

CHARACTERIZING WATERLOGGING TOLERANCE IN SOUTHERN SOYBEAN  
(GLYCINE MAX L. [MERR.]) GERMPLASM COMPARING TRADITIONAL  
PHENOTYPING TO REMOTE SENSING METHODS AND APPLYING GENOMIC  
SELECTION FOR WATERLOGGING TOLERANCE TRAITS

A Dissertation

by

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## ABSTRACT

Development of flood-tolerant crops provides a pivotal resource to agriculture, helping to reduce yield loss and plant damage from fields with water-saturated soil conditions due to heavy rains, excessive irrigation, or poorly drained, low lying areas. Water-saturated soils can create hypoxic conditions for the root system and cause the plant to turn chlorotic, resulting in premature death, a common problem for soybean [*Glycine max* (L.) Merr.]. Sufficient genetic variability is present within soybean germplasm to differentiate between susceptible and tolerant genotypes. Rating samples from the field for tolerance to flooding is a process that can be resource-intensive and ineffective at distinguishing consistent plant responses, due to genotype by environmental interactions. A comparison of traditional phenotyping to high-throughput phenotyping using the unmanned aerial vehicles (UAVs) was conducted. A selected group of elite Corteva soybean germplasm, adapted for the southern U.S., was exposed to controlled waterlogged field conditions in 2014-2015 and 2017-2018. A visual flood-tolerance field (VS\_FLTFLD) score was assigned using traditional phenotyping and red, green, blue (RGB) camera imagery using UAVs, allowing for a single-time-point flood-tolerance (RS\_FLTFLD) score and a multi-time-point flood-recovery (RS\_FLTRCV) score to be estimated. Comparisons among the remote sensing and traditional phenotyping techniques provided a clear validation, illustrating that UAVs using RGB cameras can provide accurate phenotypic characterization of waterlogging tolerance in soybean. A comparison including RS\_FLTFLD and RS\_FLTRCV was performed with

the multi-time-point measurement exhibiting improved stability year to year. High-throughput phenotyping platforms allow breeders to capture high-quality phenotypic data on an extensive scale, mitigating some of the issues associated with ‘large p, small n’ (p= number of features, n= number of samples). Genomic selection (GS) has proven to be a valuable tool when analyzing complex traits, such as flood tolerance. Trait predictions were generated using data from 2017 and 2018. Pearson correlations between the training and testing sets were performed to evaluate prediction accuracy. Prediction accuracy was 0.68 and 0.26 percent for the trait FLTRCV in the years 2017 and 2018 respectively. This demonstrates that GS selection can be a valuable tool for improving waterlogging tolerance in soybean even with significant genotype x environmental interactions.

## DEDICATION

I dedicate this dissertation to my wife, Elizabeth, I could not have done this without your support and love; to my kids Gabriel and Abigail, thanks for the joy you guys give me each day; and to my mother Sue, for always believing in me and pushing me to keep on going. I would not be where I am today without your encouragement.

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## CONTRIBUTORS AND FUNDING SOURCES

### **Contributors**

This work was supervised by a dissertation committee consisting of Professor Dr. William L. Rooney, Dr. Dirk B. Hays, and Dr. Michael J. Thomson of the Department of Crop and Soil Sciences and Dr. Mark J. Hood of Corteva Agriscience.

The phenotypic data was produced onsite at the Corteva Agriscience Research Facility West Memphis, AR. All genotypic data was provided by Corteva Agriscience at Johnston, IA campus. All other analysis and work conducted for this dissertation was completed by the student independently.

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# CHAPTER I

## INTRODUCTION

There is an ever-increasing demand to get more resources from our planet, and the limitations of these resources affect present and future quality of life for every individual. Demands on agriculture are concerning, given the constant increase in the world population. The need for food to feed efficiently the world population is at an all-time high and we are perhaps one catastrophe away from a breaking point. Farmers have the task of meeting this challenge and will need all available advancements in agricultural technology at their disposal to meet this formidable task.

The increase of yields over time is the result of both improvements in agricultural techniques and combining of better genetics. About 50% of the yield gains in soybean can be attributed to superior genetics (Specht et al., 1999). As a science, plant breeding plays a critical role in agriculture. Developing improved cultivars is a time-consuming process that requires many resources, but breeders have demonstrated gradual increases in yields over time. Some crops have demonstrated this gain to a much greater extent than others. The rate of gain comparison between corn (*Zea mays* L.) and soybean (*Glycine max* [L.] Merrill) would be an example of this. From 1924 to 2009 corn yields have shown an increase annually of 1.7 bushel/acre compared to a 0.34 bushel/acre increase in soybean. From 1990 to 2009 corn yields showed an annual gain of 2.4 bushel/acre compared to 0.30 bushel/acre for soybean. This exponential increase

in corn yields but not in soybeans can cause trepidation for a breeder (Mikel et al., 2010; Diers, 2010).

Development of soybean cultivars that possess value-added traits such as flood tolerance and other abiotic resistance is receiving more attention. As the quality of arable land becomes more limited, the use of marginal ground for crop production becomes likely. Often these lands have limitations requiring increased inputs to sustain productivity and the benefits from the soil are marginally justified. These soils frequently offer inadequate fertility, salinity, pH problems, poor physical condition, reduced water availability, or poor drainage (Havlin et al., 2005). Flood tolerant lines developed through phenotypic selection may be lower yielding than susceptible lines, most likely because high yielding lines focus all their efforts on carbon assimilation, while the tolerant lower yielding lines maintain mechanisms for flood stress adaptation. The complexities of flood stress tolerance have contributed to the difficulties in breeding flood-tolerant crop varieties. Breeding efforts have been challenging due to limited knowledge regarding the precise mechanism of flood tolerance, efficient field and/or laboratory screenings, and the development of molecular markers associated with flood tolerance.

A search of available literature revealed numerous comparisons of cited screening methods and quantitative trait loci (QTL) studies for flood tolerance in soybean using traditional phenotyping (Van Toai et al., 2001; Cornelious et al., 2005; Githiri et al., 2006; Nguyen et al., 2012; Ye et al., 2018). But identification of an accurate high-throughput phenotyping technique using digital red, green, blue (RGB)

imagery has not been thoroughly investigated in a flood screening to this author's knowledge. Using RGB digital imagery from an unmanned aerial vehicle (UAV) for the assessment of disease resistance has been validated as an effective and precise phenotyping technique in citrus and potato (Garcia-Ruiz et al., 2013; Sugiura et al., 2016).

Whole genome prediction (WGP) and genomic selection (GS) is a method which can increase the effectiveness of a breeding program via genomic estimated breeding values (GEBV) for complex traits and reduce the resources required for phenotyping in earlier generations (Meuwissen et al., 2001; Heffner et al., 2009; Jannink et al., 2010). The use of WGP and GS for increasing genetic gain for flood tolerance must be evaluated to determine if and how accurate these estimated predictions are. Thus, these and other questions need to be answered before these methods can be used in a breeding program. The objectives of the research reported herein are:

Examine the flood screening process and compare the traditional phenotyping using visual scores to those collected using the UAS RGB digital imagery. Analyze the different traits for effectively assessing flood tolerance in the field while maintaining or improving precision.

Implement genomic selection using whole-genome predictions to evaluate each year of the 2017-2018 dataset using cross-validation to assess accuracy of the training set and testing set for each year individually. Then validate across year predictions using the 2017 dataset (training set) to generate predictions for the 2018 dataset (testing set) and then correlate that with the observed flood tolerance traits.

CHAPTER II  
REVIEW OF LITERATURE\*

**Soybean Origin and Proliferation**

Soybean (*Glycine max* [L.] Merrill) is an annual legume species native to China and is a member of the genus *Glycine*, which is divided into two subgenera *Soja* and *Glycine*. *Soja* contains two species: *Glycine soja* Sieb. and Zucc. and *Glycine max* (soybean). It is believed that *G. soja* is the wild ancestor of *G. max*, which has never been identified in the wild. Soybean can trace its domestication back to the northeastern region of the country around the 11th century BCE. This region, greater China, and the Korean peninsula can be considered the primary gene center for soybean and its movement can be linked to the unification of China. Domestication was most likely a process of trial and error over several hundred years and eventually introduced to the regions of Japan, Indonesia, the Philippines, Southeast Asia, and India through the 1st - 15th Centuries. These regions encompass what is known as the “second gene center” (Hymowitz, 1970).

During the 17th century soy sauce was becoming a common trade item, but early European visitors to Asia mistook tofu for cheese, and soybean’s importance as a food product was not revealed to the western world until the publication of Engelbert

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Kaempfer's book "Amoenitatum Exoticum..." in 1712. Carl Linnaeus first described soybean in 1737, during his stay with George Clifford, who was director of the Dutch East India Company and had an extensive botanical garden at the Hartekamp estate in Heemstede, Netherlands. These early introductions to Europe were merely grown for early taxonomy work. Records identify countries like France, England, and Yugoslavia as growing soybeans, with only Yugoslavia actually harvesting the seed and using it as a supplemental feed for chickens (Hymowitz, 1986).

In 1765, Samuel Bowen introduced soybean to the Georgia Colony in North America on his plantation near Savannah. Bowen had a production process that generated soy sauce and soy noodles; he was awarded a patent for inventions involved with the manufacturing of these products. Shortly after Bowen, Benjamin Franklin shipped seed to the botanist John Bertram to plant in his garden in Pennsylvania in 1770. Eventually soybean was introduced to the Midwest by John H. Lea in the middle 19th century and was on its way to become a well-established forage crop. The first Plant Introduction number issued by the Office of Foreign Seed and Plant Introduction within the USDA was P.I. 480 originating from Serbia (Hymowitz and Harlan, 1983). It was not until the 1920's that soybeans transitioned from a forage crop to their predominance as a major grain crop in the U.S. and the world.

### **Modern Production, Use, and World Population Demand**

Soybean is an important cash crop in North America and elsewhere in the world. Fifty-nine percent of oilseed production worldwide comes from Soy. Soybean oil is one

of the most widely used edible commodities and the meal can be used for animal feed and in human food products. Nearly half of all the meal produced in the U.S. is used to feed poultry, while another quarter goes to swine. There is also a growing utilization of soybean oil in various industrial and manufacturing applications, replacing oils generated from conventional fossil fuel production; 20% of soybean oil in the U.S. is used in this manner, while the remaining 80% is utilized in edible products (Soy Stats 2018, <http://www.soystats.com>; verified January, 2019). In 2017, soybean acres were estimated at 90.1 million acres, the highest on record in the United States, and \$9.30 was the average price per bushel, with a yield average of 49.1 bushels to the acre in 2017 (National Agricultural Statistics Service, Agricultural Statistics Board, United States Department of Agriculture, 2018). The U.S. exports 56.2 million metric tons of the soybean crop, with the majority of the crop going to China, Mexico, Netherlands, and Japan. Current growth estimates indicate that the world population will be over the 9 billion mark by 2050 (U.N. World Population Prospects, The 2017 Revision, 2017). As the global population increases and the demand for food and fuel present significant challenges given the limited resources of arable land, fresh water, and changing weather patterns, food production must increase 50% before 2030 to meet the world population demand (Ki-moon, 2008).

