A	16324036
JHI_Hv50k_2016_261569	4H	N/A	16406801
JHI_Hv50k_2016_261572	4H	N/A	16407069
JHI_Hv50k_2016_261573	4H	N/A	16407140
JHI_Hv50k_2016_261630	4H	N/A	16697940
JHI_Hv50k_2016_261631	4H	N/A	16698434
JHI_Hv50k_2016_261643	4H	N/A	16884738
JHI_Hv50k_2016_261689	4H	N/A	16945177
JHI_Hv50k_2016_261690	4H	N/A	16946659
JHI_Hv50k_2016_261708	4H	N/A	17075290
JHI_Hv50k_2016_261833	4H	N/A	18257507
JHI_Hv50k_2016_262040	4H	N/A	18793904
JHI_Hv50k_2016_262239	4H	N/A	18807203
JHI_Hv50k_2016_262248	4H	N/A	18946772
JHI_Hv50k_2016_262431	4H	N/A	19034565
JHI_Hv50k_2016_262456	4H	N/A	19034585
JHI_Hv50k_2016_262494	4H	N/A	19035310
JHI_Hv50k_2016_262502	4H	N/A	19035896
JHI_Hv50k_2016_262558	4H	N/A	19036885
JHI_Hv50k_2016_262563	4H	N/A	19045295
JHI_Hv50k_2016_262564	4H	N/A	19045634
JHI_Hv50k_2016_262637	4H	N/A	19046013
JHI_Hv50k_2016_262639	4H	N/A	19046048
JHI_Hv50k_2016_262642	4H	N/A	19048181

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_262748	4H	N/A	19051321
JHI_Hv50k_2016_263100	4H	N/A	19788980
JHI_Hv50k_2016_263248	4H	N/A	20444215
JHI_Hv50k_2016_263250	4H	N/A	20471633
JHI_Hv50k_2016_263252	4H	N/A	20471893
JHI_Hv50k_2016_263262	4H	N/A	20916115
JHI_Hv50k_2016_263263	4H	N/A	20916193
JHI_Hv50k_2016_263266	4H	N/A	20916387
JHI_Hv50k_2016_263307	4H	N/A	21125465
JHI_Hv50k_2016_263331	4H	N/A	21127124
JHI_Hv50k_2016_263437	4H	N/A	21257934
JHI_Hv50k_2016_263488	4H	N/A	21725492
JHI_Hv50k_2016_264264	4H	N/A	24971733
JHI_Hv50k_2016_265457	4H	N/A	28556305
JHI_Hv50k_2016_265932	4H	N/A	30703080
JHI_Hv50k_2016_265990	4H	N/A	31032201
JHI_Hv50k_2016_266024	4H	N/A	31032981
JHI_Hv50k_2016_266028	4H	N/A	31033063
JHI_Hv50k_2016_266082	4H	N/A	31036401
JHI_Hv50k_2016_266192	4H	N/A	31036597
JHI_Hv50k_2016_266201	4H	N/A	31286038
JHI_Hv50k_2016_266314	4H	N/A	31295038
JHI_Hv50k_2016_266331	4H	N/A	31295184
JHI_Hv50k_2016_266399	4H	N/A	31360393
JHI_Hv50k_2016_266496	4H	N/A	31369105
JHI_Hv50k_2016_266659	4H	N/A	31988564
JHI_Hv50k_2016_266718	4H	N/A	31988616
JHI_Hv50k_2016_266752	4H	N/A	31989031
JHI_Hv50k_2016_266761	4H	N/A	31989315
JHI_Hv50k_2016_266765	4H	N/A	31989817
JHI_Hv50k_2016_266866	4H	N/A	32166431
JHI_Hv50k_2016_266867	4H	N/A	32166489
JHI_Hv50k_2016_267007	4H	N/A	32596474
JHI_Hv50k_2016_267212	4H	N/A	33657074
JHI_Hv50k_2016_267291	4H	N/A	33664854
JHI_Hv50k_2016_267309	4H	N/A	33665566
JHI_Hv50k_2016_267354	4H	N/A	33751558
JHI_Hv50k_2016_267514	4H	N/A	34426476
JHI_Hv50k_2016_267540	4H	N/A	34427513
JHI_Hv50k_2016_267605	4H	N/A	34427742
JHI_Hv50k_2016_267614	4H	N/A	34427853
JHI_Hv50k_2016_267619	4H	N/A	34519974

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_267629	4H	N/A	34520725
JHI_Hv50k_2016_267631	4H	N/A	34521225
JHI_Hv50k_2016_267663	4H	N/A	34523236
JHI_Hv50k_2016_267738	4H	N/A	34998141
JHI_Hv50k_2016_268482	4H	N/A	38561233
JHI_Hv50k_2016_268491	4H	N/A	38561507
JHI_Hv50k_2016_268579	4H	N/A	38664064
JHI_Hv50k_2016_268626	4H	N/A	39816265
JHI_Hv50k_2016_268808	4H	N/A	43217163
JHI_Hv50k_2016_268868	4H	N/A	47908556
JHI_Hv50k_2016_268870	4H	N/A	48068590
JHI_Hv50k_2016_269169	4H	N/A	62507755
JHI_Hv50k_2016_269205	4H	N/A	66125361
JHI_Hv50k_2016_269374	4H	N/A	70903771
JHI_Hv50k_2016_269378	4H	N/A	71123293
JHI_Hv50k_2016_269379	4H	N/A	71634568
JHI_Hv50k_2016_269524	4H	N/A	74086486
JHI_Hv50k_2016_269549	4H	N/A	74274298
JHI_Hv50k_2016_269746	4H	N/A	82000707
JHI_Hv50k_2016_270047	4H	N/A	95192811
JHI_Hv50k_2016_270319	4H	N/A	107554231
JHI_Hv50k_2016_270835	4H	N/A	129074910
JHI_Hv50k_2016_271280	4H	N/A	146523773
JHI_Hv50k_2016_271455	4H	N/A	152573751
JHI_Hv50k_2016_271457	4H	N/A	152826623
JHI_Hv50k_2016_271473	4H	N/A	154555959
JHI_Hv50k_2016_272665	4H	N/A	255509729
JHI_Hv50k_2016_272747	4H	N/A	261870386
JHI_Hv50k_2016_272900	4H	N/A	272399869
JHI_Hv50k_2016_273189	4H	N/A	291893338
JHI_Hv50k_2016_273355	4H	N/A	296948465
JHI_Hv50k_2016_273382	4H	N/A	298233447
JHI_Hv50k_2016_273393	4H	N/A	299662439
JHI_Hv50k_2016_273435	4H	N/A	305120235
JHI_Hv50k_2016_273866	4H	N/A	324160601
JHI_Hv50k_2016_273870	4H	N/A	325087815
JHI_Hv50k_2016_273871	4H	N/A	326713422
JHI_Hv50k_2016_273885	4H	N/A	328352421
JHI_Hv50k_2016_273928	4H	N/A	330160337
JHI_Hv50k_2016_273963	4H	N/A	330603965
JHI_Hv50k_2016_274170	4H	N/A	337462863
JHI_Hv50k_2016_274598	4H	N/A	346785177

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_274673	4H	N/A	348601805
JHI_Hv50k_2016_274678	4H	N/A	348789450
JHI_Hv50k_2016_274694	4H	N/A	349065357
JHI_Hv50k_2016_274789	4H	N/A	359748154
JHI_Hv50k_2016_274792	4H	N/A	360369095
JHI_Hv50k_2016_274794	4H	N/A	361137715
JHI_Hv50k_2016_274796	4H	N/A	361451256
JHI_Hv50k_2016_274812	4H	N/A	361809363
JHI_Hv50k_2016_274930	4H	N/A	361898606
JHI_Hv50k_2016_274974	4H	N/A	361904696
JHI_Hv50k_2016_275009	4H	N/A	363522847
JHI_Hv50k_2016_275355	4H	N/A	369566427
JHI_Hv50k_2016_275685	4H	N/A	372318518
JHI_Hv50k_2016_275686	4H	N/A	372387567
JHI_Hv50k_2016_275917	4H	N/A	378887008
JHI_Hv50k_2016_276040	4H	N/A	383290120
JHI_Hv50k_2016_276045	4H	N/A	384196406
JHI_Hv50k_2016_276096	4H	N/A	384684649
JHI_Hv50k_2016_276097	4H	N/A	385074179
JHI_Hv50k_2016_276100	4H	N/A	385116928
JHI_Hv50k_2016_276140	4H	N/A	386406108
JHI_Hv50k_2016_276166	4H	N/A	388974320
JHI_Hv50k_2016_276249	4H	N/A	391334121
JHI_Hv50k_2016_276268	4H	N/A	391818656
JHI_Hv50k_2016_276269	4H	N/A	392360672
JHI_Hv50k_2016_276408	4H	N/A	394296078
JHI_Hv50k_2016_276456	4H	N/A	395292890
JHI_Hv50k_2016_276475	4H	N/A	399165523
JHI_Hv50k_2016_276476	4H	N/A	399165710
JHI_Hv50k_2016_276511	4H	N/A	400235069
JHI_Hv50k_2016_276637	4H	N/A	404118330
JHI_Hv50k_2016_276705	4H	N/A	407253723
JHI_Hv50k_2016_276754	4H	N/A	408670617
JHI_Hv50k_2016_276793	4H	N/A	409683365
BOPA2_12_30591	5H	4.66	418444096
SCRI_RS_168359	5H	5.36	418450401
BOPA1_10207_1024	5H	11.32	421467260
BOPA1_2594_172	5H	28.56	430537203
BOPA1_4684_775	5H	31.06	431594380
SCRI_RS_179526	5H	35.15	440206397
SCRI_RS_220164	5H	35.15	440407894
SCRI_RS_239393	5H	43.92	475078655

Marker	Chromosome	Position (cM)	Position (BP)
BOPA2_12_30111	5H	44.99	479346433
SCRI_RS_182435	5H	44.99	480814934
SCRI_RS_188367	5H	44.99	480815073
BOPA1_3928_513	5H	64.25	483099571
BOPA1_ABC14990_1_1_126	5H	68.58	483491035
BOPA1_370_443	5H	70.31	484376635
SCRI_RS_212784	5H	71.53	485868284
SCRI_RS_147819	5H	76.14	486429124
BOPA1_ABC14689_1_9_399	5H	84.96	487799143
BOPA1_10318_572	5H	85.58	487806956
BOPA2_12_30098	5H	86.18	487888257
BOPA2_12_30855	5H	87.71	488442001
BOPA2_12_30705	5H	90.22	489487954
BOPA2_12_10752	5H	90.68	492218471
SCRI_RS_157897	5H	94.85	492844404
SCRI_RS_225268	5H	95.25	493148008
SCRI_RS_149088	5H	103.35	494101837
SCRI_RS_224501	5H	104.35	494108893
SCRI_RS_9991	5H	104.35	494113680
SCRI_RS_231239	5H	106.45	494114311
BOPA1_ConsensusGBS0531_1	5H	111.56	494680166
BOPA2_12_11298	5H	111.56	494702961
SCRI_RS_51000	5H	115.33	495149430
SCRI_RS_90070	5H	115.43	495463348
BOPA1_7167_466	5H	115.53	495700493
SCRI_RS_170159	5H	116.23	497103609
SCRI_RS_234330	5H	116.33	497105858
BOPA1_ABC17073_1_1_298	5H	116.93	498535025
SCRI_RS_188785	5H	117.43	498537242
SCRI_RS_138933	5H	126.19	499576774
SCRI_RS_141778	5H	126.19	499576853
SCRI_RS_235055	5H	126.19	499577304
BOPA1_ABC03900_1_2_406	5H	126.39	499580055
BOPA2_12_30869	5H	126.93	499580242
SCRI_RS_13320	5H	127.43	500701015
BOPA1_6450_755	5H	128.8	501182991
BOPA1_ABC03113_1_1_251	5H	128.8	501183822
SCRI_RS_102414	5H	130.03	501226980
SCRI_RS_128407	5H	130.03	501227291
SCRI_RS_175672	5H	130.03	501818824
SCRI_RS_206956	5H	130.33	501819072
BOPA2_12_31234	5H	134.2	504590955

Marker	Chromosome	Position (cM)	Position (BP)
BOPA1_1011_1338	5H	134.67	504595425
SCRI_RS_225632	5H	136.52	505208975
BOPA1_603_72	5H	149.41	511831450
SCRI_RS_155688	5H	149.41	512984373
SCRI_RS_173583	5H	149.41	513074025
SCRI_RS_224438	5H	149.41	514559621
SCRI_RS_181521	5H	153.37	514827552
BOPA2_12_30162	5H	156.7	517212860
SCRI_RS_165400	5H	156.7	517659194
BOPA1_6761_490	5H	169.97	519233358
BOPA2_12_30656	5H	169.97	519240614
SCRI_RS_141634	5H	169.97	519240722
SCRI_RS_186984	5H	169.97	519241050
SCRI_RS_13882	5H	171.06	519245435
BOPA1_3007_1337	5H	171.16	519245603
BOPA1_5145_1355	5H	171.16	519245858
SCRI_RS_167103	5H	172.13	519247797
BOPA1_2144_852	5H	172.23	519248057
BOPA1_5219_773	5H	172.25	519248445
SCRI_RS_194337	5H	176.52	519895678
SCRI_RS_194566	5H	176.73	519896366
SCRI_RS_216726	5H	176.73	519899715
SCRI_RS_206768	5H	177.43	520030220
BOPA1_6116_709	5H	177.5	520673251
SCRI_RS_167850	5H	179.17	521147320
BOPA1_6489_465	5H	179.67	521147558
BOPA2_12_31481	5H	179.67	522121511
SCRI_RS_12519	5H	180.84	523522324
SCRI_RS_219619	5H	180.84	523522553
SCRI_RS_232575	5H	180.94	524682169
SCRI_RS_193456	5H	184.75	526655447
JHI_Hv50k_2016_277585	5H	N/A	534003424
JHI_Hv50k_2016_277603	5H	N/A	534121177
JHI_Hv50k_2016_277831	5H	N/A	534766880
JHI_Hv50k_2016_277889	5H	N/A	535004576
JHI_Hv50k_2016_278063	5H	N/A	535197107
JHI_Hv50k_2016_278266	5H	N/A	535442901
JHI_Hv50k_2016_278487	5H	N/A	535811048
JHI_Hv50k_2016_278498	5H	N/A	535811358
JHI_Hv50k_2016_278708	5H	N/A	537949120
JHI_Hv50k_2016_278909	5H	N/A	540122439
JHI_Hv50k_2016_278952	5H	N/A	540585635

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_278953	5H	N/A	540590618
JHI_Hv50k_2016_279021	5H	N/A	541554917
JHI_Hv50k_2016_279217	5H	N/A	542749449
JHI_Hv50k_2016_279256	5H	N/A	543624239
JHI_Hv50k_2016_279307	5H	N/A	544245975
JHI_Hv50k_2016_279481	5H	N/A	545294986
JHI_Hv50k_2016_279492	5H	N/A	545295211
JHI_Hv50k_2016_280756	5H	N/A	547771964
JHI_Hv50k_2016_280847	5H	N/A	548133718
JHI_Hv50k_2016_280850	5H	N/A	548133848
JHI_Hv50k_2016_280854	5H	N/A	548134269
JHI_Hv50k_2016_280992	5H	N/A	551804739
JHI_Hv50k_2016_281029	5H	N/A	551820958
JHI_Hv50k_2016_281049	5H	N/A	551832905
JHI_Hv50k_2016_281145	5H	N/A	551938991
JHI_Hv50k_2016_281168	5H	N/A	551982784
JHI_Hv50k_2016_281183	5H	N/A	552530672
JHI_Hv50k_2016_281189	5H	N/A	552549773
JHI_Hv50k_2016_281221	5H	N/A	552934147
JHI_Hv50k_2016_281227	5H	N/A	552963942
JHI_Hv50k_2016_281274	5H	N/A	553190243
JHI_Hv50k_2016_281410	5H	N/A	553420492
JHI_Hv50k_2016_281761	5H	N/A	554919966
JHI_Hv50k_2016_281762	5H	N/A	554920212
JHI_Hv50k_2016_282068	5H	N/A	556972677
JHI_Hv50k_2016_282235	5H	N/A	557092970
JHI_Hv50k_2016_282279	5H	N/A	557145652
JHI_Hv50k_2016_282358	5H	N/A	557593391
JHI_Hv50k_2016_282389	5H	N/A	557742711
JHI_Hv50k_2016_282392	5H	N/A	557803007
JHI_Hv50k_2016_282655	5H	N/A	558876057
JHI_Hv50k_2016_282737	5H	N/A	559189895
JHI_Hv50k_2016_282884	5H	N/A	561573393
JHI_Hv50k_2016_282898	5H	N/A	561602001
JHI_Hv50k_2016_282946	5H	N/A	561729416
JHI_Hv50k_2016_282959	5H	N/A	561945516
JHI_Hv50k_2016_282998	5H	N/A	561955015
JHI_Hv50k_2016_283261	5H	N/A	563281196
JHI_Hv50k_2016_283305	5H	N/A	563627618
JHI_Hv50k_2016_283800	5H	N/A	565889467
JHI_Hv50k_2016_283801	5H	N/A	565889652
JHI_Hv50k_2016_284294	5H	N/A	569020292