### **Soybean Growth and Development**

Soybean is an erect and bushy plant with many branches; plants can vary in height from 1-5 feet and their roots have the potential to penetrate the soil to depths up to

5 feet. Leaves are trifoliate except for the first set of true leaves at the first node above the cotyledons. Soybean has perfect flowers that contain both male and female organelles, making it a self-pollinated crop, growing in a cluster attached by a raceme to the nodes on the plant. Soybean is grouped into two main categories for growth habit: Indeterminate (flowering begins before stem growth stops and are attached via axillary racemes) and Determinate (flowers are attached via axillary and terminal racemes, and stem growth stops with formation of terminal bud). A third growth habit type is known as Semi-determinate and is hybrid of the two main groups, this growth habit type is less prevalent in North American germplasm than Indeterminate and Determinate. Soybean matures over a wide range of photoperiods, which gives soybean excellent adaptability over a wide range of latitudes. These ranges of maturities are broken into 12 maturity groups (MG), 000 being the earliest maturity for northern Canada and IX (9) being the latest maturity for South Texas and South Florida (Sleeper and Poehlman, 2006). A standardized set of growth development stages were established in the 1970's to help the soybean research community accurately describe a precise period of growth while minimizing the variation among individuals taking notes. Soybean is divided into two growth stages, a vegetative growth period (V) and a reproductive period (R). The vegetative stage is determined by counting the number of nodes on the main stem beginning with the unifoliate; this can be VE (Emergence), VC (Cotyledon), and V(n) (nth-node). Reproduction begins with bloom (R1) and occurs when there is one open flower at any node on the main stem, R2 represents full bloom, R3 is initiation of pods, R4 full pod (at least 2cm) at one of the four uppermost nodes on the main stem with a

fully developed leaf, R5 beginning seed, R6 Full Seed, R7 start of maturity, and R8 full maturity, when 95% of pods have reached their mature pod color (Fehr et al., 1971).

### **DNA Markers, Mapping, and Underlying Genetics of Soybean**

Initially the improvement of cultivars by plant breeders was based solely on phenotypic data generated from the progeny of crossing elite by elite parents, and selecting the best available progeny (Dudley and Moll, 1969). In the 1980's the development of restricted fragment length polymorphism (RFLP) technology laid the groundwork for an increased understanding of plant genetics and a methodology to improve selection of plant traits that are polygenic, otherwise known as quantitative traits. The development of molecular markers for genetic selection has been one of the most important developments in plant breeding in the last three decades, and led to the improved selection of heritable traits; this process, better known as marker assisted selection (MAS), allows plant breeders to select lines that have only desired traits. This creates efficiency for plant breeders, by reducing the variance of the trait within the population. Any detectible polymorphic trait can be used as a marker so long as it is inherited differentially and exhibits linkage disequilibrium with a phenotypic trait of interest. The development of single nucleotide polymorphisms (SNP) and detection using high-throughput re-sequencing technologies have increased data point output exponentially, while also decreasing cost per data point just as dramatically. Next generation sequencing using reduced representation libraries (RRL's) with the sequence-by-synthesis (SBS) method processed through a clonal single molecule array (CSMA)

platform has made possible the expansive discovery of numerous SNPs in plant species (Imelfort et al., 2009).

Soybean has 20 chromosomal pairs that are theorized to be from two separate rounds of genome-wide duplication (Shoemaker et al., 1996). The soybean genome sequence assembly was first made available in 2008 and is complete except for an estimated 15% centered around pericentromeric regions believed to contain highly repetitive sequences (Schmutz et al., 2010). The soybean genome is considered moderately large and containing a relatively high gene count when compared to other plant genomes. For comparison, soybean is approximated to contain 1,150 million basepairs (Mbp) while *Arabidopsis thaliana* contains a meager 125 Mbp. This genome size and gene concentration are believed to be artifacts of the genome duplication process that occurred ~13 million years ago, (Cannon and Shoemaker, 2012). Each soybean chromosome contains long pericentromeric regions; these areas lack the number of genes located in the subsequent arms of the chromosome, or euchromatic regions. Genes located near the centromere experience far less recombination than those in euchromatic regions, consequently genes linkages can be very difficult to break. Soybean diversity can be measured using the molecular techniques and DNA sequencing described; a comparative analysis between varieties, landraces, and species can then shed light on regions of shared synteny across the genome. Several studies have reported the finding of homologous sequences among soybean and common bean (*Phaseolus vulgaris*) and other related species (Choi et al., 2004, 2006). These relatives serve as a significant gene resource for the betterment of soybean, with limited methods of

successful propagation between species preventing a more significant flow of genes. Through the process of domestication, a reduction in diversity can occur leading to genetic bottlenecks, this is a consequence of linkage disequilibrium. Numerous soybean markers have been mapped and linkage groups created, as described in: "An Integrated Genetic Linkage Map of the Soybean Genome" (Cregan et al., 1999), "A Soybean Transcript Map: Gene Distribution, Haplotype and Single-Nucleotide Polymorphism Analysis" (Choi et al., 2007), and "A High Density Integrated Genetic Linkage Map of Soybean and the Development of a 1536 Universal Soy Linkage Panel for Quantitative Trait Locus Mapping" (Hyten et al., 2010). Many soybean markers are publicly available at the USDA affiliated soybase website (<http://soybase.org/>).

While there have been numerous studies performed to identify quantitative trait loci (QTL), and this technique has developed into a comparatively routine process over the years, over 1200 studies cited in 12 major crops, the successes of taking genetic mapping information and exploiting QTL to improve cultivars is limited compared to the number of studies (Bernardo, 2008). When developing strategy for successfully utilizing MAS for improving quantitative traits one should focus on the plant breeding aspect of "how identified QTL can be exploited in a breeding program...to improve (instead of simply study) a complex trait" (Bernardo, 2008). Questions a researcher should ask before conducting QTL analysis to identify complex traits ought to be: "1. Why do I want to find QTL, 2. Procedures for marker-based selection depend on the number of QTL, 3. Estimates of QTL effects for complex traits are often inconsistent, and 4. We

need to consider gain per unit of time and cost rather than gain per cycle” (Bernardo, 2008).

Genome-wide association analysis (GWAS) is an alternative to conventional linkage QTL mapping and involves the detection of QTL in a naturally occurring population instead of a family based population, which empowers researchers to investigate species in which establishing mapping populations is not easily accomplished, thereby saving time (Hwang et al., 2014). GWAS offers high resolution and has been effective in discerning traits associated with disease resistance, yield, and other numerous traits. A critical difference between these two methods is the degree of linkage disequilibrium (LD), the non-random association of different loci in a population. Conventional populations have a defined population structure and this population structure can be a confounding factor, resulting in false positives, if not accounted for when using GWAS. There are two ways of controlling false positives in association mapping: (1) to account for population structure a Q matrix can be created using principle component analysis (PCA), which identifies subpopulations that may exist within the sample of individuals with unknown structure; (2) a kinship (K) matrix can be created from the coefficients of co-ancestry using marker data, thus estimating relative kinship based on probabilities of being identical by state; this is often denoted as the “QK model” (Bernardo, 2010). The availability of high-throughput DNA sequencing has made association mapping an effective tool using mixed linear models (MLM) to create predictions of quantitative traits effects associated with markers (Zhang et al., 2016). Genome-wide association analysis is an effective tool when looking for QTL of

complex traits. Advantages over traditional linkage mapping are: the ability to detect an assortment of loci affecting the phenotype, not only those segregating in a bi-parental cross, and the improved resolution resulting from the underlying increased number of recombinations, taking advantage of the decay in LD.

### **Biotic and Abiotic Stress in Soybean**

Soybeans are grown in many diverse environments and face many challenges out in the field, biotic and abiotic. Plants that possess the ability to maximize their yield potential in adverse conditions provide the grower with a value-added product that minimizes risk. Much of the early tolerance and resistance work in soybean has focused on the many biotic stresses a plant encounters in the field. Of these biotic diseases, Asian soybean rust (*Phakopsora pachyrhizi*) has the greatest yield reducing effects worldwide. In North America soybean yields were reduced most by cyst nematode (*Heterodera glycines*), phytophthora root and stem rot (*Phytophthora sojae*), followed by various seedling diseases (*Rhizoctonia solani*, *Pythium* spp., *Fusarium* spp., and *Phomopsis* spp.) (Wrather et al., 2010). Abiotic stresses from nutrient deficiency or toxicity, flooding or drought, and salinity are responsible for more than 50% of the yield losses worldwide (Boyer, 1982). Plants subjected to abiotic stress respond by triggering metabolic, cellular, biochemical, and physiological mechanisms in order to survive until maturity. Improvement of crops to cope with environmental stress can prove difficult without considering the various environments, types of stress, and plant genes involved in regulating a response. Traditional breeding and now modern breeding with the use of



genomics and biotechnology, have produced cultivars with improved tolerance to many environmental stresses. Recent discoveries have revealed some of the signaling pathways and biochemical components involved in initiating plant responses to abiotic stress. Manipulating or limiting reactions to these processes would be one way of providing tolerance. Classifying the plant pathways responsible for the regulation and response to abiotic stresses has made significant steps. Although currently the signaling factors themselves that activate the plant response are not completely understood, most of the pathways that conduct the responses have been identified. Specific protein kinases may coordinate signaling pathways in unison converging targeted points of multiple abiotic as well as biotic stresses. Continued genetic analysis in conjunction with plant expression modeling will further identify signaling components, and allow for the characterization of factors responsive to specific abiotic stresses and determine the complexity of the signaling process (Chinnusamy et al., 2004).

### **Flood Tolerance Responses in Crops**

As climate change causes weather to be more erratic across the globe, the potential for heavy rainfall events to have a negative impact on agriculture becomes more plausible. Flooding is one of the most severe environmental factors limiting the productivity of agricultural crops; production losses in the United States due to flooding are second only to drought (Bailey-Serres et al., 2012). Flood losses in the United States were estimated on average at \$24 billion dollars a year between 2000 and 2001, per insurance indemnities paid out to farmers as recorded by the U.S. Department of

Agriculture Risk Management Agency *Cause of Loss Historical Data* (Bailey-Serres et al., 2012). Flooding is considered an all-purpose term referring to excessively wet conditions. A unified set of terminology was recommended and agreed on at the 15th New Phytologist Workshop on Flooding Stress: (1) “waterlogging or soil flooding” is excessive water in the soil or root-zone only, (2) “partial waterlogging or soil flooding” is similar to waterlogging but different in the sense that soil is not completely saturated and the depth and degree of the flooding is described or measured, (3) “submergence” means the entire plant is under water, and (4) “partial Submergence” means the entire root system and a portion of the above ground part of the plant is submerged. This is usually documented by a measurement of either plant height in relation to water level or the depth of the water to the soil (Sasidharan et al., 2017).

Flooding causes several different crises to transpire in the plant. These were categorized by Colmer and Voesenek (2009) into five types: (1) “*Energy crisis*”. Air in the soil becomes displaced by water, creating a restriction in the plant to gas exchange, limiting access to molecular oxygen (O<sub>2</sub>) and carbon dioxide (CO<sub>2</sub>), reducing cell respiration capacity. Oxygen diffusion is ten thousand times lower in water than in air (Armstrong et al., 2009), so displacement creates an asphyxiating effect in plants. The terminology used to describe this reduction in levels of O<sub>2</sub> in the plant is known as hypoxia. Plant metabolism requires O<sub>2</sub> to carry out oxidative phosphorylation. When this ceases adenosine triphosphate (ATP) must be generated via glycolysis (2) “*Carbohydrate crisis*”. This shift in plant metabolism, going from normal aerobic respiration and photosynthesis to inefficient anaerobic ATP production, results in a

depletion of sugar and starch reserves in the plant that can lead to cell and organ failure (Bailey-Serres et al., 2012). (3) *Toxicities*. Elements and metals in the soil can be released creating high levels of  $Mn^{3+}$ ,  $Fe^{2+}$ , and  $S^{2-}$  in plant root tissues. Formation of organic acids like propionic acid and butyric acid can occur requiring an increase in plant metabolism to process the acid compounds. Excess ethanol in the plant is transformed into acetaldehyde triggering cell injury upon flood abatement. (4) *Reactive Oxygen Species* (ROS). During the onset of flooding the plant experiences elevated levels of plant derived ethylene, reactive nitrogen, and ROS. These in turn lead to the creation of superoxide, originating in the mitochondria and accumulating as hydrogen peroxide. Elevated levels of hydrogen peroxide are common in plants upon re-oxygenation. (5) “*Water Deficits*”. Flooded conditions ironically cause a wilting of the above ground portion of the plant due to loss in water pressure in plasma membranes (Holbrook and Zwieniecki, 2003).

Plants have adapted strategies for survival and these can be categorized in two main methods. (1) Avoidance phenotypes also known as “low- $O_2$  escape syndrome (LOES)” are the modifications that the plant goes through during flooded conditions to improve gas exchange. These changes are mediated by the increased ethylene accumulating in the plant. An example of these changes is the formation of air filled pockets better known as “aerenchyma” which can form in the roots, stems, and leaves providing short term relief under flooded conditions. These pockets assist with gas exchange by limiting radial diffusion of oxygen and distribution within the plant and have been documented in crops like rice and wheat (Colmer and Voesenek, 2009).

Another modification is the development of adventitious roots (AR). These are roots that typically originate from the shoot portion of the plant and can have large amounts of aerenchyma. Adventitious roots form upon flooding and tend to occur in the older nodes closer to the soil surface. Many factors contribute to the development of AR including plant developmental stage, water temperature, depth, and flood duration (Zhang et al., 2015). AR facilitate plant survival by supporting gas exchange along with continuing nutrient and water uptake compensating for the submerged roots (Sauter, 2013). The last alteration is the ability to elongate parts of the shoot, particularly their leaves, petioles, and/or stems reestablishing contact with the air above the water. This escape mechanism is termed hyponastic growth (Colmer and Voesenek, 2009). (2) “Low-O<sub>2</sub> quiescence syndrome (LOQS)” does not require a physical change the plant, as occurs with LOES, but is a metabolic change that slows growth creating a stasis like effect. This ability to regulate metabolism during periods of flooding, particularly flash flood events that produce complete submergence, allows plants to survive and experience rapid recovery once flooding has subsided. Plants that demonstrate this ability manage energy consumption during periods of low O<sub>2</sub> stress, minimize the effects of ROS activity in the plant, and increase enzymes that produce ATP economically and without O<sub>2</sub>. The best example of this being implemented in a breeding program is the introduction of the SUBMERGENCE1 (SUB1) locus from the flood-tolerant landrace FR13A into popular rice varieties for the lowlands of south-east Asia. The SUB1 varieties produced all show a significantly higher survival rate than the original recurrent parents (Septiningsih et al., 2009). The SUB1 locus encodes tandem-repeated genes which are members of a

conserved group VII ethylene-response factor (ERF-VII), transcription factors that restrict ethylene production and thus prevent the activation of elongation (Xu et al., 2006; Singh et al., 2010). This locus epitomizes the “low-O<sub>2</sub> quiescence syndrome (LOQS)” adaptive method. Two other loci, identified in rice, are also members of the ethylene response factors family. These are SNORKEL1 and SNORKEL2, which allow rice to escape flooded situations via rapid growth exemplifying the “low-O<sub>2</sub> escape syndrome (LOES)” phenotype (Hattori et al., 2009). Many studies have been conducted on flooding tolerance in plants providing key findings on plant responses and their adaptive behaviors. Understanding these morphological and metabolic adaptations will continue to illuminate the underlying molecular mechanisms conditioning flood response in plants.

### **Soybean Response to Flooding**

To date there have been numerous flood tolerance studies concerning soybean, including germination, seeding vigor, vegetative, and reproductive, all with the emphasis on lessening the impact flooding stress has on yield. Variation for waterlogging tolerance exists in soybean, and the physiological, morphological, and structural response soybean exhibits during flooding have been reported in detail extensively (Table 1, page 21). Soybean’s responses to waterlogged conditions include a reduction in yield and/or height, delayed flowering, delayed maturity, and/or changes in chlorophyll content (greenness), carbon dioxide exchange, accumulation of dry matter, nitrogen content, nodule dry weight, and nodule number to name a few. Ahmed et al.

(2013) measured yield loss due to flood treatment by growth stage and reported that soybeans are more susceptible to flooding during the reproductive phase than the vegetative phase. Yield reductions in soybean due to flooding during vegetative growth can be in the ranges of 17% to 43% and during the R2 reproductive phase were estimated at greater than 50% on average. This yield loss is highly dependent on environmental conditions, variety, and duration of the waterlogged conditions (Oosterhuis et al., 1990; VanToai et al., 2010). Measurements of root biomass and development response under hypoxic conditions can be key indicators for selecting varieties tolerant to waterlogged conditions. Susceptible genotypes exhibit root morphology in flooded treatments, including shortness, absence of secondary lateral roots, and an overall reduction of root dry weight when compared to flood tolerant genotypes, morphology analogous to non-treated controls (Sakazono et al., 2014; Nguyen et al., 2017; Suematsu et al., 2017). Continued movement of O<sub>2</sub> to the roots during hypoxic conditions gives soybean plants the ability to survive and continue growth for extended periods of flooding (Bacanamwo and Purcell, 1999). Soybeans that experience low O<sub>2</sub> conditions during flooding will experience a reduction of N<sub>2</sub> fixation rather quickly because of reduced nodule numbers and dry weight. Rhizobia are diazotrophic bacteria that biologically fix nitrogen (N<sub>2</sub>) by means of a symbiotic relationship with legumes inside the root nodules of the plant. This process is a critical component for achieving successful yields. Amarante and Sodek (2005) measured the reduction of N<sub>2</sub> production to be detectable within 10 minutes of waterlogging conditions being implemented by taking readings of the glutamine concentrations in the

xylem sap which is correlated to N<sub>2</sub> fixation in soybeans. Another response of flood tolerant soybean lines to waterlogged treatments is the formation of aerenchyma and adventitious roots more readily than their waterlogged susceptible counterparts, illustrating the “low-O<sub>2</sub> escape syndrome (LOES)” adaptive system. Adventitious root development was observed on the third day with an approximate difference of one day between a tolerant genotype and susceptible genotype (Valliyodan et al., 2014). Formation of an aerenchyma complex in soybean is typically observed three weeks after inducing flooded conditions. This delay in the development of aerenchyma is detrimental to the soybean plant. There are wetland plant species that possess these types of cells even under non-hypoxic environments and without hesitation are prepared for sudden inundations. Identifying cultivars with improved aerenchyma characteristics could be a method for developing improved flood tolerant soybeans. The production of aerenchyma was quantified via lipid peroxidation by Kim et al (2015) and found to be higher in lines that demonstrated tolerance to waterlogging treatments compared to susceptible lines. Thick cracks (i.e. hypertrophic lenticels) form in the aerenchyma and facilitate O<sub>2</sub> entry into the plant. Experiments that blocked these openings showed that O<sub>2</sub> levels significantly drop and once the obstruction was removed O<sub>2</sub> levels normalized, indicating that the aerenchyma and hypertrophic lenticels functions as a ‘snorkel’ for continued O<sub>2</sub> movement into the plant and to the roots under flooded conditions (Shimamura et al., 2010). Endogenous hormones were measured at 5 and 10 day intervals in soybeans treated to waterlogging stress. Tolerant genotypes reveal increased levels of ethylene compared to the susceptible equivalent, and conversely methionine

demonstrated a decrease in tolerant versus susceptible genotypes. Measurements of the endogenous hormones abscisic acid, proline, gibberellic acid, jasmonic acid, and salicylic acid were also conducted, with only jasmonic acid not exhibiting a significant difference between flood tolerant and flood susceptible lines on either the 5th day nor the 10th day of flood treatment (Kim et al., 2015). Each of these hormones either plays a role in plant regulation of water potential or is a stress response hormone. Analysis of differential gene expression in soybean revealed that genes associated with the endogenous hormones mentioned above, abscisic acid specifically, are indeed up and down regulated during periods of waterlogging, with a greater number of genes being downregulated than upregulated. The downregulation implies a reduction in metabolic activity exemplifying the “low-O<sub>2</sub> quiescence syndrome (LOQS)” adaptive approach. This same study also identified genes that are differentially expressing not only during flooding but also in drought environments. Additionally, genes involved with photosynthesis efficiency were likewise affected, substantiating the hypothesis that flooding stress reduces the plant’s ability to conduct photosynthesis effectively. Examination of the abscisic acid stress response in soybean, under waterlogged settings, indicated no association with the SUB1 ortholog that mediates flood tolerance in rice and Arabidopsis (Chen et al., 2016). Transcriptional response studies using proteome analysis have more recently been conducted on soybeans subjected to flooding and several candidate flood genes have been reported. One potential protein negatively associated with soybean’s response to flooding stress was mRNA expression of cytochrome P450 77A1. This protein was up-regulated at the onset of flooding and



subsided once flood treatment was removed. Uniconazole, a triazole chemical effective in restraining growth in plants, was used to inhibit P450 activity. This chemical treatment induces the low-O<sub>2</sub> quiescence strategy. Soybean seedlings were exposed to a 3-hour uniconazole treatment and then subjected to a 7-day flooding regimen along with a control group. Soybean plants treated had a less than 17% mortality rate while the untreated had 85% mortality (Yin et al., 2017). Subsequent analyses are needed to substantiate and elucidate these and additional genes responsible for flood tolerance signaling in soybean.

Table 1. List of reported waterlogged tolerant soybeans.

Germplasm	Maturity Group	Origin	Reference
Edison	MG III	USA	VanToai et al. 1994
GR 8836	MG III	USA	VanToai et al. 1994
CX 415	MG IV	USA	VanToai et al. 1994
Archer	MG II	USA	VanToai et al. 2001
Misuzudaizu	-	Japan	Githiri et al. 2006
Peking	MG IV	China	Sayama et al. 2009
Nam Vang	MG VIII	Cambodia	VanToai et al. 2010
VND2	MG VIII	China	VanToai et al. 2010
ATF15-1	MG VIII	Australia	VanToai et al. 2010
PI 408105A	MG IV	Korea	Shannon et al. 2005
Iyodaizu	-	Japan	Nguyen et al, 2017
Kokubu 7	MG VII	Japan	Suematsu et al. 2017
Maetsuezairai 90B	-	Japan	Suematsu et al. 2017
Yahagi	VII	Japan	Suematsu et al. 2017
UA 5615C	MG V	USA	Wu et al. 2017
R10-4892	-	USA	Wu et al. 2017
R13-12552	-	USA	Wu et al. 2017
R07-6669	-	USA	Wu et al. 2017
Walters	MG V	USA	Wu et al. 2017
R04-342	-	USA	Wu et al. 2017
S11-25108	-	USA	Wu et al. 2017

Table 1. Continued

Germplasm	Maturity Group	Origin	Reference
S12-1362	-	USA	Wu et al. 2017
S11-25615	-	USA	Wu et al. 2017

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Numerous studies have recognized the physical and molecular changes occurring in soybeans under waterlogged conditions revealing the natural variations that exist. High-throughput phenotyping platforms could be a cost-effective way of capturing these changes leading to the next step of integrating this natural variation into elite varieties improving the genetic base for waterlogging tolerance in soybean.