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_285355	5H	N/A	572541803
JHI_Hv50k_2016_285612	5H	N/A	573136005
JHI_Hv50k_2016_286384	5H	N/A	575310792
JHI_Hv50k_2016_286574	5H	N/A	575964718
JHI_Hv50k_2016_286578	5H	N/A	575967345
JHI_Hv50k_2016_286752	5H	N/A	576174703
JHI_Hv50k_2016_286812	5H	N/A	576199964
JHI_Hv50k_2016_286826	5H	N/A	576242994
JHI_Hv50k_2016_286830	5H	N/A	576261192
JHI_Hv50k_2016_286836	5H	N/A	576261814
JHI_Hv50k_2016_303451	5H	N/A	603029543
JHI_Hv50k_2016_303722	5H	N/A	603449953
JHI_Hv50k_2016_303778	5H	N/A	603451880
JHI_Hv50k_2016_303837	5H	N/A	603455871
JHI_Hv50k_2016_303990	5H	N/A	603536758
JHI_Hv50k_2016_304050	5H	N/A	603536995
JHI_Hv50k_2016_304060	5H	N/A	603595061
JHI_Hv50k_2016_304153	5H	N/A	604001830
JHI_Hv50k_2016_304254	5H	N/A	604362860
JHI_Hv50k_2016_305192	5H	N/A	606302384
JHI_Hv50k_2016_305552	5H	N/A	606531778
JHI_Hv50k_2016_305632	5H	N/A	607080204
JHI_Hv50k_2016_306044	5H	N/A	608906858
JHI_Hv50k_2016_306099	5H	N/A	608997867
JHI_Hv50k_2016_306547	5H	N/A	610611601
JHI_Hv50k_2016_306560	5H	N/A	610614709
JHI_Hv50k_2016_306727	5H	N/A	611101674
JHI_Hv50k_2016_306776	5H	N/A	611259159
JHI_Hv50k_2016_306878	5H	N/A	611527359
JHI_Hv50k_2016_306879	5H	N/A	611527900
JHI_Hv50k_2016_307445	5H	N/A	613720690
JHI_Hv50k_2016_307526	5H	N/A	613987849
JHI_Hv50k_2016_308003	5H	N/A	614932254
JHI_Hv50k_2016_308004	5H	N/A	614934657
JHI_Hv50k_2016_308380	5H	N/A	616649248
JHI_Hv50k_2016_308611	5H	N/A	617134179
JHI_Hv50k_2016_308692	5H	N/A	617242383
JHI_Hv50k_2016_308701	5H	N/A	617242751
JHI_Hv50k_2016_309218	5H	N/A	620800655
JHI_Hv50k_2016_309279	5H	N/A	621610345
JHI_Hv50k_2016_309326	5H	N/A	621896230
JHI_Hv50k_2016_309605	5H	N/A	622522207

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_310426	5H	N/A	626127059
JHI_Hv50k_2016_310432	5H	N/A	626128511
JHI_Hv50k_2016_310433	5H	N/A	626129224
JHI_Hv50k_2016_310517	5H	N/A	626405350
JHI_Hv50k_2016_310596	5H	N/A	626693212
JHI_Hv50k_2016_310769	5H	N/A	628372726
JHI_Hv50k_2016_311366	5H	N/A	630529752
JHI_Hv50k_2016_311378	5H	N/A	630712364
JHI_Hv50k_2016_311649	5H	N/A	631178294
JHI_Hv50k_2016_311714	5H	N/A	631185131
JHI_Hv50k_2016_311989	5H	N/A	632099096
JHI_Hv50k_2016_312045	5H	N/A	632195452
JHI_Hv50k_2016_312196	5H	N/A	632385250
JHI_Hv50k_2016_312208	5H	N/A	632531009
JHI_Hv50k_2016_312213	5H	N/A	632531147
JHI_Hv50k_2016_312267	5H	N/A	632993350
JHI_Hv50k_2016_312313	5H	N/A	633841878
JHI_Hv50k_2016_312526	5H	N/A	635426634
JHI_Hv50k_2016_312608	5H	N/A	635614898
JHI_Hv50k_2016_312680	5H	N/A	635858057
JHI_Hv50k_2016_312838	5H	N/A	635872329
JHI_Hv50k_2016_312984	5H	N/A	635935655
JHI_Hv50k_2016_313398	5H	N/A	636696667
JHI_Hv50k_2016_313399	5H	N/A	636709591
JHI_Hv50k_2016_313428	5H	N/A	636709831
JHI_Hv50k_2016_313521	5H	N/A	636944791
JHI_Hv50k_2016_313531	5H	N/A	636946173
JHI_Hv50k_2016_313554	5H	N/A	636946493
JHI_Hv50k_2016_313588	5H	N/A	637274386
JHI_Hv50k_2016_313605	5H	N/A	637279511
JHI_Hv50k_2016_313607	5H	N/A	637279953
JHI_Hv50k_2016_313840	5H	N/A	638399338
JHI_Hv50k_2016_314042	5H	N/A	639097549
JHI_Hv50k_2016_314087	5H	N/A	639132527
JHI_Hv50k_2016_314476	5H	N/A	640717681
JHI_Hv50k_2016_314519	5H	N/A	640774348
JHI_Hv50k_2016_314539	5H	N/A	640774739
JHI_Hv50k_2016_314543	5H	N/A	640774996
JHI_Hv50k_2016_314563	5H	N/A	641066028
JHI_Hv50k_2016_314594	5H	N/A	641245457
JHI_Hv50k_2016_314654	5H	N/A	641665179
JHI_Hv50k_2016_314664	5H	N/A	641666748

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_314851	5H	N/A	641774142
JHI_Hv50k_2016_314972	5H	N/A	642402563
JHI_Hv50k_2016_314979	5H	N/A	642402877
JHI_Hv50k_2016_315110	5H	N/A	642627422
JHI_Hv50k_2016_315442	5H	N/A	642961023
JHI_Hv50k_2016_315533	5H	N/A	643012658
JHI_Hv50k_2016_315688	5H	N/A	643312105
JHI_Hv50k_2016_315724	5H	N/A	643788268
JHI_Hv50k_2016_315794	5H	N/A	643854120
JHI_Hv50k_2016_315798	5H	N/A	643854166
JHI_Hv50k_2016_315800	5H	N/A	643976877
JHI_Hv50k_2016_316103	5H	N/A	644526507
JHI_Hv50k_2016_316154	5H	N/A	644821178
JHI_Hv50k_2016_316196	5H	N/A	644823475
JHI_Hv50k_2016_316198	5H	N/A	645008663
JHI_Hv50k_2016_316216	5H	N/A	645022846
JHI_Hv50k_2016_316239	5H	N/A	645023020
JHI_Hv50k_2016_316566	5H	N/A	645032698
JHI_Hv50k_2016_316567	5H	N/A	645036341
JHI_Hv50k_2016_316683	5H	N/A	645395095
JHI_Hv50k_2016_316827	5H	N/A	645997619
JHI_Hv50k_2016_316829	5H	N/A	645997737
JHI_Hv50k_2016_316833	5H	N/A	646083269
JHI_Hv50k_2016_316849	5H	N/A	646303671
JHI_Hv50k_2016_316854	5H	N/A	646304994
JHI_Hv50k_2016_316904	5H	N/A	646379409
JHI_Hv50k_2016_317225	5H	N/A	647031764
JHI_Hv50k_2016_317332	5H	N/A	647032885
JHI_Hv50k_2016_317355	5H	N/A	647033171
JHI_Hv50k_2016_317406	5H	N/A	647033425
JHI_Hv50k_2016_317579	5H	N/A	647375037
JHI_Hv50k_2016_317613	5H	N/A	647455043
JHI_Hv50k_2016_317616	5H	N/A	647457994
JHI_Hv50k_2016_317619	5H	N/A	647468408
JHI_Hv50k_2016_317701	5H	N/A	647654833
JHI_Hv50k_2016_317765	5H	N/A	648094167
JHI_Hv50k_2016_317777	5H	N/A	648410441
JHI_Hv50k_2016_317806	5H	N/A	648639126
JHI_Hv50k_2016_317807	5H	N/A	648639132
JHI_Hv50k_2016_317823	5H	N/A	648721305
JHI_Hv50k_2016_317826	5H	N/A	648722330
JHI_Hv50k_2016_317827	5H	N/A	648982044

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_317891	5H	N/A	648986696
JHI_Hv50k_2016_317938	5H	N/A	649188005
JHI_Hv50k_2016_318001	5H	N/A	649189202
JHI_Hv50k_2016_318073	5H	N/A	649619388
JHI_Hv50k_2016_318116	5H	N/A	649724208
JHI_Hv50k_2016_318569	5H	N/A	651129950
JHI_Hv50k_2016_318595	5H	N/A	651129960
JHI_Hv50k_2016_318596	5H	N/A	651130675
JHI_Hv50k_2016_318663	5H	N/A	651206520
JHI_Hv50k_2016_318705	5H	N/A	651254375
JHI_Hv50k_2016_318841	5H	N/A	651629250
JHI_Hv50k_2016_318863	5H	N/A	651918992
JHI_Hv50k_2016_318898	5H	N/A	652087422
JHI_Hv50k_2016_319018	5H	N/A	652243879
JHI_Hv50k_2016_319035	5H	N/A	652795482
JHI_Hv50k_2016_319057	5H	N/A	652878576
JHI_Hv50k_2016_319071	5H	N/A	652928814
JHI_Hv50k_2016_319075	5H	N/A	652929052
JHI_Hv50k_2016_319207	5H	N/A	653046871
JHI_Hv50k_2016_319280	5H	N/A	653613536
JHI_Hv50k_2016_319283	5H	N/A	653836171
JHI_Hv50k_2016_319284	5H	N/A	653916269
JHI_Hv50k_2016_319286	5H	N/A	653918246
JHI_Hv50k_2016_319289	5H	N/A	653924576
JHI_Hv50k_2016_319727	5H	N/A	654685221
JHI_Hv50k_2016_319731	5H	N/A	654686554
JHI_Hv50k_2016_319738	5H	N/A	654931160
JHI_Hv50k_2016_319876	5H	N/A	655009880
JHI_Hv50k_2016_319956	5H	N/A	655209971
JHI_Hv50k_2016_320591	5H	N/A	656066166
JHI_Hv50k_2016_320615	5H	N/A	656479427
JHI_Hv50k_2016_320649	5H	N/A	656515007
JHI_Hv50k_2016_320774	5H	N/A	656640170
JHI_Hv50k_2016_320844	5H	N/A	656666373
JHI_Hv50k_2016_320859	5H	N/A	656677823
JHI_Hv50k_2016_320871	5H	N/A	656836232
JHI_Hv50k_2016_320904	5H	N/A	656836454
JHI_Hv50k_2016_320980	5H	N/A	656988064
JHI_Hv50k_2016_320981	5H	N/A	656988868
JHI_Hv50k_2016_321002	5H	N/A	657005264
JHI_Hv50k_2016_321033	5H	N/A	657110091
JHI_Hv50k_2016_321044	5H	N/A	657110225

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_321137	5H	N/A	657400938
JHI_Hv50k_2016_321141	5H	N/A	657401043
JHI_Hv50k_2016_321732	5H	N/A	658362841
JHI_Hv50k_2016_321795	5H	N/A	658786657
JHI_Hv50k_2016_322078	5H	N/A	659215705
JHI_Hv50k_2016_322082	5H	N/A	659219236
JHI_Hv50k_2016_322277	5H	N/A	659697400
JHI_Hv50k_2016_322356	5H	N/A	659783874
JHI_Hv50k_2016_322375	5H	N/A	659823804
JHI_Hv50k_2016_322427	5H	N/A	659842931
JHI_Hv50k_2016_322469	5H	N/A	660065923
JHI_Hv50k_2016_322514	5H	N/A	660951502
JHI_Hv50k_2016_322523	5H	N/A	660979322
JHI_Hv50k_2016_322553	5H	N/A	661139789
JHI_Hv50k_2016_322760	5H	N/A	661219615
JHI_Hv50k_2016_322766	5H	N/A	661389287
JHI_Hv50k_2016_322771	5H	N/A	661443834
JHI_Hv50k_2016_322781	5H	N/A	661522423
JHI_Hv50k_2016_322786	5H	N/A	661522878
JHI_Hv50k_2016_322787	5H	N/A	661522879
JHI_Hv50k_2016_322789	5H	N/A	661523390
JHI_Hv50k_2016_322791	5H	N/A	661526013
JHI_Hv50k_2016_322792	5H	N/A	661526522
JHI_Hv50k_2016_322815	5H	N/A	661529319
JHI_Hv50k_2016_322825	5H	N/A	661529865
JHI_Hv50k_2016_322830	5H	N/A	661583335
JHI_Hv50k_2016_322965	5H	N/A	661771402
JHI_Hv50k_2016_322967	5H	N/A	661771471
JHI_Hv50k_2016_322978	5H	N/A	661771853
JHI_Hv50k_2016_322991	5H	N/A	661772245
JHI_Hv50k_2016_323037	5H	N/A	661789029
JHI_Hv50k_2016_323097	5H	N/A	661997658
JHI_Hv50k_2016_323121	5H	N/A	661997776
JHI_Hv50k_2016_323146	5H	N/A	661998338
JHI_Hv50k_2016_323150	5H	N/A	661998642
JHI_Hv50k_2016_323155	5H	N/A	661999165
JHI_Hv50k_2016_323179	5H	N/A	662046668
JHI_Hv50k_2016_323183	5H	N/A	662088043
JHI_Hv50k_2016_323227	5H	N/A	662197221
JHI_Hv50k_2016_323237	5H	N/A	662197837
JHI_Hv50k_2016_323248	5H	N/A	662258273
JHI_Hv50k_2016_323252	5H	N/A	662258319

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_323438	5H	N/A	662628744
JHI_Hv50k_2016_323476	5H	N/A	662748947
JHI_Hv50k_2016_323498	5H	N/A	662755078
JHI_Hv50k_2016_323547	5H	N/A	662808478
JHI_Hv50k_2016_323623	5H	N/A	663156749
JHI_Hv50k_2016_324085	5H	N/A	663498872
JHI_Hv50k_2016_324180	5H	N/A	663783974
JHI_Hv50k_2016_324297	5H	N/A	664096715
JHI_Hv50k_2016_324298	5H	N/A	664209428
JHI_Hv50k_2016_324309	5H	N/A	664210667
JHI_Hv50k_2016_324311	5H	N/A	664211097
JHI_Hv50k_2016_324380	5H	N/A	664246120
JHI_Hv50k_2016_324404	5H	N/A	664302045
JHI_Hv50k_2016_324591	5H	N/A	664626197
JHI_Hv50k_2016_324601	5H	N/A	664637724
JHI_Hv50k_2016_324685	5H	N/A	664717590
JHI_Hv50k_2016_324694	5H	N/A	664717846
JHI_Hv50k_2016_324701	5H	N/A	664718231
JHI_Hv50k_2016_324768	5H	N/A	664938381
JHI_Hv50k_2016_324769	5H	N/A	664995130
JHI_Hv50k_2016_324774	5H	N/A	665051160
JHI_Hv50k_2016_324775	5H	N/A	665051753
JHI_Hv50k_2016_325123	5H	N/A	665765536
JHI_Hv50k_2016_325133	5H	N/A	665989304
JHI_Hv50k_2016_325450	5H	N/A	666712142
JHI_Hv50k_2016_325617	5H	N/A	666827535
JHI_Hv50k_2016_325672	5H	N/A	667068876
JHI_Hv50k_2016_325943	5H	N/A	667344834
JHI_Hv50k_2016_326092	5H	N/A	667544190
JHI_Hv50k_2016_326126	5H	N/A	667546588
JHI_Hv50k_2016_326132	5H	N/A	667582670
JHI_Hv50k_2016_326144	5H	N/A	667663971
JHI_Hv50k_2016_326147	5H	N/A	667677094
JHI_Hv50k_2016_326148	5H	N/A	667677804
JHI_Hv50k_2016_326149	5H	N/A	667698865
JHI_Hv50k_2016_326289	5H	N/A	668007753
JHI_Hv50k_2016_326334	5H	N/A	668032376
JHI_Hv50k_2016_326336	5H	N/A	668032520
JHI_Hv50k_2016_326414	5H	N/A	668081413
JHI_Hv50k_2016_326785	5H	N/A	668107710
JHI_Hv50k_2016_326790	5H	N/A	668107725
JHI_Hv50k_2016_326801	5H	N/A	668161346

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_326846	5H	N/A	668165239
JHI_Hv50k_2016_326899	5H	N/A	668263274
JHI_Hv50k_2016_327020	5H	N/A	668340990
JHI_Hv50k_2016_327029	5H	N/A	668341081
JHI_Hv50k_2016_327138	5H	N/A	668607455
JHI_Hv50k_2016_327189	5H	N/A	668607733
JHI_Hv50k_2016_327190	5H	N/A	668607893
JHI_Hv50k_2016_327212	5H	N/A	668608069
JHI_Hv50k_2016_327388	5H	N/A	668638576
JHI_Hv50k_2016_327399	5H	N/A	668642360
JHI_Hv50k_2016_327426	5H	N/A	668643769
JHI_Hv50k_2016_327454	5H	N/A	668684143
JHI_Hv50k_2016_327486	5H	N/A	668686881
JHI_Hv50k_2016_327493	5H	N/A	668687251
JHI_Hv50k_2016_327702	5H	N/A	669623141
JHI_Hv50k_2016_327707	5H	N/A	669623517
JHI_Hv50k_2016_327835	5H	N/A	330411
JHI_Hv50k_2016_327871	5H	N/A	342757
JHI_Hv50k_2016_327990	5H	N/A	980568
JHI_Hv50k_2016_328943	5H	N/A	1589699
JHI_Hv50k_2016_329268	5H	N/A	3391307
JHI_Hv50k_2016_331002	5H	N/A	4890191
JHI_Hv50k_2016_331071	5H	N/A	4963187
JHI_Hv50k_2016_331093	5H	N/A	4997851
JHI_Hv50k_2016_331267	5H	N/A	5170590
JHI_Hv50k_2016_331308	5H	N/A	5174362
JHI_Hv50k_2016_331730	5H	N/A	5661183
JHI_Hv50k_2016_331947	5H	N/A	5819707
JHI_Hv50k_2016_332346	5H	N/A	6352160
JHI_Hv50k_2016_332519	5H	N/A	6979830
JHI_Hv50k_2016_332523	5H	N/A	7031590
JHI_Hv50k_2016_332591	5H	N/A	7035522
JHI_Hv50k_2016_332628	5H	N/A	7106487
JHI_Hv50k_2016_332811	5H	N/A	7539210
JHI_Hv50k_2016_332845	5H	N/A	7637833
JHI_Hv50k_2016_332921	5H	N/A	7809451
JHI_Hv50k_2016_332986	5H	N/A	7834204
JHI_Hv50k_2016_333320	5H	N/A	8038386
JHI_Hv50k_2016_333327	5H	N/A	8094559
JHI_Hv50k_2016_333334	5H	N/A	8161618
JHI_Hv50k_2016_333424	5H	N/A	8455652
JHI_Hv50k_2016_333445	5H	N/A	8539108