### **Waterlogging Tolerance Quantitative Trait Loci (QTL) in Soybean**

Multiple waterlogging tolerant quantitative trait loci (QTL) have been reported (Table 2, page 26), with the first reported QTL coming from two northern recombinant inbred line (RIL) populations ‘Archer’ x ‘Minsoy’ and ‘Archer’ x ‘Noir I’. This one major locus was a simple sequence repeat marker Sat\_064 on chromosome 18 (linkage group G) that was not associated with any other traits determined in the screening, like maturity, yield, and plant height; however, the possible association to a disease trait (*Phytophthora* genes *Rps4* and *Rps6*) could not be ruled out completely (VanToai et al., 2001). This locus was introgressed into southern germplasm via near isogenic lines (NIL) and the Sat\_064 marker was evaluated. While no significant variation associate with Sat\_064 was detected for either waterlogging injury or yield in waterlogging conditions among the NILs, there was variation within the NIL sets for both traits

(Reyna et al., 2003). Supplementary analysis of this QTL was conducted using 2 RIL populations with ‘Archer’ as a parent. In this study two additional QTL were recognized as significant using bulk segregant analysis, Satt385 on Chromosome 5 (linkage group A1) and Satt269 on Chromosome 13 (linkage group F); these alleles were traced back to ‘Archer’ (Cornelious et al., 2005). These early studies seem to signify a relationship between waterlogging tolerance and native soybean resistance to the disease *Phytophthora sojae* (*P. sojae*) due to these markers’ close association with known *Rps* genes. A QTL producing increased yields under flooded environments was reported on Chromosomes 6 (linkage group C2) by Githiri et al. (2006); however, this locus was co-located with the maturity marker *E1*, inadvertently demonstrating that later maturing lines have an advantage when exposed to waterlogging treatments due to delayed flowering. This epitomizes the need to isolate maturity effects in subsequent investigations to clarify the actual factors behind waterlogging tolerance in soybean. The “seed-flood” screening by Sayama et al. (2009) characterized flood tolerance in soybean seedlings employing a 48-hour seed soaking process compared to a control and then evaluated germination rates (seeds with radicals longer than 1cm) and normal seeding rate (seedlings without damage to cotyledon or radical) of each group. The experiment discovered 4 QTL (*Sft1*, *Sft2*, *Sft3*, and *Sft4*) using a RIL population from ‘Peking’ (a black seed coat variety) x ‘Tamahomare’ (yellow seed coat variety); tolerant QTL were associated with the ‘Peking’ genotype. *Sft1*, nearby Sat\_175 on chromosome 12 (linkage group H) and was associated with increased germination rate. *Sft2*, is co-located with the *I* (*Inhibitor*) allele controlling seed coat color on chromosome 8 (linkage group A2)

showing improved germination rates and normal seeding rate. Seed coat color was previously attributed to improved flood tolerance varieties, with pigmented seed having greater tolerance to flooded conditions than yellow seed coat varieties (Hou and Thseng, 1991). This was attributed to anthocyanins associated with the seed coat acting as antioxidants and neutralizing ROS development in the seed. *Sft3* and *Sft4* were mapped near Satt348 (Chromosome 4) and Sat\_279 (Chromosome 2) respectively, but showed only moderately increased seed-flooding tolerance. Research using the plant introduction (PI) 408105A as the flood tolerant donor in a RIL population, crossed to S99-2281, a sensitive genotype from the University of Missouri, specified the location of two putative loci, one on Chromosome 13 (linkage group F) approximate to Sct\_003 and the other on Chromosome 17 (linkage group D2) nearest to the single nucleotide polymorphism (SNP) BARC-062213-17705 marker. Both these QTL were linked not only to improved flood tolerance but also partial *P. sojae* resistance, with the chromosome 13 QTL corresponding to the QTL previously reported by Cornelious et al. (2005). PI 408105A is acknowledged as an effective source for introgression of flood tolerance QTL into elite germplasm. More recent research has looked at QTL associated with root morphology and plasticity under hypoxic environments induced by flooding. A study based in Japan developed a new phenotypic evaluation method using hydroponic and aeration for characterizing root development under hypoxic conditions (Nguyen et al., 2017). A RIL population was developed using a hypoxia susceptible (Tachinagaha) by hypoxia resistant cross from a previous study (Sakazono et al., 2014). Eight different traits were measured: root length (RL), root length development (RLD), root surface

area (RSA), root surface area development (RSAD), root diameter (RD), change in average root diameter (CARD), root dry weight (RDW), and shoot dry weight (SDW). QTL analysis was performed revealing many loci correlated with root development for the eight various traits measured under hypoxia conditions. Several QTL were also reported using a waterlogging injury score, with many overlapping with previously reported QTL. Of these the QTLs on Chromosome 12 (between Satt052 – Satt302) and 14 (between Sat\_177-Sat\_342) recurred across years. The region on Chromosome 12, which performed well under both hypoxic and waterlogged environments, was then backcrossed into the susceptible line Tachinagaha using marker assisted backcrossing to confirm the Satt052 – Satt302 region in the NIL (NIL-9-4-5). This interval on Chromosome 12 includes the QTL previously reported by Sayama et al. (2009) expressing an increased germination rate after 48-hour seed soak. Nguyen et al. (2017) noted that “many QTL for soybean seed weight were found in our introgressed region (<http://soybase.org/>)” and that seed size for the NIL was smaller than the recurrent parent Tachinagaha. Another research experiment investigating QTL’s conditioning waterlogging tolerance in soybean concentrated on creating a RIL mapping population using exotic (PI 561271) by elite (S99-2281) germplasm and then fine mapping these QTL. These loci were then incorporated into NILs with the goal of elucidating the physiological mechanisms and validating the relevance of these waterlogging QTL (Ye et al., 2018). A QTL was identified across three different years on Chromosome 3 nearest to marker Gm03\_3087237 coming from PI 561271 explaining up to 33% of the variation and named qWT\_Gm03. This QTL is nearby a known candidate gene for *Rps1*,

a *phytophthora sojae* resistance gene; it was concluded that this was not the same gene, but a different gene related to an auxin pathway. An additional minor QTL was also detected two of the three years and positioned on Chromosome 10 adjacent to marker Gm10\_43107961. NILs from the RIL population were selected that were heterozygous for qWT\_Gm03 and used to evaluate the additive effects of the QTL for waterlogging tolerance. As expected, those with the tolerant maker demonstrated enhanced tolerance to flooded environments. A consequence of this allele was improved root development under waterlogged situations; root development was more prolific with faster regeneration than in genotypes without the Chromosome 3 QTL. A list of potential candidate genes was identified using the reference genome Williams 82; among these were a pectin methyl esterase inhibitor involved in root and shoot elongation and a gene that encodes a stress response protein (Ye et al., 2018). Several QTL have been identified in soybean that can improve waterlogging tolerance; however, soybean appears to lack a single major QTL conditioning waterlogging tolerance, unlike rice. The quantitative nature of waterlogging tolerance in soybean requires the combining of multiple favorable alleles into a variety. Exploring additional avenues such as genomic selection may be a more effective method for increasing flood tolerance in soybean while still maintaining yields of elite cultivars.

Table 2. List of reported QTL associated with waterlogged tolerance in soybean. Quantitative trait loci (QTL), Parental Source QTL, Chromosome (CR), Genetic Position, Coefficient of determination ( $R^2$ ), and Literature Reference.

QTL	Parental Source QTL	CR	Genetic Position	$R^2$	Reference
Chr.3	Archer	3	Satt485	–	Cornelious et al. (2005)

Table 2. Continued

QTL	Parental Source QTL	CR	Genetic Position	R <sup>2</sup>	Reference
Chr.18	Archer	18	Sat_064	–	VanToai et al. (2001); Cornelious et al. (2005)
<i>ft1</i>	Misuzudaizu	6	Satt100	0.49	Githiri et al. (2006)
<i>ft2</i>	Misuzudaizu	2	Satt282	0.07	Githiri et al. (2006)
<i>ft3</i>	Misuzudaizu	19	A489	0.1	Githiri et al. (2006)
<i>ft4</i>	Misuzudaizu	11	A520	0.11	Githiri et al. (2006)
<i>ft5</i>	Misuzudaizu	14	A685b	0.1	Githiri et al. (2006)
<i>ft6</i>	Misuzudaizu	7	A715	0.07	Githiri et al. (2006)
<i>ft7</i>	Misuzudaizu	10	Satt477	0.07	Githiri et al. (2006)
<i>Sft 1</i>	Peking	12	Sat_175	–	Sayama et al. (2009)
<i>Sft 2</i>	Peking	8	Satt187	–	Sayama et al. (2009)
<i>Sft 3</i>	Peking	4	Satt338	–	Sayama et al. (2009)
<i>Sft 4</i>	Peking	2	Sat_279	–	Sayama et al. (2009)
<i>FTS-11</i>	PI 408105A	11	BARC- 016279- 02316	0.18	Nguyen et al. (2012)
<i>FTS-13</i>	PI 408105A	13	BARC- 024569- 04982	0.14 – 0.18	Nguyen et al. (2012)
<i>Qhti-14-1</i>	Tachinagaha	14	Sat_177- Sat_342	0.1	Nguyen et al. (2017)
<i>Qhti-12-1</i>	Tachinagaha	12	Satt052- Satt302	0.11	Nguyen et al. (2017)
<i>Qhti-14-2</i>	Tachinagaha	14	Sat_177- Sat_342	0.18	Nguyen et al. (2017)
<i>Qhti-12-2</i>	Tachinagaha	12	Satt052- Satt302	0.18	Nguyen et al. (2017)
<i>Qhti-14-3</i>	Tachinagaha	14	Satt126- Satt467	0.11	Nguyen et al. (2017)
<i>Qhti-4</i>	Tachinagaha	4	AW277661- Satt399	0.1	Nguyen et al. (2017)
<i>Qhti-9</i>	Tachinagaha	9	GMES1693 -CRRS100	0.12	Nguyen et al. (2017)
<i>Qrl-14</i>	Tachinagaha	14	Satt342- Satt126	0.23	Nguyen et al. (2017)
<i>Qrl-12</i>	Tachinagaha	12	Satt052- Satt302	0.19	Nguyen et al. (2017)
<i>Qrld-12</i>	Tachinagaha	12	Satt663- Satt362	0.15	Nguyen et al. (2017)

Table 2. Continued

QTL	Parental Source QTL	CR	Genetic Position	R <sup>2</sup>	Reference
<i>Qrsad-12</i>	Tachinagaha	12	Satt052-Satt302	0.12	Nguyen et al. (2017)
<i>Qrd-14-1</i>	Tachinagaha	14	Satt342-Satt126	0.15	Nguyen et al. (2017)
<i>Qrd-14-2</i>	Tachinagaha	14	Satt342-Satt126	0.14	Nguyen et al. (2017)
<i>Qrd-12</i>	Tachinagaha	12	Satt469-Satt302	0.22	Nguyen et al. (2017)
<i>Qcard-11</i>	Tachinagaha	11	Sct_026-Sat_364	0.11	Nguyen et al. (2017)
<i>Qcard-14</i>	Tachinagaha	14	Sat_177-Satt126	0.11	Nguyen et al. (2017)
<i>qWT_Gm03</i>	PI 561271	3	Gm03_3087 2737_A/G	0.17- .33	Ye et al. (2018)
<i>qWT_Gm10</i>	S99-2281	10	Gm10_4310 7961_A/G	0.08- 0.15	Ye et al. (2018)

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### High-Throughput Phenotyping Using Aerial Imagery

Phenotyping has been a fundamental part of field based plant breeding since its beginnings, and contemporaneously a limiting factor concerning the number of plots an individual is capable of characterizing in a season. A plant breeder's goal is quickly and accurately to capture as many phenotypic differences among genotypes within a cycle, selecting the best genotypes for advancement and increasing genetic gain. Advances in genotyping have led to large genotypic libraries that can be used in marker assisted selection (MAS), marker assisted recurrent selection (MARS), and genomic selection (GS), with traditional phenotyping creating an operational bottleneck limiting the ability to efficiently optimize genetic gain. High-throughput phenotyping (HTP) systems provide the means to alleviate this obstacle and capture large amounts of phenotypic data



previously unattainable. Some of the most frequently used crop phenotyping instruments are: digital red-green-blue (RGB), multispectral, hyperspectral, fluorescence, LiDAR (light imaging, detection, and ranging), and thermal sensors. These sensors are often integrated into a field based platform like a stationary tower, tractor or unmanned aerial vehicle (UAV). Remote field based phenotyping has a clear advantage over traditional phenotyping by reducing time required for phenotyping and being non-invasive and non-damaging. These techniques are carried out nearby the crop without having to disturb the canopy. Digital RGB cameras are presently one of the most economical and commonly used systems available and have exceeded NDVI multispectral imagery when used in vegetative indices (Araus et al., 2018). When a UAV is used, a flight plan is created and a sensor mounted on a gimble maintains alignment with the ground to prevent distortion. Captured images can be in various file formats (JPEG, TIFF, etc.) depending on user software. Raw images are then compiled and assembled via georeferencing orthomosaic employing ground control points (GCP) captured using RTK-GPS (Garcia-Ruiz et al., 2013; Sugiura et al., 2016). Individual plot clips are produced allowing each plot to be analyzed independently, the method for accomplishing this is by applying a polygon grid superimposed over the location representing range and plot arrangements (Aguate et al., 2017). Spectral bands (NDVI) or color space (RGB) is examined via software with many different programs available to users. RGB imagery is frequently evaluated using representations of the RGB color model, by hue, saturation, and value (HSV) or hue, saturation, and lightness (HSL), and permits a computer to perceive color corresponding to human vision (Sugiura et al., 2016). The classification of images is based on the

elements H value, S value, and V value parameters constructing data values for each plot. Validation of high-throughput phenotyping using UAV imagery versus traditional or “ground truth” phenotyping has demonstrated that UAVs are more accurate and these remote sensing platforms allow for optimization within the predictive agriculture space (Singh et al., 2019).