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_333580	5H	N/A	8542409
JHI_Hv50k_2016_333582	5H	N/A	8542496
JHI_Hv50k_2016_333663	5H	N/A	8563536
JHI_Hv50k_2016_333734	5H	N/A	9156204
JHI_Hv50k_2016_333873	5H	N/A	9849360
JHI_Hv50k_2016_333888	5H	N/A	9850825
JHI_Hv50k_2016_333982	5H	N/A	10326662
JHI_Hv50k_2016_334009	5H	N/A	10327299
JHI_Hv50k_2016_334019	5H	N/A	10435033
JHI_Hv50k_2016_334048	5H	N/A	10693154
JHI_Hv50k_2016_334107	5H	N/A	10714251
JHI_Hv50k_2016_334293	5H	N/A	11062630
JHI_Hv50k_2016_334470	5H	N/A	11572699
JHI_Hv50k_2016_334519	5H	N/A	11584090
JHI_Hv50k_2016_334532	5H	N/A	11591736
JHI_Hv50k_2016_334536	5H	N/A	11594356
JHI_Hv50k_2016_334556	5H	N/A	11920410
JHI_Hv50k_2016_334596	5H	N/A	11933952
JHI_Hv50k_2016_334609	5H	N/A	12013305
JHI_Hv50k_2016_334631	5H	N/A	12013658
JHI_Hv50k_2016_334734	5H	N/A	12283083
JHI_Hv50k_2016_334913	5H	N/A	12300933
JHI_Hv50k_2016_334929	5H	N/A	12304072
JHI_Hv50k_2016_335092	5H	N/A	12314220
JHI_Hv50k_2016_335112	5H	N/A	12371765
JHI_Hv50k_2016_335695	5H	N/A	13136231
JHI_Hv50k_2016_335909	5H	N/A	13764910
JHI_Hv50k_2016_335951	5H	N/A	13960725
JHI_Hv50k_2016_335957	5H	N/A	14070575
JHI_Hv50k_2016_335965	5H	N/A	14280071
JHI_Hv50k_2016_336035	5H	N/A	14330154
JHI_Hv50k_2016_336100	5H	N/A	14331834
JHI_Hv50k_2016_336182	5H	N/A	14499794
JHI_Hv50k_2016_336184	5H	N/A	14500273
JHI_Hv50k_2016_336307	5H	N/A	14563324
JHI_Hv50k_2016_336409	5H	N/A	15314726
JHI_Hv50k_2016_336485	5H	N/A	15546212
JHI_Hv50k_2016_336530	5H	N/A	15816898
JHI_Hv50k_2016_336825	5H	N/A	16214276
JHI_Hv50k_2016_336914	5H	N/A	16280175
JHI_Hv50k_2016_336981	5H	N/A	16375754
JHI_Hv50k_2016_336982	5H	N/A	16388106

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_336985	5H	N/A	16388484
JHI_Hv50k_2016_337233	5H	N/A	16442725
JHI_Hv50k_2016_337256	5H	N/A	16443423
JHI_Hv50k_2016_337292	5H	N/A	16478459
JHI_Hv50k_2016_337522	5H	N/A	16584646
JHI_Hv50k_2016_337638	5H	N/A	16632963
JHI_Hv50k_2016_337642	5H	N/A	16633246
JHI_Hv50k_2016_337685	5H	N/A	16749593
JHI_Hv50k_2016_337688	5H	N/A	16869967
JHI_Hv50k_2016_337694	5H	N/A	16877584
JHI_Hv50k_2016_337706	5H	N/A	16878353
JHI_Hv50k_2016_337709	5H	N/A	16890650
JHI_Hv50k_2016_337720	5H	N/A	16890908
JHI_Hv50k_2016_337721	5H	N/A	16892233
JHI_Hv50k_2016_337798	5H	N/A	16900130
JHI_Hv50k_2016_337800	5H	N/A	16900243
JHI_Hv50k_2016_337879	5H	N/A	17088063
JHI_Hv50k_2016_337944	5H	N/A	17551767
JHI_Hv50k_2016_337952	5H	N/A	17552594
JHI_Hv50k_2016_337966	5H	N/A	17570572
JHI_Hv50k_2016_337999	5H	N/A	17809701
JHI_Hv50k_2016_338020	5H	N/A	18484902
JHI_Hv50k_2016_338033	5H	N/A	18485894
JHI_Hv50k_2016_338081	5H	N/A	18824277
JHI_Hv50k_2016_338174	5H	N/A	18902488
JHI_Hv50k_2016_338297	5H	N/A	19314531
JHI_Hv50k_2016_338812	5H	N/A	21311510
JHI_Hv50k_2016_339757	5H	N/A	23623291
JHI_Hv50k_2016_339937	5H	N/A	24161048
JHI_Hv50k_2016_340216	5H	N/A	24645160
JHI_Hv50k_2016_340365	5H	N/A	24668006
JHI_Hv50k_2016_340515	5H	N/A	25047179
JHI_Hv50k_2016_341123	5H	N/A	26768165
JHI_Hv50k_2016_341542	5H	N/A	28205200
JHI_Hv50k_2016_341590	5H	N/A	28205270
JHI_Hv50k_2016_342331	5H	N/A	30846841
JHI_Hv50k_2016_342543	5H	N/A	30966590
JHI_Hv50k_2016_342553	5H	N/A	30969379
JHI_Hv50k_2016_342631	5H	N/A	31017513
JHI_Hv50k_2016_342636	5H	N/A	31141609
JHI_Hv50k_2016_342700	5H	N/A	31192378
JHI_Hv50k_2016_342741	5H	N/A	31198782

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_343060	5H	N/A	31704416
JHI_Hv50k_2016_343321	5H	N/A	32382209
JHI_Hv50k_2016_343370	5H	N/A	32383493
JHI_Hv50k_2016_343392	5H	N/A	33011742
JHI_Hv50k_2016_345222	5H	N/A	37477912
JHI_Hv50k_2016_346016	5H	N/A	39432561
JHI_Hv50k_2016_346198	5H	N/A	39470226
JHI_Hv50k_2016_346217	5H	N/A	39489597
JHI_Hv50k_2016_347072	5H	N/A	50799106
JHI_Hv50k_2016_347691	5H	N/A	60836368
JHI_Hv50k_2016_347951	5H	N/A	63827231
JHI_Hv50k_2016_347997	5H	N/A	64014716
JHI_Hv50k_2016_348057	5H	N/A	65596600
JHI_Hv50k_2016_348062	5H	N/A	66188950
JHI_Hv50k_2016_348156	5H	N/A	68138115
JHI_Hv50k_2016_348196	5H	N/A	69833083
JHI_Hv50k_2016_348446	5H	N/A	77382148
JHI_Hv50k_2016_348775	5H	N/A	91938522
JHI_Hv50k_2016_349258	5H	N/A	109850093
JHI_Hv50k_2016_349524	5H	N/A	118332860
JHI_Hv50k_2016_349526	5H	N/A	118535766
JHI_Hv50k_2016_349531	5H	N/A	118998875
JHI_Hv50k_2016_349861	5H	N/A	133167845
JHI_Hv50k_2016_349981	5H	N/A	136211533
JHI_Hv50k_2016_350279	5H	N/A	144739550
JHI_Hv50k_2016_350380	5H	N/A	146119058
JHI_Hv50k_2016_350559	5H	N/A	148643454
JHI_Hv50k_2016_350643	5H	N/A	149602534
JHI_Hv50k_2016_350756	5H	N/A	150490404
JHI_Hv50k_2016_351248	5H	N/A	157620109
JHI_Hv50k_2016_351364	5H	N/A	161984059
JHI_Hv50k_2016_352396	5H	N/A	187533801
JHI_Hv50k_2016_352644	5H	N/A	194659213
JHI_Hv50k_2016_352672	5H	N/A	195457853
JHI_Hv50k_2016_352997	5H	N/A	201395975
JHI_Hv50k_2016_353535	5H	N/A	223065521
JHI_Hv50k_2016_354345	5H	N/A	258343071
JHI_Hv50k_2016_354659	5H	N/A	269294155
JHI_Hv50k_2016_354871	5H	N/A	281977261
JHI_Hv50k_2016_358193	5H	N/A	353294396
JHI_Hv50k_2016_358212	5H	N/A	353406644
JHI_Hv50k_2016_358214	5H	N/A	353408348

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_358293	5H	N/A	355027322
JHI_Hv50k_2016_358309	5H	N/A	355854346
JHI_Hv50k_2016_358460	5H	N/A	363827489
JHI_Hv50k_2016_358978	5H	N/A	373947869
JHI_Hv50k_2016_359126	5H	N/A	374645453
JHI_Hv50k_2016_359251	5H	N/A	376643350
JHI_Hv50k_2016_359326	5H	N/A	378974018
JHI_Hv50k_2016_359328	5H	N/A	378976091
JHI_Hv50k_2016_359365	5H	N/A	379783564
JHI_Hv50k_2016_359405	5H	N/A	379784492
JHI_Hv50k_2016_359412	5H	N/A	379784853
JHI_Hv50k_2016_359473	5H	N/A	380200042
JHI_Hv50k_2016_359586	5H	N/A	381030642
JHI_Hv50k_2016_359855	5H	N/A	385256940
JHI_Hv50k_2016_359869	5H	N/A	386944681
JHI_Hv50k_2016_360177	5H	N/A	391871912
JHI_Hv50k_2016_360277	5H	N/A	392078244
JHI_Hv50k_2016_360294	5H	N/A	392349289
JHI_Hv50k_2016_360298	5H	N/A	392467757
JHI_Hv50k_2016_360507	5H	N/A	395215173
JHI_Hv50k_2016_360588	5H	N/A	395605995
JHI_Hv50k_2016_360644	5H	N/A	396127690
JHI_Hv50k_2016_360660	5H	N/A	396139433
JHI_Hv50k_2016_360689	5H	N/A	396144552
JHI_Hv50k_2016_360936	5H	N/A	396727882
JHI_Hv50k_2016_360937	5H	N/A	397037213
JHI_Hv50k_2016_360941	5H	N/A	397638942
JHI_Hv50k_2016_360992	5H	N/A	399379778
JHI_Hv50k_2016_360993	5H	N/A	400155607
JHI_Hv50k_2016_360994	5H	N/A	400167616
JHI_Hv50k_2016_360998	5H	N/A	400963737
JHI_Hv50k_2016_361020	5H	N/A	401161340
JHI_Hv50k_2016_361045	5H	N/A	401470999
JHI_Hv50k_2016_361069	5H	N/A	401478075
JHI_Hv50k_2016_361116	5H	N/A	402638037
JHI_Hv50k_2016_361130	5H	N/A	403606353
JHI_Hv50k_2016_361173	5H	N/A	404649084
JHI_Hv50k_2016_361175	5H	N/A	404652449
JHI_Hv50k_2016_361213	5H	N/A	405010660
JHI_Hv50k_2016_361424	5H	N/A	406915022
JHI_Hv50k_2016_361467	5H	N/A	408531208
JHI_Hv50k_2016_361479	5H	N/A	408977454

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_361562	5H	N/A	409828110
JHI_Hv50k_2016_361598	5H	N/A	410039915
JHI_Hv50k_2016_361640	5H	N/A	410500947
JHI_Hv50k_2016_361644	5H	N/A	410504163
JHI_Hv50k_2016_361670	5H	N/A	410506086
JHI_Hv50k_2016_361989	5H	N/A	417073135
JHI_Hv50k_2016_362138	5H	N/A	417612600
JHI_Hv50k_2016_362139	5H	N/A	417826795
JHI_Hv50k_2016_362170	5H	N/A	418397616
JHI_Hv50k_2016_362182	5H	N/A	418527638
JHI_Hv50k_2016_362189	5H	N/A	420832505
JHI_Hv50k_2016_362259	5H	N/A	425433102
JHI_Hv50k_2016_362340	5H	N/A	429327213
JHI_Hv50k_2016_362392	5H	N/A	431199929
JHI_Hv50k_2016_362460	5H	N/A	432541147
JHI_Hv50k_2016_362471	5H	N/A	433014087
JHI_Hv50k_2016_362549	5H	N/A	434910711
JHI_Hv50k_2016_362565	5H	N/A	435260539
JHI_Hv50k_2016_362587	5H	N/A	436278882
JHI_Hv50k_2016_362624	5H	N/A	437258974
JHI_Hv50k_2016_362645	5H	N/A	437717160
JHI_Hv50k_2016_362729	5H	N/A	439951274
JHI_Hv50k_2016_362931	5H	N/A	442930059
JHI_Hv50k_2016_362943	5H	N/A	443048015
JHI_Hv50k_2016_362947	5H	N/A	444709150
JHI_Hv50k_2016_362983	5H	N/A	446938150
JHI_Hv50k_2016_362994	5H	N/A	447499891
JHI_Hv50k_2016_362998	5H	N/A	448135436
JHI_Hv50k_2016_362999	5H	N/A	448166989
JHI_Hv50k_2016_363030	5H	N/A	450930890
JHI_Hv50k_2016_363037	5H	N/A	451266503
JHI_Hv50k_2016_363048	5H	N/A	452114186
JHI_Hv50k_2016_363055	5H	N/A	452631838
JHI_Hv50k_2016_363058	5H	N/A	454149209
JHI_Hv50k_2016_363288	5H	N/A	461079345
JHI_Hv50k_2016_363290	5H	N/A	461114068
JHI_Hv50k_2016_363306	5H	N/A	461870555
JHI_Hv50k_2016_363493	5H	N/A	462703088
JHI_Hv50k_2016_363674	5H	N/A	463683432
JHI_Hv50k_2016_363693	5H	N/A	463684004
JHI_Hv50k_2016_363801	5H	N/A	465303610
JHI_Hv50k_2016_363815	5H	N/A	465304084

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_363831	5H	N/A	465690233
JHI_Hv50k_2016_363837	5H	N/A	467890577
JHI_Hv50k_2016_363859	5H	N/A	467893402
JHI_Hv50k_2016_363863	5H	N/A	467893908
JHI_Hv50k_2016_363900	5H	N/A	469166692
JHI_Hv50k_2016_363918	5H	N/A	470634130
JHI_Hv50k_2016_364306	5H	N/A	472240778
JHI_Hv50k_2016_364522	5H	N/A	477077114
JHI_Hv50k_2016_364597	5H	N/A	477164043
JHI_Hv50k_2016_364763	5H	N/A	477800925
JHI_Hv50k_2016_364765	5H	N/A	477802316
JHI_Hv50k_2016_364768	5H	N/A	478110731
JHI_Hv50k_2016_364806	5H	N/A	478391565
JHI_Hv50k_2016_365175	5H	N/A	480000867
JHI_Hv50k_2016_365227	5H	N/A	481012963
JHI_Hv50k_2016_365259	5H	N/A	481685452
JHI_Hv50k_2016_365302	5H	N/A	481692870
JHI_Hv50k_2016_365311	5H	N/A	481836073
JHI_Hv50k_2016_365416	5H	N/A	481838876
JHI_Hv50k_2016_365534	5H	N/A	481844728
JHI_Hv50k_2016_365725	5H	N/A	481848811
JHI_Hv50k_2016_365856	5H	N/A	482555036
JHI_Hv50k_2016_365907	5H	N/A	483150567
JHI_Hv50k_2016_365954	5H	N/A	483620774
JHI_Hv50k_2016_366162	5H	N/A	488887424
JHI_Hv50k_2016_366199	5H	N/A	490060558
JHI_Hv50k_2016_366337	5H	N/A	491265347
JHI_Hv50k_2016_366349	5H	N/A	491273528
JHI_Hv50k_2016_366488	5H	N/A	493231694
JHI_Hv50k_2016_366553	5H	N/A	493901806
JHI_Hv50k_2016_366688	5H	N/A	495790017
JHI_Hv50k_2016_367342	5H	N/A	502462773
SCRI_RS_169941	6H	0.5	507569038
BOPA1_5159_579	6H	1.4	507569313
SCRI_RS_194023	6H	2.6	507759961
SCRI_RS_211856	6H	5.87	510422150
SCRI_RS_202485	6H	9.89	512009155
SCRI_RS_206183	6H	10.29	512009252
BOPA1_ConsensusGBS0346_1	6H	14.26	512226026
BOPA1_2795_1707	6H	15.16	512837699
SCRI_RS_139715	6H	16.16	513103090
SCRI_RS_202723	6H	16.56	513118642

Marker	Chromosome	Position (cM)	Position (BP)
SCRI_RS_20187	6H	16.66	514043517
BOPA1_1769_545	6H	17.58	514099813
SCRI_RS_222092	6H	30.99	516261542
BOPA1_3164_1386	6H	41.35	517931163
BOPA1_12210_480	6H	50.41	518254158
BOPA1_5448_298	6H	50.61	519247281
SCRI_RS_119674	6H	54.1	521539362
SCRI_RS_151282	6H	54.1	522149972
SCRI_RS_168111	6H	54.1	522151623
SCRI_RS_196459	6H	54.1	522764494
SCRI_RS_200882	6H	54.1	522942007
SCRI_RS_236452	6H	54.1	524080668
SCRI_RS_234724	6H	54.2	525418280
SCRI_RS_192720	6H	55.08	526470988
SCRI_RS_239962	6H	55.08	526479600
BOPA2_12_30782	6H	55.36	526683519
BOPA2_12_30510	6H	55.48	526685179
BOPA1_4070_386	6H	55.9	527175033
SCRI_RS_116842	6H	55.9	527176552
BOPA1_1009_1089	6H	56.78	527401592
BOPA2_12_30473	6H	57.64	528059388
SCRI_RS_13935	6H	59.21	534740966
BOPA1_3656_341	6H	59.33	535400590
SCRI_RS_174583	6H	60.71	535842978
SCRI_RS_129321	6H	62.91	535848272
SCRI_RS_170672	6H	63.9	535848905
SCRI_RS_232544	6H	63.9	535849165
BOPA1_2298_1526	6H	64.29	536025416
BOPA1_832_1040	6H	65.08	536069662
SCRI_RS_211289	6H	65.08	536069757
SCRI_RS_137824	6H	65.28	536069852
SCRI_RS_167	6H	65.38	536081466
BOPA1_5554_1971	6H	71.69	536282758
BOPA2_12_31289	6H	74.18	537723034
SCRI_RS_175370	6H	75.2	538086674
BOPA2_12_31101	6H	76.14	538352769
SCRI_RS_205971	6H	77.4	538635801
SCRI_RS_231790	6H	77.7	538643382
SCRI_RS_152324	6H	78.06	538665726
SCRI_RS_167655	6H	78.06	539063294
SCRI_RS_145279	6H	78.26	539063939
SCRI_RS_143317	6H	78.53	539063996

Marker	Chromosome	Position (cM)	Position (BP)
BOPA1_4454_1080	6H	78.76	539363533
SCRI_RS_129756	6H	79.43	539878351
SCRI_RS_137870	6H	79.83	540211481
SCRI_RS_13815	6H	79.83	540214402
SCRI_RS_193336	6H	79.83	540576612
SCRI_RS_206976	6H	80.23	540809136
BOPA1_2047_850	6H	80.31	540811295
SCRI_RS_170674	6H	83.73	541278010
SCRI_RS_153166	6H	87.72	541491436
SCRI_RS_164037	6H	92.72	541821951
SCRI_RS_182637	6H	96.47	542336536
SCRI_RS_120442	6H	100.63	542940342
BOPA1_3349_759	6H	102.03	543370234
SCRI_RS_158871	6H	102.63	543533490
BOPA2_12_10704	6H	106.49	543533512
SCRI_RS_8034	6H	107.43	543604352
BOPA1_10687_540	6H	110.59	543610730
SCRI_RS_3070	6H	110.59	543611669
BOPA1_3047_1400	6H	110.79	543737952
BOPA1_428_1519	6H	110.79	543738318
SCRI_RS_128218	6H	111.09	543738599
SCRI_RS_626	6H	115.09	544657143
SCRI_RS_144541	6H	115.49	545266695
BOPA1_4396_567	6H	122.99	545563147
BOPA2_12_31126	6H	124.21	545727109
BOPA1_ABC08038_1_3_160	6H	124.72	545736928
SCRI_RS_226875	6H	126.01	545954958
SCRI_RS_205578	6H	126.11	546165565
SCRI_RS_9648	6H	129.12	546518078
SCRI_RS_223104	6H	136.62	546760377
SCRI_RS_229960	6H	136.62	546761285
BOPA2_12_30956	6H	139.39	546897085
JHI_Hv50k_2016_367980	6H	N/A	547085267
JHI_Hv50k_2016_368196	6H	N/A	547251071
JHI_Hv50k_2016_368230	6H	N/A	547256507
JHI_Hv50k_2016_368691	6H	N/A	548146024
JHI_Hv50k_2016_368692	6H	N/A	548245869
JHI_Hv50k_2016_368699	6H	N/A	548249202
JHI_Hv50k_2016_368707	6H	N/A	548290007
JHI_Hv50k_2016_368708	6H	N/A	548433147
JHI_Hv50k_2016_368893	6H	N/A	549256145
JHI_Hv50k_2016_369164	6H	N/A	550504158

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_369506	6H	N/A	552736800
JHI_Hv50k_2016_369893	6H	N/A	553922774
JHI_Hv50k_2016_370436	6H	N/A	555831111
JHI_Hv50k_2016_370791	6H	N/A	557854612
JHI_Hv50k_2016_370838	6H	N/A	557943048
JHI_Hv50k_2016_371127	6H	N/A	558862422
JHI_Hv50k_2016_371325	6H	N/A	558902973
JHI_Hv50k_2016_371331	6H	N/A	559351392
JHI_Hv50k_2016_371347	6H	N/A	559467449
JHI_Hv50k_2016_371357	6H	N/A	559467566
JHI_Hv50k_2016_371365	6H	N/A	559470101
JHI_Hv50k_2016_371378	6H	N/A	559707003
JHI_Hv50k_2016_371390	6H	N/A	559750255
JHI_Hv50k_2016_371391	6H	N/A	559751312
JHI_Hv50k_2016_371398	6H	N/A	559840153
JHI_Hv50k_2016_371418	6H	N/A	559876316
JHI_Hv50k_2016_371498	6H	N/A	560045056
JHI_Hv50k_2016_371503	6H	N/A	560054931
JHI_Hv50k_2016_371508	6H	N/A	560157418
JHI_Hv50k_2016_371598	6H	N/A	560159921
JHI_Hv50k_2016_371605	6H	N/A	560435971
JHI_Hv50k_2016_371619	6H	N/A	560626610
JHI_Hv50k_2016_371631	6H	N/A	560911867
JHI_Hv50k_2016_371719	6H	N/A	560912986
JHI_Hv50k_2016_371727	6H	N/A	560913362
JHI_Hv50k_2016_371731	6H	N/A	560913526
JHI_Hv50k_2016_371732	6H	N/A	560913899
JHI_Hv50k_2016_371826	6H	N/A	560914456
JHI_Hv50k_2016_371873	6H	N/A	560914566
JHI_Hv50k_2016_372009	6H	N/A	561098751
JHI_Hv50k_2016_372059	6H	N/A	561098823
JHI_Hv50k_2016_372259	6H	N/A	561400729
JHI_Hv50k_2016_372298	6H	N/A	561564843
JHI_Hv50k_2016_372356	6H	N/A	561584301
JHI_Hv50k_2016_372364	6H	N/A	561618730
JHI_Hv50k_2016_372369	6H	N/A	561626309
JHI_Hv50k_2016_372815	6H	N/A	561628538
JHI_Hv50k_2016_372826	6H	N/A	561628642
JHI_Hv50k_2016_372848	6H	N/A	561629538
JHI_Hv50k_2016_372853	6H	N/A	561629557
JHI_Hv50k_2016_372879	6H	N/A	561630110
JHI_Hv50k_2016_372938	6H	N/A	561630494

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_372953	6H	N/A	561632274
JHI_Hv50k_2016_373042	6H	N/A	561832544
JHI_Hv50k_2016_373104	6H	N/A	561991408
JHI_Hv50k_2016_373107	6H	N/A	561998798
JHI_Hv50k_2016_373113	6H	N/A	562087742
JHI_Hv50k_2016_373307	6H	N/A	562781468
JHI_Hv50k_2016_373354	6H	N/A	562812780
JHI_Hv50k_2016_373372	6H	N/A	562815089
JHI_Hv50k_2016_373399	6H	N/A	562817604
JHI_Hv50k_2016_373484	6H	N/A	562864810
JHI_Hv50k_2016_373554	6H	N/A	563076620
JHI_Hv50k_2016_373745	6H	N/A	563282001
JHI_Hv50k_2016_373819	6H	N/A	563561183
JHI_Hv50k_2016_373821	6H	N/A	563562045
JHI_Hv50k_2016_373942	6H	N/A	563842808
JHI_Hv50k_2016_374006	6H	N/A	563994904
JHI_Hv50k_2016_374033	6H	N/A	564073929
JHI_Hv50k_2016_374056	6H	N/A	564085976
JHI_Hv50k_2016_374260	6H	N/A	565059591
JHI_Hv50k_2016_374302	6H	N/A	565062211
JHI_Hv50k_2016_374479	6H	N/A	565493522
JHI_Hv50k_2016_374480	6H	N/A	565493630
JHI_Hv50k_2016_374661	6H	N/A	565493928
JHI_Hv50k_2016_374701	6H	N/A	565495409
JHI_Hv50k_2016_374972	6H	N/A	565497124
JHI_Hv50k_2016_375012	6H	N/A	565497477
JHI_Hv50k_2016_375013	6H	N/A	565497503
JHI_Hv50k_2016_375081	6H	N/A	565576337
JHI_Hv50k_2016_375198	6H	N/A	565615314
JHI_Hv50k_2016_375488	6H	N/A	565731953
JHI_Hv50k_2016_375489	6H	N/A	565733142
JHI_Hv50k_2016_376156	6H	N/A	566296744
JHI_Hv50k_2016_376157	6H	N/A	566370701
JHI_Hv50k_2016_376166	6H	N/A	566410167
JHI_Hv50k_2016_376229	6H	N/A	566413812
JHI_Hv50k_2016_376446	6H	N/A	566449245
JHI_Hv50k_2016_376871	6H	N/A	567134476
JHI_Hv50k_2016_377032	6H	N/A	567208867
JHI_Hv50k_2016_377043	6H	N/A	567221199
JHI_Hv50k_2016_377313	6H	N/A	567649884
JHI_Hv50k_2016_377325	6H	N/A	567652676
JHI_Hv50k_2016_377329	6H	N/A	567911525

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_377341	6H	N/A	567912968
JHI_Hv50k_2016_377413	6H	N/A	568224978
JHI_Hv50k_2016_377566	6H	N/A	568278035
JHI_Hv50k_2016_377584	6H	N/A	568280437
JHI_Hv50k_2016_377636	6H	N/A	568302735
JHI_Hv50k_2016_377649	6H	N/A	568302969
JHI_Hv50k_2016_377667	6H	N/A	568303103
JHI_Hv50k_2016_377672	6H	N/A	568303144
JHI_Hv50k_2016_377677	6H	N/A	568472235
JHI_Hv50k_2016_377710	6H	N/A	569743557
JHI_Hv50k_2016_377723	6H	N/A	569745449
JHI_Hv50k_2016_377772	6H	N/A	570053771
JHI_Hv50k_2016_377788	6H	N/A	570137780
JHI_Hv50k_2016_377802	6H	N/A	570261682
JHI_Hv50k_2016_377851	6H	N/A	570406533
JHI_Hv50k_2016_377942	6H	N/A	570955817
JHI_Hv50k_2016_378043	6H	N/A	571406660
JHI_Hv50k_2016_378295	6H	N/A	571848152
JHI_Hv50k_2016_378309	6H	N/A	571851512
JHI_Hv50k_2016_378310	6H	N/A	571851645
JHI_Hv50k_2016_378314	6H	N/A	571852437
JHI_Hv50k_2016_378826	6H	N/A	573485616
JHI_Hv50k_2016_378831	6H	N/A	573489280
JHI_Hv50k_2016_378854	6H	N/A	573534087
JHI_Hv50k_2016_378880	6H	N/A	573659868
JHI_Hv50k_2016_379186	6H	N/A	575061137
JHI_Hv50k_2016_379225	6H	N/A	575160623
JHI_Hv50k_2016_379329	6H	N/A	575422609
JHI_Hv50k_2016_379632	6H	N/A	576454210
JHI_Hv50k_2016_379641	6H	N/A	576454692
JHI_Hv50k_2016_379653	6H	N/A	576479375
JHI_Hv50k_2016_380005	6H	N/A	577460714
JHI_Hv50k_2016_380301	6H	N/A	577615089
JHI_Hv50k_2016_380356	6H	N/A	577769461
JHI_Hv50k_2016_380360	6H	N/A	577774107
JHI_Hv50k_2016_380422	6H	N/A	577828241
JHI_Hv50k_2016_380489	6H	N/A	578238672
JHI_Hv50k_2016_380600	6H	N/A	578396049
JHI_Hv50k_2016_380732	6H	N/A	578720838
JHI_Hv50k_2016_380948	6H	N/A	578870420
JHI_Hv50k_2016_381219	6H	N/A	578970224
JHI_Hv50k_2016_381291	6H	N/A	579213240

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_381312	6H	N/A	579219212
JHI_Hv50k_2016_381313	6H	N/A	579229349
JHI_Hv50k_2016_381396	6H	N/A	579290143
JHI_Hv50k_2016_381471	6H	N/A	579490548
JHI_Hv50k_2016_381518	6H	N/A	579519901
JHI_Hv50k_2016_381520	6H	N/A	579522181
JHI_Hv50k_2016_381804	6H	N/A	579612988
JHI_Hv50k_2016_381817	6H	N/A	579615905
JHI_Hv50k_2016_381828	6H	N/A	579818116
JHI_Hv50k_2016_381829	6H	N/A	579825513
JHI_Hv50k_2016_381860	6H	N/A	579836546
JHI_Hv50k_2016_381882	6H	N/A	579839037
JHI_Hv50k_2016_381948	6H	N/A	579884304
JHI_Hv50k_2016_382095	6H	N/A	580187141
JHI_Hv50k_2016_382157	6H	N/A	580195488
JHI_Hv50k_2016_382190	6H	N/A	580309552
JHI_Hv50k_2016_382495	6H	N/A	580852616
JHI_Hv50k_2016_382520	6H	N/A	580874412
JHI_Hv50k_2016_382597	6H	N/A	581247100
JHI_Hv50k_2016_382827	6H	N/A	581608152
JHI_Hv50k_2016_382955	6H	N/A	582529842
JHI_Hv50k_2016_382974	6H	N/A	582529873
JHI_Hv50k_2016_383140	6H	N/A	582685965
JHI_Hv50k_2016_383163	6H	N/A	582686485
JHI_Hv50k_2016_383175	6H	N/A	582776560
JHI_Hv50k_2016_383177	6H	N/A	582788155
JHI_Hv50k_2016_383208	6H	N/A	583046407
JHI_Hv50k_2016_383221	6H	N/A	583046671
JHI_Hv50k_2016_383447	6H	N/A	583266279
JHI_Hv50k_2016_383480	6H	N/A	583268459
JHI_Hv50k_2016_383599	6H	N/A	583312020
JHI_Hv50k_2016_383738	6H	N/A	84953
JHI_Hv50k_2016_383767	6H	N/A	86515
JHI_Hv50k_2016_383773	6H	N/A	86682
JHI_Hv50k_2016_383807	6H	N/A	280101
JHI_Hv50k_2016_384217	6H	N/A	1393685
JHI_Hv50k_2016_385422	6H	N/A	3380638
JHI_Hv50k_2016_385462	6H	N/A	3393998
JHI_Hv50k_2016_385463	6H	N/A	3407292
JHI_Hv50k_2016_385675	6H	N/A	3453473
JHI_Hv50k_2016_385744	6H	N/A	3689463
JHI_Hv50k_2016_385826	6H	N/A	3689970

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_385857	6H	N/A	3737456
JHI_Hv50k_2016_385944	6H	N/A	3756293
JHI_Hv50k_2016_386104	6H	N/A	3761274
JHI_Hv50k_2016_386179	6H	N/A	3767825
JHI_Hv50k_2016_386217	6H	N/A	3849335
JHI_Hv50k_2016_386349	6H	N/A	3994225
JHI_Hv50k_2016_386678	6H	N/A	4104059
JHI_Hv50k_2016_386716	6H	N/A	4104121
JHI_Hv50k_2016_387175	6H	N/A	4427562
JHI_Hv50k_2016_387236	6H	N/A	4427621
JHI_Hv50k_2016_387338	6H	N/A	4532177
JHI_Hv50k_2016_387677	6H	N/A	4816610
JHI_Hv50k_2016_388223	6H	N/A	5165949
JHI_Hv50k_2016_388506	6H	N/A	5267791
JHI_Hv50k_2016_388579	6H	N/A	5389278
JHI_Hv50k_2016_388653	6H	N/A	5389395
JHI_Hv50k_2016_389292	6H	N/A	5927449
JHI_Hv50k_2016_389675	6H	N/A	6312488
JHI_Hv50k_2016_389838	6H	N/A	6717486
JHI_Hv50k_2016_390429	6H	N/A	7760158
JHI_Hv50k_2016_390441	6H	N/A	8000663
JHI_Hv50k_2016_390444	6H	N/A	8000949
JHI_Hv50k_2016_390481	6H	N/A	8010696
JHI_Hv50k_2016_390504	6H	N/A	8017070
JHI_Hv50k_2016_390577	6H	N/A	8017354
JHI_Hv50k_2016_391188	6H	N/A	8554691
JHI_Hv50k_2016_392114	6H	N/A	9454846
JHI_Hv50k_2016_395737	6H	N/A	16576405
JHI_Hv50k_2016_396736	6H	N/A	18345101
JHI_Hv50k_2016_397916	6H	N/A	20024504
JHI_Hv50k_2016_398886	6H	N/A	24043924
JHI_Hv50k_2016_399580	6H	N/A	24685425
JHI_Hv50k_2016_399819	6H	N/A	24685804
JHI_Hv50k_2016_400174	6H	N/A	25008942
JHI_Hv50k_2016_400635	6H	N/A	25375817
JHI_Hv50k_2016_400665	6H	N/A	25375971
JHI_Hv50k_2016_400711	6H	N/A	25426080
JHI_Hv50k_2016_400728	6H	N/A	25438196
JHI_Hv50k_2016_400736	6H	N/A	25439751
JHI_Hv50k_2016_401825	6H	N/A	26814992
JHI_Hv50k_2016_402178	6H	N/A	27157531
JHI_Hv50k_2016_402765	6H	N/A	27776690