Aside from platform type, understanding the characteristics of the trait being evaluated and the timing of flights are key to producing quality HTP data. These decisions have the same impact that erroneous data from traditional phenotyping would have on a breeding program. It has been acknowledged that utilizing data from multiple time points in a model improves predictions when contrasted to single time point models (Aguate et al., 2017). Araus et al. (2018) created three separate categories of traits captured using RGB: counting (e.g. stand counts), monitoring (e.g. disease and maturity evaluation), and three-dimensional reconstruction (e.g. plant canopy height). Beyond simply using HTP to characterize genotypes in a breeding program, one can exploit this abundance of data to evaluate microenvironments in field experiments and correct for these effects, thereby improving heritability and increasing selection accuracy. Big data using HTP has also renewed interest in crop modeling by enhancing the prediction capabilities of crop growth models addressing the complexities of genotype x environment x management interactions (Cooper et al., 2014).

## Genomic Selection

Genomic selection (GS), or genome-wide selection, is a form of genetic marker based selection that leverages dense marker maps across the entire genome and depends on the probability that segments of linkage disequilibrium (LD) and quantitative trait loci (QTL) are similar in a validation population as the reference population. Bayesian methods are then used to estimate marker effects across the entire genome and predict breeding values for individuals (Meuwissen et al., 2001). The genomic selection method utilizes a ‘reference population’ or training population (training set) representing a relevant group of breeding individuals that have been phenotyped across a range of environments, genotyped, kinship, and/or population structure information to develop a model that estimates all marker effects simultaneously for a ‘validation population’ or prediction population (prediction set) containing only genotypic information. These estimates are referred to as genomic estimated breeding values (GEBVs) and are the summation of all marker effects for a given individual (Meuwissen et al., 2001). Genome-wide selection has shifted the paradigm in breeding programs, offering significant increases in genetic gain for complex quantitative traits when combined with methods to condense cycle times. Early methods of GS created issues using multiple linear regression. GEBVs are calculated using the linear model,  $y_i = \mu + \sum_{j=1}^p x_{ij} \beta_j$ , where  $\mu$  is an intercept,  $x_{ij}$  is the genotype of the  $i$ th individual at the  $j$ th marker and  $\beta_j$  is the corresponding marker effect (de los Campos et al., 2013). An inherent danger when using multiple linear regression is multicollinearity of predictors, or correlation of independent variables, causing an overfitting of the model. This problem of ‘large  $p$

(number of markers), small n (number of phenotyped individuals)' leads to a lack of degrees of freedom (Jannink et al., 2010). To manage overestimation, procedures that utilize variable selection or a shrinkage of estimates are applied, e.g. genomic best linear unbiased prediction, Bayesian ridge regression, Bayesian regression, kernel regression, and machine learning methods, when creating GS models (Jannink et al., 2010). Best linear unbiased prediction with a genomic relationship matrix, also known as genomic best linear unbiased prediction (GBLUP) or kinship-BLUP, is a widely-used method for creating GEBVs and was first implemented in dairy cattle breeding (Hayes et al., 2009; Endelman, 2011). GBLUP is comparable to the standard pedigree based relationship matrix commonly used in a traditional BLUP; however, the pedigree based relationship matrix is replaced with a marker based estimate of additive relationships (de los Campos et al., 2013). The basic GBLUP model is  $y = Wg + e$ , where  $g \sim N(0, K\sigma^2)$ ,  $g$  is a vector of genotypic values and  $W$  is the design matrix connecting lines to phenotypic observations.  $K$  is the marker based additive kinship matrix and  $K=GG'$ , where  $G$  is the genotype matrix (Endelman, 2011). GBLUP methods were superior to marker assisted recurrent selection but, in animal breeding Bayesian approaches outperformed GBLUP when populations were from a multi-breed parentage (Bernardo, 2010; Hayes et al., 2009).

Bayesian statistics is a form of statistical inference that answers unknown parameters using probability statements even when there's limited data. Prior knowledge is utilized to create a distribution that is combined with current data using a likelihood function characterizing the current state of information called the posterior distribution

(Ghosh, 2010). These methods were previously computationally taxing; however, the advent of modern computing has now made generating optimal Bayes estimates routine. Bayesian models build predictions presuming “*a priori*” that only a few markers have an effect that differs from zero, allowing for variable selection (Meuwissen and Godard, 2010). Priors can be broken-down into four separate categories based on how thick or flat the tails of the distribution: (1) Gaussian prior has two hyperparameters, the first being the mean and usually set to zero and the second is the variance. This is the RR estimate better known as Bayesian ridge regression (BRR), also known as Ridge Regression Best Linear Unbiased Predictor (RR-BLUP). RR is a penalized method, which estimates regression coefficients by minimizing residual sum of squares by applying a limitation on the size of the regression coefficients. When the intercept and variance parameters are identified, the posterior distribution of marker effects will be multivariate normal and the posterior mean of marker effects is given by the equation  $\beta = [X'X + \sigma^2 \sigma_\beta^{-2} I]^{-1} X' \tilde{y}$ , where X is a matrix of marker genotypes,  $\tilde{y}$  is a vector of centered phenotypes,  $\sigma^2$  is the phenotypic variance and  $\sigma_\beta^2$  is the known marker variance hyperparameter (de los Campos et al., 2013). BRR approach may not be ideal in cases where some markers are linked to QTL while others are in regions that are not affecting the trait, as this method performs shrinkage of estimates that is equal across all markers (de los Campos et al., 2013). (2) Thick-tailed priors are comparable to Gaussian except for the higher mass at zero producing a significant shrinkage approaching zero on markers with minor effects. Examples of thick-tailed priors are: Bayesian least absolute angle and selection operator (LASSO), using the double-exponential or Laplace prior

(Park and Casella 2008); and the BayesA using the scaled-t density prior which was used in the pioneering genomic selection article by Meuwissen et al. (2001). (3) Spike-slab priors or finite mixture models are a combination of Gaussian components, a small variance centered on zero (the “spike”) and large variance also centered on zero (the “slab”). The model Bayes stochastic search variable selection (SSVS) is an example of this variable selection technique. A drawback of this model is the required knowledge in stochastic processes and the need to interpret which proportion effects are coming from the small variance. (4) Point of mass at zero and slab priors are priors that induce an assortment of variable selection and shrinkage. BayesB incorporates a point of mass at zero distribution, where the variance is zero, and a slab prior distribution, which has larger variance and is a scaled-t density (de los Campos et al., 2013). Having prior distribution mass at zero allows for markers to be estimated with zero influence, aligning with an accurate representation of how some genomic regions would carry no QTL for a trait (Heffner et al., 2009). Analogous to BayesB, BayesC method uses a point of mass at zero and slab density, but in this case the slab is a normal density (de los Campos et al., 2013). BayesC( $\pi$ ) was developed to address the drawbacks of BayesA and BayesB. Using a flawed probability of markers with null effects can negatively influence accuracy of predictions this is because the reduction of a markers influence is affected by the quantity of markers with insignificant effects. Habier et al. (2011) concluded that the probability of markers with null effects should be considered as an unknown and extrapolated from the data, as is the case with BayesC( $\pi$ ). Lastly, semi-parametric and nonparametric approaches, which determine regression coefficients from the data, such

as reproducing kernel Hilbert spaces regression (RKHS), random forests (RF) and neural networks (NN) can be used to model the regression functions. These types of procedures incorporate machine learning and go beyond the abilities of linear regression models, capturing non-additive genetic effects. These applications are on the forefront of genomic predictions and for the most part currently in proof of concept phase (Gianola et al., 2006; Jannink et al., 2010; Li et al., 2018). Among these linear models, Bayesian regression and GBLUP are the most frequently implemented and examined methods involving GS. The leading advantage related to GBLUP remains simplistic implementation with many software packages available, and the benefit of Bayesian methods is that they permit deviations from the infinitesimal model (de los Campos et al., 2013). Bayesian methods have been shown to provide higher prediction accuracies by performing selection and shrinkage when compared to other models like penalized regression in empirical studies, with the caveat that low marker density could have contributed to the results in this study (Solberg et al., 2009; Heslot et al., 2012).

Factors that can influence genomic selection prediction accuracy include: model choice, genetic architecture, marker density, and training population design. (1) Model choice has been demonstrated via simulations to effect GS accuracy; these differences are often dependent on genetic architecture (de los Campos et al., 2013). Inconsistencies among models are generally small when using real data, but Bayesian models (e.g. Bayes SSVS, BayesB, BayesA, and BayesC) typically outperformed other model types (e.g. Ridge Regression, GBLUP, and LASSO) (Jannink et al., 2010; de los Campos et al., 2013). It is generally expected that any model that is flexible and can accommodate

various types of genetic architecture will produce best results. (2) Trait architecture cannot be controlled, and traits with higher heritability and Mendelian in nature, should have improved accuracies compared to low heritability, polygenic traits. A question concerning genetic architecture arises from simulated studies where these architecture types are established, unlike empirical data where these can be quite complex (de los Campos et al., 2013). (3) Marker density can also influence GS accuracy. Meuwissen et al. (2009) demonstrated using a simulated study that lower marker densities reduced the accuracy of GBLUP models and BayesB was an improved model in such cases. Conversely, there is also a diminishing rate of increase to marker density, reported by Lorenzana and Bernardo (2009), indicating that a maximum marker density of 10cM evenly spaced across the genome is sufficient for genomic selection in biparental plant breeding populations. An empirical study using dairy cattle conducted by VanRaden et al. (2009) revealed that reducing marker numbers (38,416 SNPs) by 75% led to a reduction in accuracy; however, this reduction was minimal, from 0.53 to 0.50. (4) In this same study a reduction in training population reduced accuracy from 0.53 to 0.35; this illustrates that designing the training population is the most critical step in GS and modifications to the training population can have the most dramatic effects (Jannink et al., 2010). The objective of training a population design is to reduce the cost to phenotyping by utilizing only the genotypes necessary to accurately predict individuals in the validation population; this requires a balance between acceptable accuracy levels and resource allocation (Lorenz and Nice, 2017). Increasing the number of individuals in a training population, using both empirical and simulation studies, significantly increases



the prediction accuracy regardless of model choice or marker density (Meuwissen, 2009; Lorenzana and Bernardo, 2009; Zhang et al., 2017). Relationships of the training population to the validation population must also be considered when deciding which genotypes to include or leave out. Prediction accuracy is negatively impacted when training populations are not closely related to the validation population; this has been reported in studies for both animals and plants (Pszczola et al., 2012; Albrecht et al., 2014). Including one or both parents in a training population is one way of accomplishing this. Genotypes that are unrelated to the prediction set often result in prediction accuracies of zero or near-zero (Jacobson et al., 2014). An exception illustrated by Hickey et al. (2014) showed that with increased marker numbers (10,000) and significantly larger populations (20,000 individuals), models could achieve accuracies upwards of 70% using genotypes from a training set predicted onto an unrelated prediction set. Of these aspects contributing to genomic selection accuracy, the ones that can be manipulated by plant breeders to achieve best results are: size and design of the training population, genomic relationships between individuals in the training set and prediction set, and marker density and spacing across the genome.

### **Genomic Selection in Soybean**

In soybean, genomic selection studies have been reported for several traits, including yield, seed composition (protein and oil) and disease resistance, all with promising results (Bao et al., 2015; Jarquin et al., 2016; Zhang et al., 2016). Bao et al. (2015) implemented association mapping and genomic selection techniques for

improved Sudden Death Syndrome (SDS) resistance. A panel of 282 breeding lines from the University of Minnesota were used and identified several known regions of SDS resistance along with some novel QTL previously unreported. Cross-validation was used to estimate prediction accuracy of GS for SDS resistance. Out of the four traits captured during the experiment, RLS (Root Lesion Score), FSS (Foliar Symptom Score), RR (Root Retention), and DMR (Dry Matter Reduction), GS using RLS gave an accuracy of 0.64, which led the authors to conclude that genomic selection can be used successfully to evaluate breeding candidates for SDS resistance in a soybean breeding program.

Using 18,480 accessions from the USDA Soybean Germplasm Collection representing a diverse group of relative maturities (RM0 – RM9), Jarquin et al. (2016) evaluated prediction accuracies of seed protein, oil, and yield and reported positive prediction accuracies using three separate cross-validation models: GBLUP, BayesB, and Bayesian LASSO. The average prediction correlations were moderate to very high for the three traits across the various subgroups of germplasm, with the oil median prediction around 0.69, protein median prediction of 0.56, and yield median prediction of 0.64. The poorest predictions were those where no genetic relationship existed across the diverse group of accessions, predominantly northern germplasm used to predict southern germplasm and vice versa (Jarquin et al., 2016). Genomic selection for seed weight (SW) in soybean, using 309 plant introductions (PIs), was evaluated by Zhang et al. (2016). This study compared the use of GS to marker assisted selection (MAS) and reported prediction accuracies of 0.75-0.87 and 0.62-0.75 respectively, and validated that genomic selection is a valuable tool for selecting seed weight and superior to MAS.

## Summary

Natural variation exists in soybean for waterlogging tolerance, resulting in numerous comparisons of screening methods and reported quantitative trait loci (QTL) studies using traditional phenotyping. The availability of high-throughput phenotyping techniques using UAVs and digital imagery provides a precipitous and efficient phenotyping method that ought to enhance the assessment of waterlogging tolerance in soybean, whether through improved accuracy or by reducing laborious phenotyping. These new phenotyping platforms could illuminate and/or confirm QTL for waterlogging tolerance in soybean assist in providing more precise allele locations for improving waterlogging tolerance using marker assisted selection.

Genomic selection (GS) using whole genome predictions (WGP) is a method which can increase the effectiveness of a breeding program via genomic estimated breeding values (GEBV) for complex traits and reduce the resources required for phenotyping in earlier generations. The use of WGP and GS holds the potential for accelerated development of soybean varieties with improved waterlogged tolerance. The present research will explore the feasibility of using high-throughput phenotyping for screening soybeans in flooded conditions and evaluate GS as a potential tool for improving waterlogging tolerance in soybean.

CHAPTER III  
CHARACTERIZING FLOOD TOLERANCE USING TRADITIONAL  
PHENOTYPING AND UNMANNED AERIAL VEHICLES

**Introduction**

Soybean (*Glycine max* [L.] Merrill) is an important food and feed crop in North America and elsewhere in the world. Soybean oil is one of the most widely used edible commodities and the meal can be used for animal feed and in human food products. Abiotic stresses from nutrient deficiency or toxicity, flooding or drought, and salinity are responsible for more than 50% of the yield losses worldwide (Boyer, 1982). Drought is the number one abiotic cause of yield loss in soybean with flooding following second. Yield loss from flooding can occur at all stages of soybean development.

Flooded soil conditions that create excessive water in the soil or root-zone only are characterized as “waterlogging or soil flooding”, while flooded conditions in which the entire root system and a portion of the above ground part of the plant is submerged are termed “partial submergence”; this is usually documented by a measurement of either plant height in relation to water level or the depth of the water to the soil (Sasidharan et al., 2017). Under waterlogged conditions soybeans experience visual symptoms of suppressed height, loss of chlorophyll content (greenness), canopy collapse, chlorosis of the leaves, and, depending on duration of flood, eventual death. Ahmed et al. (2013) measured yield loss due to flood treatment by growth stage and reported that soybeans are more susceptible to flooding during the reproductive phase

than the vegetative phase. Susceptible genotypes exhibit root morphology in flooded treatments including shortness, lack of secondary lateral roots, and an overall reduction of root dry weight when compared to flood tolerant genotypes that is analogous to that of non-treated controls (Sakazono et al., 2014; Nguyen et al., 2017; Suematsu et al., 2017). Continued movement of O<sub>2</sub> to the roots during hypoxic conditions gives soybean plants the ability to survive and continue growth for extended periods of flooding (Bacanamwo and Purcell, 1999). Formation of aerenchyma and adventitious roots is indicative of tolerant varieties in contrast to waterlogged susceptible counterparts, illustrative of the “low-O<sub>2</sub> escape syndrome (LOES)” adaptive system. Adventitious root development in tolerant varieties has been observed typically three days into flooded treatment with susceptible genotype lagging in adventitious root development (Valliyodan et al., 2014). The production of aerenchyma was quantified via lipid peroxidation by Kim et al. (2015) and found to be higher in lines that demonstrated tolerance to waterlogging treatments compared to susceptible lines. Thick cracks (i.e. hypertrophic lenticels) form in the aerenchyma and facilitate O<sub>2</sub> entry into the plant. Genes associated with the production of abscisic acid specifically are down regulated during periods of waterlogging. The downregulation implies a reduction in metabolic activity exemplifying the “low-O<sub>2</sub> quiescence syndrome (LOQS)” adaptive approach. Additionally, genes involved with photosynthesis efficiency were likewise affected, substantiating the hypothesis that flooding stress reduces the plant’s ability to conduct photosynthesis effectively.

Natural variation, in response to waterlogging conditions, has been reported in numerous soybean studies. Tolerance to waterlogging conditions appears to be

quantitative, controlled by many individual loci having minor effects, requiring the combining of multiple favorable alleles into a variety (VanToai et al., 2001; Cornelious et al., 2005; Githiri et al., 2006; Sayama et al., 2009; Nguyen et al., 2017; Ye et al., 2018). These studies typically measure the root and/or shoot portions of the plant characterizing responses to hypoxic conditions induced by flooding. These responses are typically conducted from a visual phenotyping perspective; infrequently some studies characterize waterlogged plant responses by measuring fluids, hormone levels, and gases within the plant (Bacanamwo and Purcell, 1999; Amarante and Sodek, 2005; Kim et al., 2015; Chen et al., 2016). Currently no studies report the use of high-throughput phenotyping as a method for characterizing soybean plant's responses to waterlogging conditions. Improving waterlogging tolerance in soybean would prevent crop losses in poorly drained areas often distressed by heavy rains or irrigation followed by rain events.

The objective of this research was to develop a screening process that evaluated the effectiveness of characterizing waterlogged soybeans under flooded field conditions, representative of what farmers might experience in a real-world setting, using both traditional phenotyping or “ground truthing” (visual scores) and comparing those to remote sensing traits captured utilizing high-throughput phenotyping methods employing unmanned aerial vehicles and digital imagery.

## Materials and Methods

### Plant Material

A total of 704 soybean genotypes representing maturity groups (MG) MG3 through MG7 were characterized for waterlogging tolerance in response to flooded field experiments from 2014-2015 and 2017-2018. These genotypes were selected from various Corteva soybean breeding programs and represent entries from wide-area yield trials of elite soybean cultivars. Genotypes were grouped into categories based on growth habit (GH), indeterminate and determinate, using a proprietary Corteva single nucleotide polymorphism (SNP) associated with growth habit in soybean. Within GH categories, genotypes were separated by maturity groups to minimize the maturity effects in response to waterlogged treatments. The number of genotypes in each GH and MG, classified by years of flood screening, appears in Table 3. During the flood tolerance screening, genotypes were added and dropped each year with selected genotypes repeating over multiple years.

Table 3. 2014-2015 and 2017-2018 Flood tolerance screening summary of genotypes classified by: growth habit, determinate (DET) and indeterminate (IND), and maturity group (MG).

Year	DET				IND				Total
	MG5	MG6	MG7	Total	MG3	MG4	MG5	Total	
2014	33	3	2	38	23	62	9	94	132
2015	37	10	5	52	52	121	15	188	240
2017	44	9	3	56	20	108	18	146	202
2018	26	12	6	44	11	67	8	86	130
Grand Total	140	34	16	190	106	358	50	514	704

## Field Management and Data Collection

The 4-year field evaluations for soybean waterlogging tolerance were conducted at the Corteva Agriscience Research Station in Proctor, Arkansas (34.146°N, -90.321°W) on Sharkey silt clay (very-fine, smectitic, thermic Chromic Epiaquerts). This soils series “consist of very deep poorly and very poorly drained, very slowly permeable solid that formed in clayey alluvium” (<https://websoilsurvey.sc.egov.usda.gov/>, Accessed 01/21/2019). Each flood treatment location contained experiments grown as randomized complete block design (RCBD) with 5 replications (rep) in 2014-2015 and 4 reps in 2017-2018. Genotypes with similar maturities were blocked together to minimize maturity effects. An identical neighboring control location was also planted that was furrow irrigated only. Differences were observed between the treated and control locations for the same genotype in both the visual scores and digital images (Figure 1, page 48). Plots were 7ft (2.13m) long single row and spaced 36 inches (0.91m) apart. The planting rate was 50 seeds per plot, or 7.14 seeds ft<sup>2</sup> not including alley spacing. The planting dates for the four experimental locations were June 20, 2014; June 12, 2015; May 18, 2017; and May 14, 2018, respectively. A series of levees were constructed (Figure 2a, page 49) to separate growth habits and maturities with spill gates (Figure 2b, page 49), resembling those used in rice production, on the lower side used to manage water levels targeting 5-10cm of water above the soil during flood treatment (Figure 2c, page 49) ensuring soil remained saturated during treatment for each separate block (Ye et al., 2018). All plots were surrounded to prevent un-bordered edge effects from occurring; this response was hypothesized by Cornelious et al. (2005) to be from



excessive water temperatures due to unshaded areas within the field experiment. Once maturity groups reached the R1 growth stage (beginning bloom), one open flower on any node on the main stem (Fehr et al., 1971), flood treatment was initiated for that block. This water level was maintained for a period of 9-12 days until flood stress symptomology began to develop (Wu et al., 2017). After flood treatment, plots were watered using furrow irrigation as needed.

All plots received a visual rating labeled visual flood tolerance field (VS\_FLTFLD) for waterlogging injury 7-10 days after treatment was removed (Cornelius et al., 2005). The injury rating scale was the following: 9 indicated less than 10% damage ( $\geq 90\%$  healthy plants) and 1 was greater than 85% of the plants showing foliar damage and/or death ( $\leq 15\%$  healthy plants), correspondingly (9 = 0%-10%; 8 = 11%-20%; 7 = 21%-30%; 6 = 31%-40%; 5 = 41%-50%; 4 = 51%-60%; 3 = 61%-70%; 2 = 71%-85%; 1 = 86%-100%) (Figure 2d, page 49). This rating scale is analogous to those reported by Wu et al. (2017); however, a reversed scoring system was implemented corresponding with the standardized scoring system historically utilized across all crops at Corteva in which a “9” is always the “better/more desirable” score while a “1” is the “poorest/least desirable” score, for a given trait.