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_402835	6H	N/A	27776943
JHI_Hv50k_2016_403264	6H	N/A	28116257
JHI_Hv50k_2016_403321	6H	N/A	28772177
JHI_Hv50k_2016_403398	6H	N/A	29235937
JHI_Hv50k_2016_403427	6H	N/A	29241965
JHI_Hv50k_2016_403454	6H	N/A	29243140
JHI_Hv50k_2016_403587	6H	N/A	29729422
JHI_Hv50k_2016_403637	6H	N/A	29824105
JHI_Hv50k_2016_403761	6H	N/A	29984004
JHI_Hv50k_2016_403905	6H	N/A	30200161
JHI_Hv50k_2016_403948	6H	N/A	30211460
JHI_Hv50k_2016_404291	6H	N/A	30563152
JHI_Hv50k_2016_404362	6H	N/A	30701874
JHI_Hv50k_2016_404658	6H	N/A	31046895
JHI_Hv50k_2016_404715	6H	N/A	31279790
JHI_Hv50k_2016_404798	6H	N/A	31298851
JHI_Hv50k_2016_404853	6H	N/A	31299698
JHI_Hv50k_2016_405435	6H	N/A	31393930
JHI_Hv50k_2016_405533	6H	N/A	31569124
JHI_Hv50k_2016_405598	6H	N/A	31744040
JHI_Hv50k_2016_405730	6H	N/A	31747115
JHI_Hv50k_2016_405806	6H	N/A	31750796
JHI_Hv50k_2016_405814	6H	N/A	31793062
JHI_Hv50k_2016_405815	6H	N/A	31955282
JHI_Hv50k_2016_405816	6H	N/A	31955568
JHI_Hv50k_2016_405846	6H	N/A	32003409
JHI_Hv50k_2016_405888	6H	N/A	32256851
JHI_Hv50k_2016_406397	6H	N/A	32899627
JHI_Hv50k_2016_406537	6H	N/A	33043619
JHI_Hv50k_2016_406685	6H	N/A	34596090
JHI_Hv50k_2016_406722	6H	N/A	34596344
JHI_Hv50k_2016_406870	6H	N/A	34820327
JHI_Hv50k_2016_407107	6H	N/A	35109064
JHI_Hv50k_2016_407259	6H	N/A	36876621
JHI_Hv50k_2016_407303	6H	N/A	36912536
JHI_Hv50k_2016_407417	6H	N/A	37308520
JHI_Hv50k_2016_407516	6H	N/A	37805069
JHI_Hv50k_2016_408424	6H	N/A	42073144
JHI_Hv50k_2016_408985	6H	N/A	44222907
JHI_Hv50k_2016_409027	6H	N/A	44318055
JHI_Hv50k_2016_409208	6H	N/A	45864389
JHI_Hv50k_2016_409636	6H	N/A	46842102

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_409707	6H	N/A	47035938
JHI_Hv50k_2016_410367	6H	N/A	49217273
JHI_Hv50k_2016_410861	6H	N/A	50282984
JHI_Hv50k_2016_410961	6H	N/A	50546041
JHI_Hv50k_2016_411580	6H	N/A	52168557
JHI_Hv50k_2016_412204	6H	N/A	52939132
JHI_Hv50k_2016_412238	6H	N/A	52939434
JHI_Hv50k_2016_412497	6H	N/A	54433173
JHI_Hv50k_2016_412507	6H	N/A	54433547
JHI_Hv50k_2016_412585	6H	N/A	54651216
JHI_Hv50k_2016_412783	6H	N/A	55008900
JHI_Hv50k_2016_412816	6H	N/A	55136501
JHI_Hv50k_2016_412817	6H	N/A	55237717
JHI_Hv50k_2016_412828	6H	N/A	55241859
JHI_Hv50k_2016_412908	6H	N/A	55515270
JHI_Hv50k_2016_413007	6H	N/A	56622231
JHI_Hv50k_2016_413026	6H	N/A	56623782
JHI_Hv50k_2016_413027	6H	N/A	56656041
JHI_Hv50k_2016_413028	6H	N/A	56668736
JHI_Hv50k_2016_413036	6H	N/A	56670392
JHI_Hv50k_2016_413045	6H	N/A	56673684
JHI_Hv50k_2016_413090	6H	N/A	56674411
JHI_Hv50k_2016_413143	6H	N/A	57444222
JHI_Hv50k_2016_413234	6H	N/A	57649623
JHI_Hv50k_2016_413564	6H	N/A	58421486
JHI_Hv50k_2016_413579	6H	N/A	58430975
JHI_Hv50k_2016_413581	6H	N/A	58432697
JHI_Hv50k_2016_413603	6H	N/A	58907081
JHI_Hv50k_2016_413976	6H	N/A	61029514
JHI_Hv50k_2016_414010	6H	N/A	61030036
JHI_Hv50k_2016_414036	6H	N/A	61030214
JHI_Hv50k_2016_414205	6H	N/A	61032176
JHI_Hv50k_2016_414224	6H	N/A	61032760
JHI_Hv50k_2016_414229	6H	N/A	61032866
JHI_Hv50k_2016_414250	6H	N/A	61032962
JHI_Hv50k_2016_414256	6H	N/A	61033075
JHI_Hv50k_2016_414260	6H	N/A	61033368
JHI_Hv50k_2016_414275	6H	N/A	61033515
JHI_Hv50k_2016_414287	6H	N/A	61033666
JHI_Hv50k_2016_414296	6H	N/A	61034085
JHI_Hv50k_2016_414297	6H	N/A	61034316
JHI_Hv50k_2016_414345	6H	N/A	61034772

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_414666	6H	N/A	62199745
JHI_Hv50k_2016_414749	6H	N/A	62238600
JHI_Hv50k_2016_415465	6H	N/A	66043847
JHI_Hv50k_2016_415471	6H	N/A	66167452
JHI_Hv50k_2016_415491	6H	N/A	66943782
JHI_Hv50k_2016_415494	6H	N/A	66945898
JHI_Hv50k_2016_415571	6H	N/A	68615178
JHI_Hv50k_2016_415572	6H	N/A	68751821
JHI_Hv50k_2016_415577	6H	N/A	68752432
JHI_Hv50k_2016_415578	6H	N/A	68752518
JHI_Hv50k_2016_415581	6H	N/A	68762210
JHI_Hv50k_2016_415585	6H	N/A	68768119
JHI_Hv50k_2016_415592	6H	N/A	69085278
JHI_Hv50k_2016_415593	6H	N/A	69305016
JHI_Hv50k_2016_415600	6H	N/A	69933106
JHI_Hv50k_2016_415602	6H	N/A	69934186
JHI_Hv50k_2016_415617	6H	N/A	69981977
JHI_Hv50k_2016_415624	6H	N/A	70162390
JHI_Hv50k_2016_415625	6H	N/A	70260800
JHI_Hv50k_2016_415658	6H	N/A	70265030
JHI_Hv50k_2016_415738	6H	N/A	70505091
JHI_Hv50k_2016_415739	6H	N/A	70505748
JHI_Hv50k_2016_415741	6H	N/A	70581371
JHI_Hv50k_2016_415843	6H	N/A	72602355
JHI_Hv50k_2016_415847	6H	N/A	72605059
JHI_Hv50k_2016_415895	6H	N/A	72974660
JHI_Hv50k_2016_415971	6H	N/A	74207487
JHI_Hv50k_2016_415974	6H	N/A	74251791
JHI_Hv50k_2016_415975	6H	N/A	74252709
JHI_Hv50k_2016_416000	6H	N/A	74253068
JHI_Hv50k_2016_416017	6H	N/A	74461644
JHI_Hv50k_2016_416043	6H	N/A	74462597
JHI_Hv50k_2016_416067	6H	N/A	74798729
JHI_Hv50k_2016_416153	6H	N/A	75585441
JHI_Hv50k_2016_416155	6H	N/A	75585506
JHI_Hv50k_2016_416162	6H	N/A	75904305
JHI_Hv50k_2016_416163	6H	N/A	75905380
JHI_Hv50k_2016_416166	6H	N/A	77003147
JHI_Hv50k_2016_416171	6H	N/A	77006201
JHI_Hv50k_2016_416172	6H	N/A	77006278
JHI_Hv50k_2016_416642	6H	N/A	84523339
JHI_Hv50k_2016_416643	6H	N/A	84523491

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_416678	6H	N/A	84523553
JHI_Hv50k_2016_416777	6H	N/A	84525575
JHI_Hv50k_2016_416934	6H	N/A	84642849
JHI_Hv50k_2016_417151	6H	N/A	87070632
JHI_Hv50k_2016_417170	6H	N/A	87070780
JHI_Hv50k_2016_417204	6H	N/A	87921419
JHI_Hv50k_2016_417245	6H	N/A	87958437
JHI_Hv50k_2016_417327	6H	N/A	88750621
JHI_Hv50k_2016_417337	6H	N/A	89200436
JHI_Hv50k_2016_418658	6H	N/A	97470472
JHI_Hv50k_2016_418674	6H	N/A	97662528
JHI_Hv50k_2016_418675	6H	N/A	97678115
JHI_Hv50k_2016_418730	6H	N/A	97734689
JHI_Hv50k_2016_418731	6H	N/A	97735118
JHI_Hv50k_2016_418740	6H	N/A	97738171
JHI_Hv50k_2016_418778	6H	N/A	97742113
JHI_Hv50k_2016_418829	6H	N/A	97752409
JHI_Hv50k_2016_418841	6H	N/A	97762077
JHI_Hv50k_2016_418848	6H	N/A	98043009
JHI_Hv50k_2016_418874	6H	N/A	98043584
JHI_Hv50k_2016_419069	6H	N/A	101902669
JHI_Hv50k_2016_419073	6H	N/A	101904949
JHI_Hv50k_2016_419096	6H	N/A	102611500
JHI_Hv50k_2016_419118	6H	N/A	102938480
JHI_Hv50k_2016_419155	6H	N/A	102939069
JHI_Hv50k_2016_419181	6H	N/A	104383705
JHI_Hv50k_2016_419362	6H	N/A	112347053
JHI_Hv50k_2016_419390	6H	N/A	112360299
JHI_Hv50k_2016_419579	6H	N/A	114660408
JHI_Hv50k_2016_419702	6H	N/A	115429145
JHI_Hv50k_2016_419705	6H	N/A	115429729
JHI_Hv50k_2016_419724	6H	N/A	115430019
JHI_Hv50k_2016_419783	6H	N/A	116740227
JHI_Hv50k_2016_420068	6H	N/A	117700457
JHI_Hv50k_2016_420098	6H	N/A	118260059
JHI_Hv50k_2016_420119	6H	N/A	118260502
JHI_Hv50k_2016_420176	6H	N/A	118690321
JHI_Hv50k_2016_420182	6H	N/A	119003644
JHI_Hv50k_2016_420201	6H	N/A	120010328
JHI_Hv50k_2016_420704	6H	N/A	126300006
JHI_Hv50k_2016_420761	6H	N/A	127126670
JHI_Hv50k_2016_420815	6H	N/A	141856892

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_420918	6H	N/A	144121020
JHI_Hv50k_2016_420919	6H	N/A	144181030
JHI_Hv50k_2016_421045	6H	N/A	144289984
JHI_Hv50k_2016_421054	6H	N/A	145959028
JHI_Hv50k_2016_421057	6H	N/A	146052648
JHI_Hv50k_2016_421484	6H	N/A	160219976
JHI_Hv50k_2016_421521	6H	N/A	162073005
JHI_Hv50k_2016_421777	6H	N/A	206559049
JHI_Hv50k_2016_421920	6H	N/A	222930913
JHI_Hv50k_2016_422456	6H	N/A	226515605
JHI_Hv50k_2016_422458	6H	N/A	226516584
JHI_Hv50k_2016_422459	6H	N/A	226516747
JHI_Hv50k_2016_422808	6H	N/A	228013325
JHI_Hv50k_2016_422903	6H	N/A	229714820
JHI_Hv50k_2016_423202	6H	N/A	235076776
JHI_Hv50k_2016_423290	6H	N/A	237170381
JHI_Hv50k_2016_423487	6H	N/A	240630446
JHI_Hv50k_2016_423492	6H	N/A	241657572
JHI_Hv50k_2016_423565	6H	N/A	243842823
JHI_Hv50k_2016_423572	6H	N/A	244652325
JHI_Hv50k_2016_423588	6H	N/A	248225521
JHI_Hv50k_2016_423595	6H	N/A	250835778
JHI_Hv50k_2016_423596	6H	N/A	251131740
JHI_Hv50k_2016_423604	6H	N/A	253835070
JHI_Hv50k_2016_423606	6H	N/A	254432159
JHI_Hv50k_2016_423636	6H	N/A	254790488
JHI_Hv50k_2016_423703	6H	N/A	255348646
JHI_Hv50k_2016_423785	6H	N/A	257808508
JHI_Hv50k_2016_423830	6H	N/A	260961516
JHI_Hv50k_2016_424223	6H	N/A	283472098
JHI_Hv50k_2016_424341	6H	N/A	289647982
JHI_Hv50k_2016_424485	6H	N/A	298441510
JHI_Hv50k_2016_425174	6H	N/A	323672640
JHI_Hv50k_2016_425588	6H	N/A	366101514
JHI_Hv50k_2016_425708	6H	N/A	374349520
JHI_Hv50k_2016_425728	6H	N/A	378968820
JHI_Hv50k_2016_425771	6H	N/A	384439643
JHI_Hv50k_2016_426443	6H	N/A	419566799
JHI_Hv50k_2016_426599	6H	N/A	426427413
JHI_Hv50k_2016_426633	6H	N/A	427038848
JHI_Hv50k_2016_426692	6H	N/A	428680332
JHI_Hv50k_2016_426780	6H	N/A	430582698

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_426822	6H	N/A	432044295
JHI_Hv50k_2016_426825	6H	N/A	433605984
JHI_Hv50k_2016_426841	6H	N/A	434011971
JHI_Hv50k_2016_426862	6H	N/A	434287108
JHI_Hv50k_2016_426925	6H	N/A	434880492
JHI_Hv50k_2016_427158	6H	N/A	437147190
JHI_Hv50k_2016_427554	6H	N/A	445818208
JHI_Hv50k_2016_427573	6H	N/A	445844413
JHI_Hv50k_2016_427722	6H	N/A	449920300
JHI_Hv50k_2016_427726	6H	N/A	450201620
JHI_Hv50k_2016_427731	6H	N/A	450209328
JHI_Hv50k_2016_428207	6H	N/A	456221912
JHI_Hv50k_2016_428246	6H	N/A	456226177
JHI_Hv50k_2016_428348	6H	N/A	461023389
JHI_Hv50k_2016_428664	6H	N/A	489455165
JHI_Hv50k_2016_428706	6H	N/A	489497000
JHI_Hv50k_2016_428726	6H	N/A	489931373
JHI_Hv50k_2016_428780	6H	N/A	489932680
JHI_Hv50k_2016_428860	6H	N/A	491565395
JHI_Hv50k_2016_428953	6H	N/A	492012069
JHI_Hv50k_2016_429028	6H	N/A	493319522
JHI_Hv50k_2016_429064	6H	N/A	493520859
JHI_Hv50k_2016_429073	6H	N/A	493524489
JHI_Hv50k_2016_429731	6H	N/A	499796121
JHI_Hv50k_2016_430267	6H	N/A	502379197
JHI_Hv50k_2016_430590	6H	N/A	503361302
JHI_Hv50k_2016_430650	6H	N/A	503500166
JHI_Hv50k_2016_430663	6H	N/A	503828289
JHI_Hv50k_2016_430676	6H	N/A	504506882
JHI_Hv50k_2016_430712	6H	N/A	505003291
JHI_Hv50k_2016_430713	6H	N/A	505007825
JHI_Hv50k_2016_430717	6H	N/A	505359523
JHI_Hv50k_2016_430796	6H	N/A	505809723
JHI_Hv50k_2016_430886	6H	N/A	507026063
JHI_Hv50k_2016_431285	6H	N/A	511816512
JHI_Hv50k_2016_431358	6H	N/A	512085679
JHI_Hv50k_2016_431359	6H	N/A	512596401
JHI_Hv50k_2016_431555	6H	N/A	514975871
JHI_Hv50k_2016_431559	6H	N/A	514976282
JHI_Hv50k_2016_431811	6H	N/A	515903719
JHI_Hv50k_2016_431836	6H	N/A	516169732
JHI_Hv50k_2016_431839	6H	N/A	516170411