In addition to recording the visual scores in 2017-2018, a digital image was captured for each plot employing the DJI Matrice 600 Pro unmanned aerial vehicle (UAV) or drone, with a Sony Alpha 6000 35mm digital camera mounted to a Gremsy T1 gimbal; the gimbal maintains alignment with the ground to prevent image distortion. A flight plan was created for the field; the drone flew at a height of about fifty meters. Raw

images were compiled and assembled creating an orthomosaic via Agisoft Photoscan, employing geospatial reference points or ground control points (GCP) captured using a SPS 585 handheld Trimble GNSS unit (Garcia-Ruiz et al., 2013; Sugiura et al., 2016; Lussem et al., 2018). Individual plot clips were produced via ArcMap (Esri's ArcGIS suite of geospatial processing programs) allowing each plot to be analyzed independently. Digital red-green-blue (RGB) imagery was analyzed via proprietary Corteva script producing three separate remote sensing (RS) traits using RGB vegetation indices (VIs): (1) Canopy Cover (RS\_CANCVR) is the general percent green canopy cover in the plot from remote sensing, or  $(\text{number of green pixels} / \text{the total image pixels}) * 100$  (2) Canopy Health (RS\_CANHLTH) is the general health of the plot canopy and is based on the density and intensity of greenness compared to all other colors using RS. This exploits a normalized green excess of all pixels to normalize the image removing lighting effects and quantify greenness (Meyer and Neto, 2008). Higher values are an indication of more green tissue. (3) Green Hue (RS\_GRNHUE) is a measure of the intensity or hue of green color for only the green pixels from RS; this exploits a normalized green excess of only the green pixels with higher values exhibiting a darker green color.

A single-time-point and a multi-time-point measurement, using an index of the three RS traits, was developed creating a remote sensing flood tolerance field (RS\_FLTFLD) trait and a remote sensing flood tolerance recovery (RS\_FLTRCV) trait, with the null hypothesis being that multi-time-point measurements will not perform as well or better than single-time-point measurements. The RS\_FLTFLD trait was a

composite of the RS traits (RS\_CANCVR, RS\_CANHLTH, and RS\_GRNHUE) from a single point in time for each year with the values then converted to a 1-9 score; the RS\_FLTRCV trait captures the change of the three RS traits using three distinct points in time for each RS trait during the flood treatment, values were calculated and then also converted to a 1-9 score (Aguate et al., 2017), The values for RS\_FLTFLD and RS\_FLTRCV were identical in scale to the visual score VS\_FLTFLD.

Plot maintenance is a critical component for enabling the drone to capture the highest quality images, thus delivering accurate data. Weeds within a plot are the number one reason for erroneous data and plots should be weed free prior to any flights. There were sixteen different flights in 2017, with the first flight commencing on June 21st (pre-flood treatment), eight separate flights during flooding treatment occurring June 26th - July 7th, and seven post flood treatment flights transpiring July 10th - 24th. The flight schedule for the 2017 control experiment (irrigated only) followed the same flight plan as the flood treated. In 2018, a total of ten flights were logged with the initial flight transpiring on June 29th (pre-flood treatment), four subsequent flights during flooding treatment occurring July 2nd - 12th, and five succeeding flood treatment flights transpiring July 17th - August 2nd. Yield data was collected for each plot for the years 2014 (excluded), 2017, and 2018. Seed yield was measured using bushels/acre (lbs., adjusted to 13% moisture) and harvested with an Almaco Split Harvest Pro (SHP50). Plant height (distance from the soil surface to the end of main stem), and days to maturity (the time from planting until 95% of the pods are mature (R8)) was also collected.



**Figure 1. Digital imagery of the same genotype (COR-B-137) in both the flood treated and control locations. Images were captured concurrently throughout pre-flood, during flood, and post flood treatment in 2017.**



**Figure 2. Field management techniques for inducing waterlogging conditions in soybean, photographed throughout the flooding treatment. (A) Levee system used to separate different material types to ensure even flooding at R1 growth stage. (B) Spill gate used to maintain water levels during treatment, and (C) flood level all through the course of treatment. (D) Example of soybeans variable response to waterlogged conditions, with plot on the left scoring 8 and the plot on the right scoring 1.**

### Statistical Analysis

The analysis of variance (ANOVA) for the VS\_FLTFLD, RS\_FLTFLD, RS\_FLTRCV, RS\_CANCVR, RS\_CANHLTH, RS\_GRNHUE, and Yield was done for both individual years and combined years for the traits mentioned, using the Fit Model for different genotypes and groups using JMP®, Version 14.3 (SAS Institute Inc., 2017

SAS/STAT 14.3 User's Guide. Cary, NC: SAS Institute Inc.). Significant differences among different treatments were calculated using LSMeans difference Student's t-test with a confidence level of  $\alpha < .05$ . Genotypes were considered fixed effects and replications were considered random effects for the individual years' analysis and replications and year were considered random for the multi-year analysis. Pearson correlation coefficients among traits based on the genotypic means were calculated for 2017-2018 and grouped by growth habit using JMP®, Version 14.3 (SAS Institute Inc., 2017 SAS/STAT 14.3 User's Guide. Cary, NC: SAS Institute Inc.). One of the most important measures of trait is heritability. Often utilized by plant breeders, heritability is a critical component in determining a trait's response to selection. There are two types of heritability: broad sense ( $H^2$ ) and narrow sense ( $h^2$ ) heritability.

$$H^2 = \frac{\sigma_g^2}{\sigma_p^2} \qquad h^2 = \frac{\sigma_a^2}{\sigma_p^2}$$

Broad sense heritability is defined as the proportion of phenotypic variance that is explained by the genetic variance, and genetic variance is comprised of additive, dominance, and epistatic effects. Narrow sense heritability is defined as the proportion of phenotypic variance that is explained by only the additive variance (Falconer and Mackey, 1996). In the strict sense heritability estimates are balanced genotypes chosen at random from a population and having a defined relationship. Broad sense heritability and repeatability have similar meanings if we consider the ratio of genotypic to phenotypic variance, with repeatability often demonstrating the maximum for broad sense heritability (Fehr, 1987; Falconer and Mackey, 1996). Piepho et al. (2007) and

Schmidt et al. (2019) proposed calculating broad sense heritability ( $H^2$ ) on unbalanced yield trials where genotypes were dropped and added as one might do in a real-world breeding program. Estimates of variance components for a mixed model were calculated applying the Sommer package (Covarrubias-Pazarán, 2016) in R software (R Development Core Team, 2018) denoting the variance-covariance structure and calculating repeatability, the upper-limit broad sense heritability employing only the phenotypic data and a broad sense heritability approximation using both phenotypic data and relationship matrices constructed using high density genome-wide markers.

#### Genotypic Data Collection

All Corteva Agriscience lines grown in 2014-2015 and 2017-2018 were genotyped using DNA analysis. Each genotype was screened with genome-wide single-nucleotide polymorphisms (SNP) markers proprietary to Corteva Agriscience. Genetic and physical positions of the proprietary SNP markers on the *Glycine max* Consensus 4.0 genetic map (Hyten et al., 2010) were estimated based on the Illumina Infinium BeadChip containing over 50,000 SNP markers published by Song et al. (2013). Marker density varied year to year with 2,258, 5,287, 2,012, and 5,581 markers for the years 2014, 2015, 2017, and 2018 respectively (Table A, page 112). SNP markers used in this study are listed in Appendix A (page 112). This variation in marker numbers year to year was due to the addition and subtraction of genotypes in the waterlogging tolerance screening. Additionally, markers were excluded that had missing data among genotypes greater than 25% after imputation and when minor allele frequency was less than 5%.

Numerical imputation was done via TASSEL (Trait Analysis by aSSociation, Evolution and Linkage) using k-nearest-neighbors with a default value of  $k = 5$  and distance type Euclidean. This imputation method compares missing genotypic data to other neighbors that are similar and uses an average of the neighbors to fill in the missing SNP data. This serves to provide a marker matrix with no missing data. The TASSEL software can be found at: <http://sourceforge.net/projects/tassel> (Bradbury et al., 2007).

## **Results and Discussion**

The effects of the waterlogging treatment were observed for all years and genotypes displayed varying degrees of response to the flooded conditions. Aerenchyma and adventitious root formation were more readily observed in tolerant varieties than their susceptible counterparts. Adventitious root development was typically observed 4-5 days into flooded treatment (Figure 3, page 58). The VS\_FLTFLD, RS\_FLTFLD, and RS\_FLTRCV trait scores covered the full range of 1-9 scale for all years, RS\_CANCVR had a range of values from 66.36% to 14.62% across years, RS\_CANHLTH had a range of values from 66.40% to 53.69% across years, RS\_GRNHUE had a range of values from 77.32% to 56.24% across years, and Yield had a range of data from 84.20bu/a 60# to 4.60bu/a 60# across years. Summary statistics for 2014, 2015, and 2017 had similar variances, standard deviations, and standard errors, while 2018 deviated from the three previous years demonstrating elevated measurements (Table 4A, 4B, 4C, 4D, 4E, 4F, and 4G, pages 60-62). Coefficients of determination ( $R^2$ ), the proportion of the variance explained by each trait, were lower for all traits in 2018 than in previous years, apart



from the remote sensing trait RS\_GRNHUE. Biplots also illustrate these year to year differences, with RS trait vectors in 2018 less correlated than the 2017 RS trait vectors (Figures 5, 6, and 7, pages 66, 67, and 68). This difference in 2018 was attributed in part to an increase in temperature and lack of precipitation (See Table 5 with weather data occurring during flood treatment, page 62). Increased temperatures in conjunction with less rain fall during treatment can exacerbate symptoms from waterlogging conditions; water temperatures in stagnant water can elevate quickly and cause scalding of plants resulting in all plants exhibiting susceptible symptoms (Cornelious et al., 2005; Wu et al. 2017). Another explanation behind these elevated statistics is the increased number of suppressed plots that exhibited premature death prior to and during early flood treatment. This was ascribed to an unusually elevated incidence of fungal disease pressure, not seen in the previous years, and purported to be *Rhizoctonia*, *Fusarium*, *Phytophthora*, or a complex of all three.

Analysis of variance for all traits (VS\_FLTFLD, RS\_FLTFLD, RS\_FLTRCV, RS\_CANCVR, RS\_CANHLTH, RS\_GRNHUE, and Yield) exhibited highly significant differences among genotypes ( $p < .0001$ ) and genotypes accounted for a significant proportion of the variance in response to the flooding treatment when examined across years (Table 6, page 63). When individual years were analyzed independently, all years again showed a significance of  $p \leq .01$  for all traits (Table 7, pages 64-65).

Applying a mixed model analysis, where genotypes were considered fixed effects and replications were considered random effects for individual years, LSMeans Differences Student's *t* indicated significant differences among genotypes for each trait

allowing, genotypes to be assigned a corresponding value for each of the six distinct traits, these can be found in the appendix B (Table B1, B2, B3 and B4, pages 302-322). Comparing LSMMeans from 2017-2018, overall values for VS\_FLTFLD, RS\_FLTFLD, and RS\_GRNHUE were lower in 2018 than the previous year; the inverse was observed for the traits RS\_CANCVR and RS\_CANHLTH, and very little difference was observed for the RS\_FLTRCV trait. This implies that the multi-time-point measurement, RS\_FLTRCV, experiences less fluctuation from environmental factors than the single-time-point measurements, VS\_FLTFLD and RS\_FLTFLD, providing improved phenotypic characterization of waterlogging tolerance in soybean year to year.