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_431844	6H	N/A	516658283
JHI_Hv50k_2016_431958	6H	N/A	517210780
JHI_Hv50k_2016_432001	6H	N/A	517560223
JHI_Hv50k_2016_432075	6H	N/A	517977728
JHI_Hv50k_2016_432076	6H	N/A	518164951
JHI_Hv50k_2016_432120	6H	N/A	518602773
JHI_Hv50k_2016_432126	6H	N/A	518602866
JHI_Hv50k_2016_432229	6H	N/A	518783609
JHI_Hv50k_2016_432334	6H	N/A	519720699
JHI_Hv50k_2016_432461	6H	N/A	520460312
JHI_Hv50k_2016_432552	6H	N/A	521168703
JHI_Hv50k_2016_432653	6H	N/A	521340775
JHI_Hv50k_2016_432683	6H	N/A	521508298
JHI_Hv50k_2016_432703	6H	N/A	521711090
JHI_Hv50k_2016_432752	6H	N/A	522262665
JHI_Hv50k_2016_433038	6H	N/A	524332552
JHI_Hv50k_2016_433188	6H	N/A	525217306
JHI_Hv50k_2016_433222	6H	N/A	525523403
JHI_Hv50k_2016_433341	6H	N/A	527477102
JHI_Hv50k_2016_433405	6H	N/A	527760632
JHI_Hv50k_2016_433420	6H	N/A	527989789
JHI_Hv50k_2016_433455	6H	N/A	528585066
JHI_Hv50k_2016_433807	6H	N/A	530821827
JHI_Hv50k_2016_433873	6H	N/A	531975687
JHI_Hv50k_2016_433973	6H	N/A	532352862
JHI_Hv50k_2016_434092	6H	N/A	534770702
JHI_Hv50k_2016_434164	6H	N/A	534938213
JHI_Hv50k_2016_434502	6H	N/A	537881567
JHI_Hv50k_2016_434541	6H	N/A	537951457
JHI_Hv50k_2016_434656	6H	N/A	538828953
SCRI_RS_160297	7H	2.82	546913302
BOPA1_1073_916	7H	16.78	571215612
BOPA1_4275_1288	7H	19.22	573569122
SCRI_RS_197190	7H	19.72	573626645
SCRI_RS_127224	7H	26.72	574100921
SCRI_RS_166520	7H	26.72	574102474
SCRI_RS_128121	7H	27.32	574967595
SCRI_RS_148318	7H	27.32	574971799
SCRI_RS_160641	7H	28.62	575019694
SCRI_RS_204453	7H	28.62	575021237
BOPA1_8365_454	7H	29.62	575839410
BOPA2_12_30780	7H	29.62	575839827

Marker	Chromosome	Position (cM)	Position (BP)
SCRI_RS_219709	7H	30.02	577607695
SCRI_RS_150053	7H	32.81	577610227
BOPA2_12_30141	7H	32.88	577611129
BOPA2_12_30219	7H	32.88	577611187
BOPA1_1511_545	7H	34.74	577611224
BOPA1_2124_984	7H	34.74	577611494
BOPA2_12_30894	7H	38.31	578286969
BOPA2_12_30895	7H	38.31	578287057
BOPA2_12_31305	7H	44.58	578293579
SCRI_RS_209176	7H	45.14	578364770
BOPA2_12_30065	7H	46.74	578365518
BOPA1_398_1244	7H	46.89	578369210
SCRI_RS_91662	7H	48.16	578964494
BOPA1_2585_2901	7H	48.74	580316082
BOPA2_12_10979	7H	48.74	580503239
BOPA2_12_30143	7H	48.86	580778369
SCRI_RS_187827	7H	51.26	581639227
SCRI_RS_200387	7H	54.63	582607553
SCRI_RS_125000	7H	55.83	583114594
BOPA2_12_30752	7H	56.83	584952172
SCRI_RS_172335	7H	56.83	586309869
SCRI_RS_146114	7H	57.83	588903868
BOPA2_12_10696	7H	57.99	589098317
SCRI_RS_187590	7H	59.13	589913203
SCRI_RS_196063	7H	60.13	590154312
BOPA1_1107_392	7H	72.84	591544202
SCRI_RS_154193	7H	73.46	591781703
BOPA2_12_30496	7H	73.81	592140333
SCRI_RS_152074	7H	74.31	592633710
BOPA2_12_30835	7H	78.07	598949504
BOPA2_12_31140	7H	78.07	598953220
SCRI_RS_112718	7H	78.07	598976150
SCRI_RS_133777	7H	78.07	599176128
SCRI_RS_135346	7H	78.07	599395544
SCRI_RS_148407	7H	78.07	599788233
SCRI_RS_154111	7H	78.07	600399970
SCRI_RS_219291	7H	78.07	600892548
BOPA2_12_10125	7H	80.47	602202847
BOPA2_12_30506	7H	80.47	602203052
BOPA1_ConsensusGBS0132_4	7H	82.16	602207307
SCRI_RS_122512	7H	83.19	602888003
SCRI_RS_133026	7H	84.09	603449891

Marker	Chromosome	Position (cM)	Position (BP)
BOPA1_3140_491	7H	84.79	603701443
SCRI_RS_194841	7H	88.29	604481194
SCRI_RS_200020	7H	91.39	604483540
BOPA2_12_30806	7H	95.7	604525609
BOPA2_12_31395	7H	95.7	604525814
SCRI_RS_146157	7H	95.7	604526281
SCRI_RS_148722	7H	95.7	604526457
BOPA1_4791_1541	7H	99.9	604527293
BOPA1_12027_128	7H	101.99	604528426
SCRI_RS_174327	7H	108.9	604697010
BOPA1_1178_279	7H	110.4	604697126
SCRI_RS_182503	7H	110.6	604698016
SCRI_RS_124251	7H	114.1	604699015
BOPA2_12_30368	7H	119.33	604865857
BOPA1_6470_1005	7H	138.76	605191582
SCRI_RS_180889	7H	143.14	606866283
SCRI_RS_187873	7H	143.14	606867865
BOPA1_7356_1241	7H	150.36	607945719
SCRI_RS_138598	7H	150.36	607954353
BOPA2_12_30593	7H	150.86	608808550
SCRI_RS_184967	7H	156.54	608826566
SCRI_RS_197550	7H	156.54	608826839
SCRI_RS_4604	7H	156.54	608827049
SCRI_RS_752	7H	158.29	609245933
SCRI_RS_200397	7H	166.25	609392442
SCRI_RS_6252	7H	166.25	609392649
SCRI_RS_157219	7H	166.45	609392873
SCRI_RS_169268	7H	166.55	609406570
BOPA1_1437_687	7H	168.94	609661971
JHI_Hv50k_2016_435981	7H	N/A	611214628
JHI_Hv50k_2016_437530	7H	N/A	613539606
JHI_Hv50k_2016_438984	7H	N/A	616907083
JHI_Hv50k_2016_441810	7H	N/A	623648062
JHI_Hv50k_2016_441962	7H	N/A	623755687
JHI_Hv50k_2016_441967	7H	N/A	623759383
JHI_Hv50k_2016_442168	7H	N/A	623915826
JHI_Hv50k_2016_444108	7H	N/A	626496239
JHI_Hv50k_2016_444110	7H	N/A	626525213
JHI_Hv50k_2016_444111	7H	N/A	626553563
JHI_Hv50k_2016_444112	7H	N/A	626554540
JHI_Hv50k_2016_444114	7H	N/A	626555948
JHI_Hv50k_2016_444132	7H	N/A	626944906

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_444808	7H	N/A	628172615
JHI_Hv50k_2016_444990	7H	N/A	628365528
JHI_Hv50k_2016_445177	7H	N/A	628367577
JHI_Hv50k_2016_445336	7H	N/A	628424282
JHI_Hv50k_2016_451565	7H	N/A	638727503
JHI_Hv50k_2016_451875	7H	N/A	639840098
JHI_Hv50k_2016_451928	7H	N/A	639921834
JHI_Hv50k_2016_451963	7H	N/A	639943346
JHI_Hv50k_2016_452259	7H	N/A	640835395
JHI_Hv50k_2016_452616	7H	N/A	641092474
JHI_Hv50k_2016_452617	7H	N/A	641092737
JHI_Hv50k_2016_452620	7H	N/A	641093063
JHI_Hv50k_2016_452621	7H	N/A	641096075
JHI_Hv50k_2016_452623	7H	N/A	641169375
JHI_Hv50k_2016_452624	7H	N/A	641173348
JHI_Hv50k_2016_452628	7H	N/A	641265145
JHI_Hv50k_2016_452747	7H	N/A	641654524
JHI_Hv50k_2016_452788	7H	N/A	641769867
JHI_Hv50k_2016_452825	7H	N/A	641796875
JHI_Hv50k_2016_452912	7H	N/A	642028967
JHI_Hv50k_2016_452991	7H	N/A	642082112
JHI_Hv50k_2016_453022	7H	N/A	642084655
JHI_Hv50k_2016_453149	7H	N/A	642239712
JHI_Hv50k_2016_453277	7H	N/A	642286189
JHI_Hv50k_2016_453321	7H	N/A	642474377
JHI_Hv50k_2016_453331	7H	N/A	642644899
JHI_Hv50k_2016_453335	7H	N/A	642657653
JHI_Hv50k_2016_453342	7H	N/A	642671008
JHI_Hv50k_2016_453372	7H	N/A	642908866
JHI_Hv50k_2016_453475	7H	N/A	643019164
JHI_Hv50k_2016_453491	7H	N/A	643338698
JHI_Hv50k_2016_453628	7H	N/A	643823157
JHI_Hv50k_2016_453659	7H	N/A	643845158
JHI_Hv50k_2016_453705	7H	N/A	643845380
JHI_Hv50k_2016_453740	7H	N/A	643846804
JHI_Hv50k_2016_453831	7H	N/A	643928169
JHI_Hv50k_2016_453875	7H	N/A	643928210
JHI_Hv50k_2016_454038	7H	N/A	644076613
JHI_Hv50k_2016_454044	7H	N/A	644139446
JHI_Hv50k_2016_454077	7H	N/A	644257663
JHI_Hv50k_2016_454121	7H	N/A	644291132
JHI_Hv50k_2016_454176	7H	N/A	644417367

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_454224	7H	N/A	644482042
JHI_Hv50k_2016_454307	7H	N/A	644608075
JHI_Hv50k_2016_454318	7H	N/A	644608283
JHI_Hv50k_2016_454320	7H	N/A	644608358
JHI_Hv50k_2016_454325	7H	N/A	644608547
JHI_Hv50k_2016_454335	7H	N/A	644608687
JHI_Hv50k_2016_454690	7H	N/A	644948099
JHI_Hv50k_2016_454930	7H	N/A	645031864
JHI_Hv50k_2016_454997	7H	N/A	645271303
JHI_Hv50k_2016_455127	7H	N/A	645378333
JHI_Hv50k_2016_455152	7H	N/A	645490810
JHI_Hv50k_2016_455479	7H	N/A	645922287
JHI_Hv50k_2016_455618	7H	N/A	646005817
JHI_Hv50k_2016_455680	7H	N/A	646120339
JHI_Hv50k_2016_455686	7H	N/A	646120429
JHI_Hv50k_2016_455759	7H	N/A	646188863
JHI_Hv50k_2016_455760	7H	N/A	646189265
JHI_Hv50k_2016_455809	7H	N/A	646433917
JHI_Hv50k_2016_455865	7H	N/A	646493271
JHI_Hv50k_2016_455911	7H	N/A	646890966
JHI_Hv50k_2016_455933	7H	N/A	646914070
JHI_Hv50k_2016_455948	7H	N/A	646917329
JHI_Hv50k_2016_456115	7H	N/A	647072573
JHI_Hv50k_2016_456239	7H	N/A	647471990
JHI_Hv50k_2016_456434	7H	N/A	647647892
JHI_Hv50k_2016_456787	7H	N/A	647664231
JHI_Hv50k_2016_456902	7H	N/A	647715581
JHI_Hv50k_2016_456991	7H	N/A	647913740
JHI_Hv50k_2016_457183	7H	N/A	648189859
JHI_Hv50k_2016_457219	7H	N/A	648198602
JHI_Hv50k_2016_457247	7H	N/A	648208727
JHI_Hv50k_2016_457385	7H	N/A	648260376
JHI_Hv50k_2016_457386	7H	N/A	648260464
JHI_Hv50k_2016_457490	7H	N/A	648298963
JHI_Hv50k_2016_457627	7H	N/A	648890976
JHI_Hv50k_2016_457677	7H	N/A	648928635
JHI_Hv50k_2016_457680	7H	N/A	648928830
JHI_Hv50k_2016_457691	7H	N/A	648929105
JHI_Hv50k_2016_457712	7H	N/A	648929649
JHI_Hv50k_2016_457875	7H	N/A	649047115
JHI_Hv50k_2016_457880	7H	N/A	649047578
JHI_Hv50k_2016_457952	7H	N/A	649062355

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_458072	7H	N/A	649104347
JHI_Hv50k_2016_458079	7H	N/A	649104580
JHI_Hv50k_2016_458622	7H	N/A	649559029
JHI_Hv50k_2016_458640	7H	N/A	649693776
JHI_Hv50k_2016_458763	7H	N/A	649792469
JHI_Hv50k_2016_458805	7H	N/A	649998027
JHI_Hv50k_2016_459053	7H	N/A	650001952
JHI_Hv50k_2016_459080	7H	N/A	650002371
JHI_Hv50k_2016_459302	7H	N/A	650219851
JHI_Hv50k_2016_459431	7H	N/A	650554578
JHI_Hv50k_2016_459432	7H	N/A	650554654
JHI_Hv50k_2016_459470	7H	N/A	650562603
JHI_Hv50k_2016_459578	7H	N/A	650671123
JHI_Hv50k_2016_459663	7H	N/A	651313302
JHI_Hv50k_2016_459698	7H	N/A	651379790
JHI_Hv50k_2016_459734	7H	N/A	651428678
JHI_Hv50k_2016_459759	7H	N/A	651449375
JHI_Hv50k_2016_459849	7H	N/A	651601946
JHI_Hv50k_2016_459853	7H	N/A	651601983
JHI_Hv50k_2016_459904	7H	N/A	651602136
JHI_Hv50k_2016_459924	7H	N/A	651602310
JHI_Hv50k_2016_460028	7H	N/A	651729207
JHI_Hv50k_2016_460104	7H	N/A	651765922
JHI_Hv50k_2016_460111	7H	N/A	651902808
JHI_Hv50k_2016_460161	7H	N/A	652201479
JHI_Hv50k_2016_460172	7H	N/A	652202135
JHI_Hv50k_2016_460173	7H	N/A	652297593
JHI_Hv50k_2016_460927	7H	N/A	654145693
JHI_Hv50k_2016_460995	7H	N/A	654151575
JHI_Hv50k_2016_461007	7H	N/A	654158432
JHI_Hv50k_2016_461120	7H	N/A	654385866
JHI_Hv50k_2016_461130	7H	N/A	654412799
JHI_Hv50k_2016_461139	7H	N/A	654416131
JHI_Hv50k_2016_461150	7H	N/A	654419217
JHI_Hv50k_2016_461166	7H	N/A	654900595
JHI_Hv50k_2016_461174	7H	N/A	654991703
JHI_Hv50k_2016_461181	7H	N/A	655554682
JHI_Hv50k_2016_461186	7H	N/A	655967387
JHI_Hv50k_2016_461190	7H	N/A	655968393
JHI_Hv50k_2016_461193	7H	N/A	655997968
JHI_Hv50k_2016_461194	7H	N/A	656029690
JHI_Hv50k_2016_461201	7H	N/A	656038171

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_461203	7H	N/A	656039010
JHI_Hv50k_2016_461212	7H	N/A	656046754
JHI_Hv50k_2016_461213	7H	N/A	656046906
JHI_Hv50k_2016_461214	7H	N/A	656047025
JHI_Hv50k_2016_461215	7H	N/A	656047151
JHI_Hv50k_2016_461220	7H	N/A	656047154
JHI_Hv50k_2016_461223	7H	N/A	656047454
JHI_Hv50k_2016_461255	7H	N/A	656048561
JHI_Hv50k_2016_461259	7H	N/A	656048737
JHI_Hv50k_2016_461261	7H	N/A	656048840
JHI_Hv50k_2016_461280	7H	N/A	656049524
JHI_Hv50k_2016_461351	7H	N/A	656051697
JHI_Hv50k_2016_461390	7H	N/A	656054225
JHI_Hv50k_2016_461473	7H	N/A	656054979
JHI_Hv50k_2016_461483	7H	N/A	656055192
JHI_Hv50k_2016_461488	7H	N/A	656055408
JHI_Hv50k_2016_461503	7H	N/A	656055483
JHI_Hv50k_2016_461537	7H	N/A	656056686
JHI_Hv50k_2016_461631	7H	N/A	656057759
JHI_Hv50k_2016_461678	7H	N/A	656328731
JHI_Hv50k_2016_461843	7H	N/A	656941572
JHI_Hv50k_2016_461928	7H	N/A	49731819
JHI_Hv50k_2016_461938	7H	N/A	49747828
JHI_Hv50k_2016_461949	7H	N/A	49764289
JHI_Hv50k_2016_462081	7H	N/A	49812469
JHI_Hv50k_2016_462268	7H	N/A	50105014
JHI_Hv50k_2016_462288	7H	N/A	50107397
JHI_Hv50k_2016_462624	7H	N/A	50289849
JHI_Hv50k_2016_462670	7H	N/A	50291953
JHI_Hv50k_2016_462760	7H	N/A	50541347
JHI_Hv50k_2016_462842	7H	N/A	50627840
JHI_Hv50k_2016_462910	7H	N/A	50928928
JHI_Hv50k_2016_462915	7H	N/A	50929137
JHI_Hv50k_2016_462950	7H	N/A	50933685
JHI_Hv50k_2016_462952	7H	N/A	50934056
JHI_Hv50k_2016_463087	7H	N/A	51059176
JHI_Hv50k_2016_463111	7H	N/A	51179511
JHI_Hv50k_2016_463268	7H	N/A	52114280
JHI_Hv50k_2016_463273	7H	N/A	52114486
JHI_Hv50k_2016_463374	7H	N/A	52394960
JHI_Hv50k_2016_463406	7H	N/A	52450538
JHI_Hv50k_2016_463438	7H	N/A	52559807

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_463534	7H	N/A	52938596
JHI_Hv50k_2016_463545	7H	N/A	52939303
JHI_Hv50k_2016_463563	7H	N/A	53032252
JHI_Hv50k_2016_463570	7H	N/A	53034168
JHI_Hv50k_2016_463773	7H	N/A	53822333
JHI_Hv50k_2016_463781	7H	N/A	53823511
JHI_Hv50k_2016_463829	7H	N/A	54083373
JHI_Hv50k_2016_464005	7H	N/A	54434146
JHI_Hv50k_2016_464031	7H	N/A	54650072
JHI_Hv50k_2016_464069	7H	N/A	54704239
JHI_Hv50k_2016_464336	7H	N/A	55256340
JHI_Hv50k_2016_464337	7H	N/A	55256480
JHI_Hv50k_2016_464339	7H	N/A	55256600
JHI_Hv50k_2016_464775	7H	N/A	57589802
JHI_Hv50k_2016_464786	7H	N/A	57649623
JHI_Hv50k_2016_464788	7H	N/A	57650557
JHI_Hv50k_2016_464790	7H	N/A	57651214
JHI_Hv50k_2016_464792	7H	N/A	57652509
JHI_Hv50k_2016_464793	7H	N/A	57652511
JHI_Hv50k_2016_464812	7H	N/A	57900984
JHI_Hv50k_2016_464826	7H	N/A	58106793
JHI_Hv50k_2016_464832	7H	N/A	58179904
JHI_Hv50k_2016_464874	7H	N/A	58419709
JHI_Hv50k_2016_464875	7H	N/A	58419742
JHI_Hv50k_2016_464882	7H	N/A	58421486
JHI_Hv50k_2016_464910	7H	N/A	58430975
JHI_Hv50k_2016_464912	7H	N/A	58432697
JHI_Hv50k_2016_464944	7H	N/A	58906885
JHI_Hv50k_2016_464952	7H	N/A	58908865
JHI_Hv50k_2016_464953	7H	N/A	58909037
JHI_Hv50k_2016_464956	7H	N/A	59140375
JHI_Hv50k_2016_464958	7H	N/A	59141247
JHI_Hv50k_2016_464959	7H	N/A	59141335
JHI_Hv50k_2016_464963	7H	N/A	59282013
JHI_Hv50k_2016_464986	7H	N/A	59577498
JHI_Hv50k_2016_465016	7H	N/A	59718648
JHI_Hv50k_2016_465054	7H	N/A	59722157
JHI_Hv50k_2016_465171	7H	N/A	60221144
JHI_Hv50k_2016_465172	7H	N/A	60221650
JHI_Hv50k_2016_465225	7H	N/A	60549354
JHI_Hv50k_2016_465267	7H	N/A	60851413
JHI_Hv50k_2016_465368	7H	N/A	61029919

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_465378	7H	N/A	61030656
JHI_Hv50k_2016_465380	7H	N/A	61030771
JHI_Hv50k_2016_465381	7H	N/A	61030891
JHI_Hv50k_2016_465409	7H	N/A	61032866
JHI_Hv50k_2016_465411	7H	N/A	61032962
JHI_Hv50k_2016_465415	7H	N/A	61033075
JHI_Hv50k_2016_465418	7H	N/A	61033348
JHI_Hv50k_2016_465419	7H	N/A	61033368
JHI_Hv50k_2016_465440	7H	N/A	61034772
JHI_Hv50k_2016_465478	7H	N/A	61039695
JHI_Hv50k_2016_466210	7H	N/A	63136224
JHI_Hv50k_2016_466639	7H	N/A	64455893
JHI_Hv50k_2016_466668	7H	N/A	64672518
JHI_Hv50k_2016_466939	7H	N/A	65425339
JHI_Hv50k_2016_467042	7H	N/A	65972420
JHI_Hv50k_2016_467284	7H	N/A	66606776
JHI_Hv50k_2016_467349	7H	N/A	66743526
JHI_Hv50k_2016_467569	7H	N/A	67854410
JHI_Hv50k_2016_467621	7H	N/A	68338821
JHI_Hv50k_2016_467738	7H	N/A	68752432
JHI_Hv50k_2016_468052	7H	N/A	69938536
JHI_Hv50k_2016_468061	7H	N/A	69981977
JHI_Hv50k_2016_468106	7H	N/A	70260800
JHI_Hv50k_2016_468108	7H	N/A	70261536
JHI_Hv50k_2016_468110	7H	N/A	70263222
JHI_Hv50k_2016_468182	7H	N/A	70505091
JHI_Hv50k_2016_468192	7H	N/A	70525896
JHI_Hv50k_2016_468635	7H	N/A	72973960
JHI_Hv50k_2016_468637	7H	N/A	72974660
JHI_Hv50k_2016_468713	7H	N/A	73547589
JHI_Hv50k_2016_468757	7H	N/A	74251791
JHI_Hv50k_2016_469166	7H	N/A	77738670
JHI_Hv50k_2016_469196	7H	N/A	78269585
JHI_Hv50k_2016_469206	7H	N/A	78305183
JHI_Hv50k_2016_469881	7H	N/A	83688073
JHI_Hv50k_2016_469882	7H	N/A	83688305
JHI_Hv50k_2016_470138	7H	N/A	84526338
JHI_Hv50k_2016_470839	7H	N/A	88011930
JHI_Hv50k_2016_470952	7H	N/A	88750621
JHI_Hv50k_2016_471007	7H	N/A	89201131
JHI_Hv50k_2016_471014	7H	N/A	89202460
JHI_Hv50k_2016_471234	7H	N/A	90404401

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_471764	7H	N/A	93122083
JHI_Hv50k_2016_472094	7H	N/A	96376724
JHI_Hv50k_2016_472850	7H	N/A	102188119
JHI_Hv50k_2016_472878	7H	N/A	102190040
JHI_Hv50k_2016_472911	7H	N/A	102531859
JHI_Hv50k_2016_472936	7H	N/A	102622948
JHI_Hv50k_2016_473455	7H	N/A	112347053
JHI_Hv50k_2016_473460	7H	N/A	112359993
JHI_Hv50k_2016_473723	7H	N/A	114743286
JHI_Hv50k_2016_473775	7H	N/A	115429729
JHI_Hv50k_2016_473777	7H	N/A	115430019
JHI_Hv50k_2016_474102	7H	N/A	118690254
JHI_Hv50k_2016_474553	7H	N/A	123914750
JHI_Hv50k_2016_474644	7H	N/A	125375014
JHI_Hv50k_2016_475645	7H	N/A	170493763
JHI_Hv50k_2016_475672	7H	N/A	190137585
JHI_Hv50k_2016_475717	7H	N/A	218524828
JHI_Hv50k_2016_475876	7H	N/A	225228013
JHI_Hv50k_2016_475891	7H	N/A	225250766
JHI_Hv50k_2016_475914	7H	N/A	225593178
JHI_Hv50k_2016_476002	7H	N/A	226516059
JHI_Hv50k_2016_476351	7H	N/A	228012854
JHI_Hv50k_2016_476354	7H	N/A	228013325
JHI_Hv50k_2016_476379	7H	N/A	228409137
JHI_Hv50k_2016_476424	7H	N/A	228937255
JHI_Hv50k_2016_477147	7H	N/A	238445429
JHI_Hv50k_2016_477559	7H	N/A	246825885
JHI_Hv50k_2016_477617	7H	N/A	248145706
JHI_Hv50k_2016_477630	7H	N/A	248450449
JHI_Hv50k_2016_477722	7H	N/A	251131740
JHI_Hv50k_2016_477901	7H	N/A	253835070
JHI_Hv50k_2016_478140	7H	N/A	257144126
JHI_Hv50k_2016_478197	7H	N/A	258864076
JHI_Hv50k_2016_478220	7H	N/A	259543043
JHI_Hv50k_2016_478345	7H	N/A	261929580
JHI_Hv50k_2016_478437	7H	N/A	264034139
JHI_Hv50k_2016_478448	7H	N/A	264053653
JHI_Hv50k_2016_478689	7H	N/A	270643772
JHI_Hv50k_2016_478768	7H	N/A	271971645
JHI_Hv50k_2016_478957	7H	N/A	276430799
JHI_Hv50k_2016_479018	7H	N/A	277632918
JHI_Hv50k_2016_479125	7H	N/A	279658373

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_479625	7H	N/A	290895048
JHI_Hv50k_2016_479696	7H	N/A	292456681
JHI_Hv50k_2016_479944	7H	N/A	297408667
JHI_Hv50k_2016_480015	7H	N/A	298437563
JHI_Hv50k_2016_480103	7H	N/A	301830374
JHI_Hv50k_2016_480133	7H	N/A	302723361
JHI_Hv50k_2016_480176	7H	N/A	304808992
JHI_Hv50k_2016_480546	7H	N/A	314057938
JHI_Hv50k_2016_481749	7H	N/A	338763694
JHI_Hv50k_2016_482084	7H	N/A	346191747
JHI_Hv50k_2016_482497	7H	N/A	357463060
JHI_Hv50k_2016_482529	7H	N/A	359551703
JHI_Hv50k_2016_483004	7H	N/A	368916425
JHI_Hv50k_2016_483121	7H	N/A	374054963
JHI_Hv50k_2016_483131	7H	N/A	374349520
JHI_Hv50k_2016_483227	7H	N/A	378968820
JHI_Hv50k_2016_483361	7H	N/A	387995997
JHI_Hv50k_2016_483417	7H	N/A	393643387
JHI_Hv50k_2016_485148	7H	N/A	427098295
JHI_Hv50k_2016_485500	7H	N/A	432044295
JHI_Hv50k_2016_487016	7H	N/A	451595038
JHI_Hv50k_2016_487134	7H	N/A	453527111
JHI_Hv50k_2016_487196	7H	N/A	453954076
JHI_Hv50k_2016_487314	7H	N/A	456221912
JHI_Hv50k_2016_487321	7H	N/A	456226518
JHI_Hv50k_2016_487464	7H	N/A	487882158
JHI_Hv50k_2016_487569	7H	N/A	489497000
JHI_Hv50k_2016_487580	7H	N/A	489929693
JHI_Hv50k_2016_488570	7H	N/A	501750617
JHI_Hv50k_2016_488572	7H	N/A	501750916
JHI_Hv50k_2016_488599	7H	N/A	502378845
JHI_Hv50k_2016_488609	7H	N/A	502930075
JHI_Hv50k_2016_488612	7H	N/A	502931286
JHI_Hv50k_2016_488948	7H	N/A	509846808
JHI_Hv50k_2016_489020	7H	N/A	511819481
JHI_Hv50k_2016_489873	7H	N/A	520955010
JHI_Hv50k_2016_490370	7H	N/A	524822249
JHI_Hv50k_2016_490424	7H	N/A	525217306
JHI_Hv50k_2016_490522	7H	N/A	526375795
JHI_Hv50k_2016_490564	7H	N/A	527476895
JHI_Hv50k_2016_490805	7H	N/A	531973117
JHI_Hv50k_2016_490847	7H	N/A	532355891

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_491005	7H	N/A	535606555
JHI_Hv50k_2016_491428	7H	N/A	546345094
JHI_Hv50k_2016_491442	7H	N/A	546397166
JHI_Hv50k_2016_491470	7H	N/A	546632220
JHI_Hv50k_2016_491472	7H	N/A	546632335
JHI_Hv50k_2016_491475	7H	N/A	546913302
JHI_Hv50k_2016_491539	7H	N/A	569006824
JHI_Hv50k_2016_491569	7H	N/A	570492768
JHI_Hv50k_2016_491618	7H	N/A	570709610
JHI_Hv50k_2016_491626	7H	N/A	570713962
JHI_Hv50k_2016_491677	7H	N/A	571062538
JHI_Hv50k_2016_491720	7H	N/A	572947346
JHI_Hv50k_2016_491733	7H	N/A	573568916
JHI_Hv50k_2016_491734	7H	N/A	573569122
JHI_Hv50k_2016_491759	7H	N/A	574100921
JHI_Hv50k_2016_491802	7H	N/A	575005145
JHI_Hv50k_2016_491872	7H	N/A	575492610
JHI_Hv50k_2016_491926	7H	N/A	576217891
JHI_Hv50k_2016_492050	7H	N/A	577609887
JHI_Hv50k_2016_492054	7H	N/A	577610014
JHI_Hv50k_2016_492057	7H	N/A	577610681
JHI_Hv50k_2016_492058	7H	N/A	577611129
JHI_Hv50k_2016_492060	7H	N/A	577611224
JHI_Hv50k_2016_492061	7H	N/A	577611494
JHI_Hv50k_2016_492135	7H	N/A	577791932
JHI_Hv50k_2016_492138	7H	N/A	577792366
JHI_Hv50k_2016_492222	7H	N/A	578293290
JHI_Hv50k_2016_492223	7H	N/A	578293579
JHI_Hv50k_2016_492238	7H	N/A	578364770
JHI_Hv50k_2016_492253	7H	N/A	578366693
JHI_Hv50k_2016_492267	7H	N/A	578369210
JHI_Hv50k_2016_492363	7H	N/A	581639227
JHI_Hv50k_2016_492408	7H	N/A	582606742
JHI_Hv50k_2016_492431	7H	N/A	583031646
JHI_Hv50k_2016_492795	7H	N/A	590232908
JHI_Hv50k_2016_492881	7H	N/A	590607072
JHI_Hv50k_2016_492940	7H	N/A	590877293
JHI_Hv50k_2016_493017	7H	N/A	591509869
JHI_Hv50k_2016_493602	7H	N/A	593205388
JHI_Hv50k_2016_493604	7H	N/A	593206327
JHI_Hv50k_2016_493632	7H	N/A	593307985
JHI_Hv50k_2016_493991	7H	N/A	597526275

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_494106	7H	N/A	598365899
JHI_Hv50k_2016_494138	7H	N/A	598676556
JHI_Hv50k_2016_494239	7H	N/A	598975681
JHI_Hv50k_2016_494393	7H	N/A	599176128
JHI_Hv50k_2016_494775	7H	N/A	600399854
JHI_Hv50k_2016_494781	7H	N/A	600400259
JHI_Hv50k_2016_494887	7H	N/A	600443428
JHI_Hv50k_2016_495162	7H	N/A	600888996
JHI_Hv50k_2016_495212	7H	N/A	600950453
JHI_Hv50k_2016_495236	7H	N/A	600964142
JHI_Hv50k_2016_495237	7H	N/A	600964892
JHI_Hv50k_2016_495457	7H	N/A	602206678
JHI_Hv50k_2016_495622	7H	N/A	602632593
JHI_Hv50k_2016_495677	7H	N/A	602678956
JHI_Hv50k_2016_495719	7H	N/A	602888003
JHI_Hv50k_2016_495726	7H	N/A	602888429
JHI_Hv50k_2016_496001	7H	N/A	604234356
JHI_Hv50k_2016_496078	7H	N/A	604332790
JHI_Hv50k_2016_496284	7H	N/A	604481140
JHI_Hv50k_2016_496334	7H	N/A	604483774
JHI_Hv50k_2016_496554	7H	N/A	604694279
JHI_Hv50k_2016_496594	7H	N/A	604698267
JHI_Hv50k_2016_497010	7H	N/A	605593985
JHI_Hv50k_2016_497105	7H	N/A	606866283
JHI_Hv50k_2016_497157	7H	N/A	606976871
JHI_Hv50k_2016_497266	7H	N/A	607681093
JHI_Hv50k_2016_497323	7H	N/A	607826653
JHI_Hv50k_2016_497329	7H	N/A	607827246
JHI_Hv50k_2016_497524	7H	N/A	608261022
JHI_Hv50k_2016_497584	7H	N/A	608811182
JHI_Hv50k_2016_497598	7H	N/A	608825777
JHI_Hv50k_2016_497605	7H	N/A	608826839
JHI_Hv50k_2016_497608	7H	N/A	608827049
JHI_Hv50k_2016_497610	7H	N/A	608827225
JHI_Hv50k_2016_497612	7H	N/A	608827493
JHI_Hv50k_2016_497615	7H	N/A	608827998
JHI_Hv50k_2016_497639	7H	N/A	609010093
JHI_Hv50k_2016_497745	7H	N/A	609597227
JHI_Hv50k_2016_498048	7H	N/A	610741494
JHI_Hv50k_2016_498052	7H	N/A	610741784
JHI_Hv50k_2016_498292	7H	N/A	611187812
JHI_Hv50k_2016_498293	7H	N/A	611187874

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_498334	7H	N/A	611195413
JHI_Hv50k_2016_498634	7H	N/A	612101916
JHI_Hv50k_2016_498676	7H	N/A	612215023
JHI_Hv50k_2016_498906	7H	N/A	613715990
JHI_Hv50k_2016_499690	7H	N/A	616320519
JHI_Hv50k_2016_500130	7H	N/A	617098230
JHI_Hv50k_2016_500141	7H	N/A	617099533
JHI_Hv50k_2016_501477	7H	N/A	621060220
JHI_Hv50k_2016_501635	7H	N/A	621837647
JHI_Hv50k_2016_501781	7H	N/A	622249778
JHI_Hv50k_2016_501795	7H	N/A	622363099
JHI_Hv50k_2016_502660	7H	N/A	623415884
JHI_Hv50k_2016_502996	7H	N/A	623648062
JHI_Hv50k_2016_503128	7H	N/A	623700499
JHI_Hv50k_2016_503145	7H	N/A	623754132
JHI_Hv50k_2016_503157	7H	N/A	623755590
JHI_Hv50k_2016_503176	7H	N/A	623759162
JHI_Hv50k_2016_503199	7H	N/A	623889668
JHI_Hv50k_2016_503216	7H	N/A	623915889
JHI_Hv50k_2016_503320	7H	N/A	624137848
JHI_Hv50k_2016_503428	7H	N/A	624290318
JHI_Hv50k_2016_503436	7H	N/A	624291161
JHI_Hv50k_2016_503500	7H	N/A	624624085
JHI_Hv50k_2016_503673	7H	N/A	624872977
JHI_Hv50k_2016_503922	7H	N/A	625634466
JHI_Hv50k_2016_504306	7H	N/A	626027118
JHI_Hv50k_2016_504572	7H	N/A	626401264
JHI_Hv50k_2016_504766	7H	N/A	626555948
JHI_Hv50k_2016_505010	7H	N/A	627089515
JHI_Hv50k_2016_505356	7H	N/A	627972394
JHI_Hv50k_2016_505375	7H	N/A	628036064
JHI_Hv50k_2016_505381	7H	N/A	628036392
JHI_Hv50k_2016_505483	7H	N/A	628172671
JHI_Hv50k_2016_505690	7H	N/A	628540308
JHI_Hv50k_2016_505752	7H	N/A	628552853
JHI_Hv50k_2016_505798	7H	N/A	628808572
JHI_Hv50k_2016_505809	7H	N/A	628811351
JHI_Hv50k_2016_506018	7H	N/A	629227980
JHI_Hv50k_2016_506093	7H	N/A	629278692
JHI_Hv50k_2016_506095	7H	N/A	629278820
JHI_Hv50k_2016_506121	7H	N/A	629447468
JHI_Hv50k_2016_506300	7H	N/A	629692134

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_506899	7H	N/A	632230284
JHI_Hv50k_2016_507221	7H	N/A	632757023
JHI_Hv50k_2016_507349	7H	N/A	633239253
JHI_Hv50k_2016_507921	7H	N/A	635206434
JHI_Hv50k_2016_507933	7H	N/A	635207230
JHI_Hv50k_2016_507943	7H	N/A	635208027
JHI_Hv50k_2016_508332	7H	N/A	636141347
JHI_Hv50k_2016_508384	7H	N/A	636149606
JHI_Hv50k_2016_508440	7H	N/A	636275734
JHI_Hv50k_2016_508538	7H	N/A	636407425
JHI_Hv50k_2016_508605	7H	N/A	636564877
JHI_Hv50k_2016_509054	7H	N/A	637199506
JHI_Hv50k_2016_509135	7H	N/A	637354942
JHI_Hv50k_2016_509271	7H	N/A	637561584
JHI_Hv50k_2016_509682	7H	N/A	638205148
JHI_Hv50k_2016_509793	7H	N/A	638450000
JHI_Hv50k_2016_509843	7H	N/A	638453743
JHI_Hv50k_2016_509849	7H	N/A	638454128
JHI_Hv50k_2016_509869	7H	N/A	638456804
JHI_Hv50k_2016_509951	7H	N/A	638524684
JHI_Hv50k_2016_510759	7H	N/A	639323737
JHI_Hv50k_2016_510951	7H	N/A	639794274
JHI_Hv50k_2016_511012	7H	N/A	639922665
JHI_Hv50k_2016_511279	7H	N/A	640412752
JHI_Hv50k_2016_511285	7H	N/A	640413174
JHI_Hv50k_2016_511966	7H	N/A	641265145
JHI_Hv50k_2016_511969	7H	N/A	641265656
JHI_Hv50k_2016_512328	7H	N/A	641796875
JHI_Hv50k_2016_512393	7H	N/A	641843766
JHI_Hv50k_2016_512497	7H	N/A	642028895
JHI_Hv50k_2016_512597	7H	N/A	642108062
JHI_Hv50k_2016_512648	7H	N/A	642238644
JHI_Hv50k_2016_512666	7H	N/A	642243408
JHI_Hv50k_2016_512813	7H	N/A	642428389
JHI_Hv50k_2016_512962	7H	N/A	642644011
JHI_Hv50k_2016_513173	7H	N/A	643310605
JHI_Hv50k_2016_513297	7H	N/A	644235980
JHI_Hv50k_2016_513337	7H	N/A	644417367
JHI_Hv50k_2016_513499	7H	N/A	644608075
JHI_Hv50k_2016_513501	7H	N/A	644608283
JHI_Hv50k_2016_513572	7H	N/A	644690963
JHI_Hv50k_2016_513690	7H	N/A	644915722

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_513720	7H	N/A	644920717
JHI_Hv50k_2016_513737	7H	N/A	644948099
JHI_Hv50k_2016_513834	7H	N/A	645014940
JHI_Hv50k_2016_513921	7H	N/A	645074827
JHI_Hv50k_2016_514223	7H	N/A	645824189
JHI_Hv50k_2016_514551	7H	N/A	646433917
JHI_Hv50k_2016_514581	7H	N/A	646477116
JHI_Hv50k_2016_514865	7H	N/A	647041370
JHI_Hv50k_2016_515347	7H	N/A	647662879
JHI_Hv50k_2016_515788	7H	N/A	648290452
JHI_Hv50k_2016_516627	7H	N/A	649693776
JHI_Hv50k_2016_516642	7H	N/A	649703235
JHI_Hv50k_2016_516758	7H	N/A	649996580
JHI_Hv50k_2016_516759	7H	N/A	649996790
JHI_Hv50k_2016_516784	7H	N/A	650002371
JHI_Hv50k_2016_516793	7H	N/A	650027103
JHI_Hv50k_2016_516830	7H	N/A	650047199
JHI_Hv50k_2016_516836	7H	N/A	650047698
JHI_Hv50k_2016_516996	7H	N/A	650601219
JHI_Hv50k_2016_517580	7H	N/A	652764553
JHI_Hv50k_2016_517858	7H	N/A	653119501
JHI_Hv50k_2016_518007	7H	N/A	653235708
JHI_Hv50k_2016_518631	7H	N/A	654157650
JHI_Hv50k_2016_518698	7H	N/A	654356383
JHI_Hv50k_2016_518741	7H	N/A	654410604
JHI_Hv50k_2016_518796	7H	N/A	654417653
JHI_Hv50k_2016_518804	7H	N/A	654541183
JHI_Hv50k_2016_518857	7H	N/A	654900532
JHI_Hv50k_2016_519240	7H	N/A	655967387
JHI_Hv50k_2016_519246	7H	N/A	655968393
JHI_Hv50k_2016_519249	7H	N/A	655968493
JHI_Hv50k_2016_519306	7H	N/A	656029690
JHI_Hv50k_2016_519329	7H	N/A	656040492
JHI_Hv50k_2016_519330	7H	N/A	656040562
JHI_Hv50k_2016_519350	7H	N/A	656047151
JHI_Hv50k_2016_519351	7H	N/A	656047154
JHI_Hv50k_2016_519353	7H	N/A	656047454
JHI_Hv50k_2016_519357	7H	N/A	656047687
JHI_Hv50k_2016_519358	7H	N/A	656047762
JHI_Hv50k_2016_519371	7H	N/A	656048737
JHI_Hv50k_2016_519376	7H	N/A	656049138
JHI_Hv50k_2016_519379	7H	N/A	656049524

Marker	Chromosome	Position (cM)	Position (BP)
JHI_Hv50k_2016_519390	7H	N/A	656050120
JHI_Hv50k_2016_519394	7H	N/A	656050247
JHI_Hv50k_2016_519408	7H	N/A	656051796
JHI_Hv50k_2016_519410	7H	N/A	656051812
JHI_Hv50k_2016_519413	7H	N/A	656051990
JHI_Hv50k_2016_519433	7H	N/A	656054712
JHI_Hv50k_2016_519437	7H	N/A	656055192
JHI_Hv50k_2016_519447	7H	N/A	656056686
JHI_Hv50k_2016_519454	7H	N/A	656057042
JHI_Hv50k_2016_519479	7H	N/A	656087668
JHI_Hv50k_2016_519604	7H	N/A	656717508
JHI_Hv50k_2016_519616	7H	N/A	656740990
BOPA1_2511_533	NA		N/A
BOPA1_6468_770	NA		N/A
BOPA2_12_10623	NA		N/A
BOPA2_12_11208	NA		N/A
BOPA2_12_20359	NA		N/A
BOPA2_12_21157	NA		N/A
BOPA2_12_30003	NA		N/A
BOPA2_12_30424	NA		N/A
BOPA2_12_30848	NA		N/A
BOPA2_12_30926	NA		N/A
BOPA2_12_30939	NA		N/A
BOPA2_12_31059	NA		N/A
BOPA2_12_31151	NA		N/A
BOPA2_12_31219	NA		N/A
BOPA2_12_31241	NA		N/A
BOPA2_12_31357	NA		N/A
BOPA2_12_31408	NA		N/A
SCRI_RS_102455	NA		N/A
SCRI_RS_103211	NA		N/A
SCRI_RS_10386	NA		N/A
SCRI_RS_110647	NA		N/A
SCRI_RS_114631	NA		N/A
SCRI_RS_114639	NA		N/A
SCRI_RS_115369	NA		N/A
SCRI_RS_11640	NA		N/A
SCRI_RS_117006	NA		N/A
SCRI_RS_119308	NA		N/A
SCRI_RS_119390	NA		N/A
SCRI_RS_119848	NA		N/A
SCRI_RS_122796	NA		N/A

Marker	Chromosome	Position (cM)	Position (BP)
SCRI_RS_123172	NA		N/A
SCRI_RS_123364	NA		N/A
SCRI_RS_124478	NA		N/A
SCRI_RS_126972	NA		N/A
SCRI_RS_128375	NA		N/A
SCRI_RS_129821	NA		N/A
SCRI_RS_130891	NA		N/A
SCRI_RS_132067	NA		N/A
SCRI_RS_132345	NA		N/A
SCRI_RS_13322	NA		N/A
SCRI_RS_133334	NA		N/A
SCRI_RS_13460	NA		N/A
SCRI_RS_13570	NA		N/A
SCRI_RS_136981	NA		N/A
SCRI_RS_137464	NA		N/A
SCRI_RS_13780	NA		N/A
SCRI_RS_137825	NA		N/A
SCRI_RS_138142	NA		N/A
SCRI_RS_138918	NA		N/A
SCRI_RS_139073	NA		N/A
SCRI_RS_139690	NA		N/A
SCRI_RS_139876	NA		N/A
SCRI_RS_139937	NA		N/A
SCRI_RS_140831	NA		N/A
SCRI_RS_140931	NA		N/A
SCRI_RS_140972	NA		N/A
SCRI_RS_141226	NA		N/A
SCRI_RS_14174	NA		N/A
SCRI_RS_142177	NA		N/A
SCRI_RS_142295	NA		N/A
SCRI_RS_142851	NA		N/A
SCRI_RS_143018	NA		N/A
SCRI_RS_143059	NA		N/A
SCRI_RS_144091	NA		N/A
SCRI_RS_144322	NA		N/A
SCRI_RS_144448	NA		N/A
SCRI_RS_145190	NA		N/A
SCRI_RS_145343	NA		N/A
SCRI_RS_146068	NA		N/A
SCRI_RS_146246	NA		N/A
SCRI_RS_147052	NA		N/A
SCRI_RS_1473	NA		N/A

Marker	Chromosome	Position (cM)	Position (BP)
SCRI_RS_147318	NA		N/A
SCRI_RS_1474	NA		N/A
SCRI_RS_147618	NA		N/A
SCRI_RS_147692	NA		N/A
SCRI_RS_148694	NA		N/A
SCRI_RS_148773	NA		N/A
SCRI_RS_149172	NA		N/A
SCRI_RS_150517	NA		N/A
SCRI_RS_152144	NA		N/A
SCRI_RS_152472	NA		N/A
SCRI_RS_153227	NA		N/A
SCRI_RS_153435	NA		N/A
SCRI_RS_154075	NA		N/A
SCRI_RS_154658	NA		N/A
SCRI_RS_155407	NA		N/A
SCRI_RS_155489	NA		N/A
SCRI_RS_156633	NA		N/A
SCRI_RS_157181	NA		N/A
SCRI_RS_157277	NA		N/A
SCRI_RS_157334	NA		N/A
SCRI_RS_158011	NA		N/A
SCRI_RS_159158	NA		N/A
SCRI_RS_159555	NA		N/A
SCRI_RS_159611	NA		N/A
SCRI_RS_160288	NA		N/A
SCRI_RS_160461	NA		N/A
SCRI_RS_161117	NA		N/A
SCRI_RS_161381	NA		N/A
SCRI_RS_161503	NA		N/A
SCRI_RS_162539	NA		N/A
SCRI_RS_163062	NA		N/A
SCRI_RS_16311	NA		N/A
SCRI_RS_163463	NA		N/A
SCRI_RS_164399	NA		N/A
SCRI_RS_165600	NA		N/A
SCRI_RS_165792	NA		N/A
SCRI_RS_166239	NA		N/A
SCRI_RS_168461	NA		N/A
SCRI_RS_169005	NA		N/A
SCRI_RS_170857	NA		N/A
SCRI_RS_172761	NA		N/A
SCRI_RS_175551	NA		N/A

Marker	Chromosome	Position (cM)	Position (BP)
SCRI_RS_179003	NA		N/A
SCRI_RS_179005	NA		N/A
SCRI_RS_179987	NA		N/A
SCRI_RS_180081	NA		N/A
SCRI_RS_181570	NA		N/A
SCRI_RS_182016	NA		N/A
SCRI_RS_182584	NA		N/A
SCRI_RS_182947	NA		N/A
SCRI_RS_185319	NA		N/A
SCRI_RS_186760	NA		N/A
SCRI_RS_187114	NA		N/A
SCRI_RS_187354	NA		N/A
SCRI_RS_189122	NA		N/A
SCRI_RS_189457	NA		N/A
SCRI_RS_189611	NA		N/A
SCRI_RS_189790	NA		N/A
SCRI_RS_189936	NA		N/A
SCRI_RS_190423	NA		N/A
SCRI_RS_190870	NA		N/A
SCRI_RS_192515	NA		N/A
SCRI_RS_193122	NA		N/A
SCRI_RS_194036	NA		N/A
SCRI_RS_194080	NA		N/A
SCRI_RS_194345	NA		N/A
SCRI_RS_195914	NA		N/A
SCRI_RS_196673	NA		N/A
SCRI_RS_196748	NA		N/A
SCRI_RS_196862	NA		N/A
SCRI_RS_197269	NA		N/A
SCRI_RS_197287	NA		N/A
SCRI_RS_198009	NA		N/A
SCRI_RS_198544	NA		N/A
SCRI_RS_198617	NA		N/A
SCRI_RS_199887	NA		N/A
SCRI_RS_199964	NA		N/A
SCRI_RS_200011	NA		N/A
SCRI_RS_200406	NA		N/A
SCRI_RS_200890	NA		N/A
SCRI_RS_20168	NA		N/A
SCRI_RS_201987	NA		N/A
SCRI_RS_201988	NA		N/A
SCRI_RS_202406	NA		N/A

Marker	Chromosome	Position (cM)	Position (BP)
SCRI_RS_202438	NA		N/A
SCRI_RS_203147	NA		N/A
SCRI_RS_203776	NA		N/A
SCRI_RS_203799	NA		N/A
SCRI_RS_204145	NA		N/A
SCRI_RS_206492	NA		N/A
SCRI_RS_206532	NA		N/A
SCRI_RS_206537	NA		N/A
SCRI_RS_206867	NA		N/A
SCRI_RS_207257	NA		N/A
SCRI_RS_208647	NA		N/A
SCRI_RS_212890	NA		N/A
SCRI_RS_214037	NA		N/A
SCRI_RS_214533	NA		N/A
SCRI_RS_219551	NA		N/A
SCRI_RS_219728	NA		N/A
SCRI_RS_220076	NA		N/A
SCRI_RS_220221	NA		N/A
SCRI_RS_220780	NA		N/A
SCRI_RS_221130	NA		N/A
SCRI_RS_221876	NA		N/A
SCRI_RS_223166	NA		N/A
SCRI_RS_224335	NA		N/A
SCRI_RS_226190	NA		N/A
SCRI_RS_226342	NA		N/A
SCRI_RS_2273	NA		N/A
SCRI_RS_230672	NA		N/A
SCRI_RS_230980	NA		N/A
SCRI_RS_231735	NA		N/A
SCRI_RS_231916	NA		N/A
SCRI_RS_232705	NA		N/A
SCRI_RS_233246	NA		N/A
SCRI_RS_233901	NA		N/A
SCRI_RS_234587	NA		N/A
SCRI_RS_235046	NA		N/A
SCRI_RS_235762	NA		N/A
SCRI_RS_236545	NA		N/A
SCRI_RS_237021	NA		N/A
SCRI_RS_237307	NA		N/A
SCRI_RS_238610	NA		N/A
SCRI_RS_239399	NA		N/A
SCRI_RS_239653	NA		N/A

Marker	Chromosome	Position (cM)	Position (BP)
SCRI_RS_240090	NA		N/A
SCRI_RS_2513	NA		N/A
SCRI_RS_4707	NA		N/A
SCRI_RS_48925	NA		N/A
SCRI_RS_4952	NA		N/A
SCRI_RS_6793	NA		N/A
SCRI_RS_7115	NA		N/A
SCRI_RS_7189	NA		N/A
SCRI_RS_7219	NA		N/A
SCRI_RS_739	NA		N/A
SCRI_RS_81903	NA		N/A
SCRI_RS_88466	NA		N/A
SCRI_RS_88710	NA		N/A
SCRI_RS_9350	NA		N/A