Pearson correlation coefficients were calculated for each trait comparison by growth habit utilizing the genotypic means for 2017-2018, with a perfect positive linear correlation between traits indicated by  $r = 1$  and a perfect negative linear correlation designated by  $r = -1$ . Correlations of all traits in 2017 were significantly positive (Table 8, pages 69-70), with RS\_CANCVR having the highest correlations to RS\_FLTFLD (DET  $r = 0.87$  and IND  $r = 0.84$ ) and RS\_FLTRCV (DET  $r = 0.85$  and IND  $r = 0.83$ ). The trait RS\_FLTRCV had the highest correlations to all three remote sensing traits, RS\_CANCVR, RS\_CANHLTH, and RS\_GRNHUE, captured by the drone in 2017, with  $r$  values of 0.85, 0.84, and 0.78 for DET and 0.83, 0.72, and 0.70 for IND respectively. The visual scores (VS\_FLTFLD) also demonstrated a positive correlation to the three remote sensing traits, RS\_CANCVR, RS\_CANHLTH, and RS\_GRNHUE, with  $r$  values of 0.70, 0.54, and 0.67 for DET and 0.74, 0.20, 0.34 for IND respectively. Ultimately the most important trait association is the comparison between waterlogging

tolerance traits and yield performance under flooded conditions, with VS\_FLTFLD (DET  $r = 0.35$  and IND  $r = 0.35$ ), RS\_FLTFLD (DET  $r = 0.42$  and IND  $r = 0.50$ ), RS\_FLTRCV (DET  $r = 0.43$  and IND  $r = 0.58$ ), RS\_CANCVR (DET  $r = 0.48$  and IND  $r = 0.57$ ), RS\_CANHLTH (DET  $r = 0.25$  and IND  $r = 0.45$ ), and RS\_GRNHUE (DET  $r = 0.43$  and IND  $r = 0.50$ ) all sharing a positive relationship in 2017. The following year some correlations had slightly negative correlations. These were particularly apparent in the determinate germplasm group, with the highest negative correlation between the traits RS\_GRNHUE and RS\_CANHLTH with a value of  $r = -0.11$  in the DET. RS\_GRNHUE was ineffective in characterizing waterlogging performance compared to the other remote sensing traits in 2018. Several plots maintained modest levels of greenness (RS\_GRNHUE) with little to no growth during flooding treatment, causing a divergence from the other remote sensing traits RS\_CANCVR and RS\_CANHLTH. Comparisons to yield also revealed the deviation of RS\_GRNHUE in 2018, with a correlation of  $r = 0.02$  for the DET and  $r = -0.05$  for the IND. The other traits all exhibited positive relationships with yield as in 2017: VS\_FLTFLD (DET  $r = 0.89$  and IND  $r = 0.75$ ), RS\_FLTFLD (DET  $r = 0.91$  and IND  $r = 0.77$ ), RS\_FLTRCV (DET  $r = 0.64$  and IND  $r = 0.44$ ), RS\_CANCVR (DET  $r = 0.62$  and IND  $r = 0.41$ ), and RS\_CANHLTH (DET  $r = 0.64$  and IND  $r = 0.47$ ).

Variance components were analyzed via the Sommer package (Covarrubias-Pazaran, 2016) in R software (R Development Core Team, 2018). Variance estimates were used to approximate repeatability and broad sense heritability values. Repeatability estimates utilized only phenotypic data while broad sense heritability estimates utilized

covariance structures by means of a relationship matrix constructed via molecular marker data in conjunction with the phenotypic data from all genotypes within each year. Repeatability estimates were calculated for the trait VS\_FLTFLD in 2014, 2015, 2017, and 2018, whereas traits RS\_FLTFLD, RS\_FLTRCV, RS\_CANCVR, RS\_CANHLTH, and RS\_GRNHUE were calculated in 2017-2018. Broad sense heritability estimates were approximated for the traits VS\_FLTFLD, RS\_FLTFLD, RS\_FLTRCV, RS\_CANCVR, RS\_CANHLTH, and RS\_GRNHUE using the 2017-2018 dataset. Repeatability estimates were indeed higher than the broad sense heritability estimate, which used molecular markers to create relationship matrices, with the highest repeatability estimates occurring in 2017 for the remote sensing traits RS\_CANCVR (repeatability = 0.76) and RS\_GRNHUE (repeatability = 0.77); these same traits were again the two highest in 2018. Out of the three traits, VS\_FLTFLD, RS\_FLTFLD, RS\_FLTRCV, that utilized the 1-9 scoring scale, RS\_FLTRCV was the most consistent for both years 2017 and 2018, with estimates of 0.69 and 0.66 respectively. The traits VS\_FLTFLD and RS\_FLTFLD had larger fluctuations year to year: VS\_FLTFLD was approximated at 0.66 and 0.39 for the years 2017 and 2018 respectively, while RS\_FLTFLD was approximated at 0.70 and 0.48 for the years 2017 and 2018 respectively. VS\_FLTFLD in 2014, 2015, and 2017 showed steady improvement in repeatability estimates until 2018 (Table 9, pages 71-72). Broad sense heritability estimates for the three flood tolerance scores and the three remote sensing traits in 2017 ranged from 0.33 to 0.62, with RS\_GRNHUE and VS\_FLTFLD having the highest approximations, 0.62 and 0.61 respectively. This range corresponds to what others have

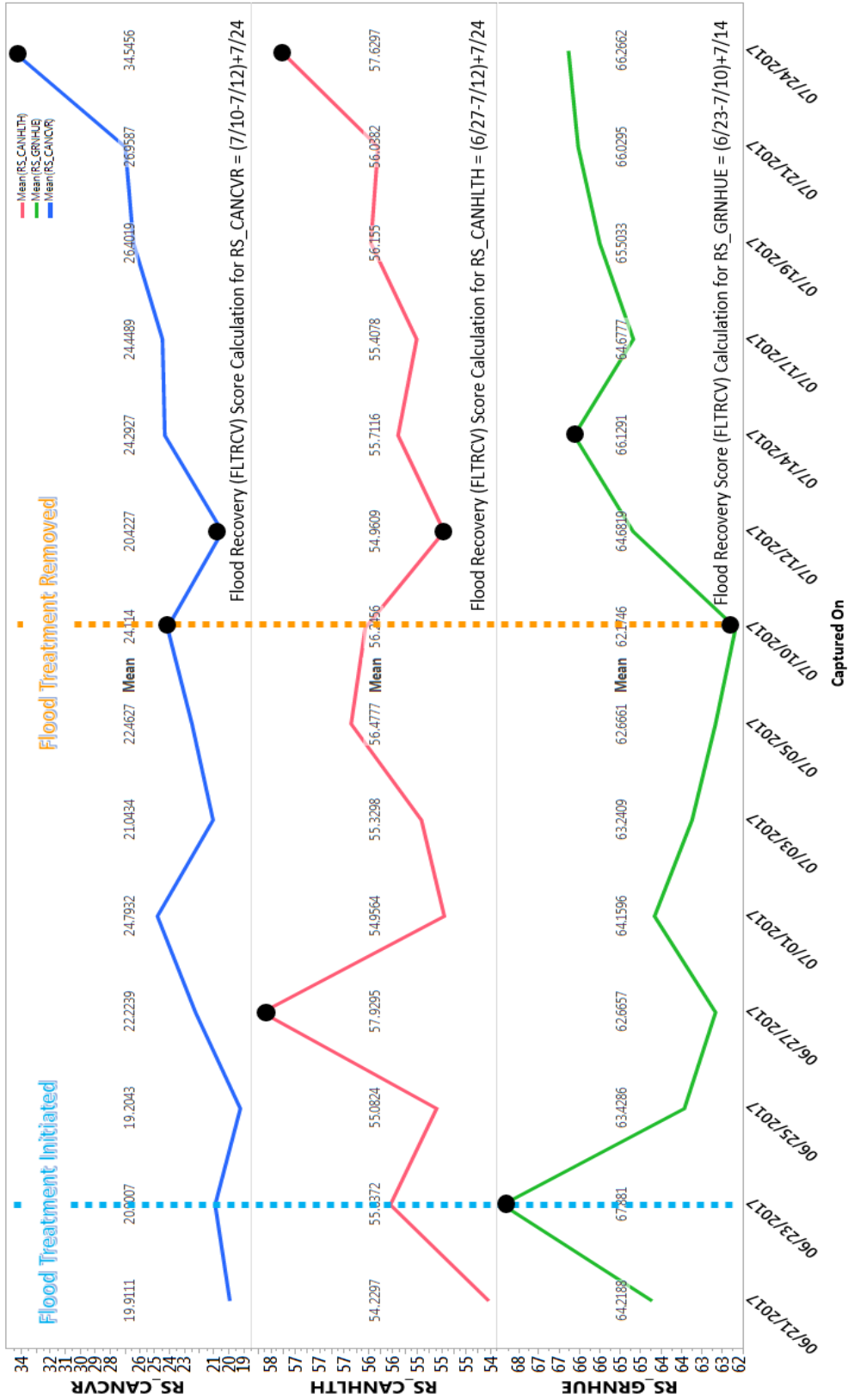
reported in various studies (Ye et al., 2018). Again, consistent with the repeatability results, 2018 demonstrated a reduction in heritability estimate values, however these were more pronounced and can be attributed to the increase in residual (error) variance for 2018 (Table 10, page 73). This year to year variation in heritability has been reported in other soybean traits. Jauregui et al. (2011) acknowledged a similar occurrence in soybean food-grade traits, also previous waterlogging tolerance research indicated that variation of genotype injury scores and genotype x environment interactions can be highly significant for waterlogging injury (Conelious et al., 2006; Wu et al., 2017).

In conclusion, comparisons of the remote sensing traits to traditional or “ground truth” phenotyping provides validation of high-throughput phenotyping using UAV imagery, illustrating that the UAVs using remote sensing devices (RGB cameras) can provide an accurate phenotypic characterization of waterlogging tolerance in soybean. High-throughput remote sensing platforms provide opportunities to capture data that is considered equal to or even an improvement over traditional phenotyping methods. Environmental factors such as temperature and disease can cause genotype x environment interactions and play a significant role in the severity of waterlogging symptomology in a field setting. To minimize these environmental factors, a comparison between single-time-point and a multi-time-point measurements, using an index of the three remote sensing traits, was developed creating a remote sensing flood tolerance field (RS\_FLTFLD) and remote sensing flood tolerance recovery (RS\_FLTRCV) score respectively. The multi-time-point measurement exhibited increased stability for phenotype characterization year to year compared to single-time-point measurement.

Figure 4 (page 59) illustrates the response observed for the three remote sensing traits, RS\_CANCVR, RS\_CANHLTH, and RS\_GRNHUE, during flooded treatment and shows how the multi-time-point measurement (RS\_FLTRCV) was calculated. As this technological space becomes more refined in the field of crop science these platforms will allow breeders to capture high quality phenotypic data on an immense scale not previously possible, mitigating some of the issues associated with “large p (number of markers), small n (number of phenotyped individuals)” (Jannink et al., 2010).



**Figure 3. Image of aerenchyma and adventitious root formation in soybeans occurring 4-5 days after flood treatment was initiated.**



**Figure 4. Response observed for the three remote sensing traits, RS\_CANCVR, RS\_CANHLTH, and RS\_GRNHUE, during flooded treatment. Example of how the multi-time-point measurement (RS\_FLTRCV) was calculated vs. the single-time-point measurement (RS\_FLTFLD) which used data collected on 7/12/2017.**

Table 4A. Summary statistics for the trait visual flood field (VS\_FLTFLD) score by years and all years combined; Maximum (Max) VS\_FLTFLD score, Minimal (Min) VS\_FLTFLD score, VS\_FLTFLD variance, VS\_FLTFLD standard deviation (Std Dev), VS\_FLTFLD standard error (Std Err), and VS\_FLTFLD coefficient of variation (CV).

Analysis Statistics	VS_FLTFLD D (score) Max	VS_FLTFLD D (score) Min	VS_FLTFLD D (score) Variance	VS_FLTFLD D (score) Std Dev	VS_FLTFLD D (score) Std Err	VS_FLTFLD D (score) CV
2014	9	1	3.79	1.95	0.07	36.43
2015	9	1	3.56	1.89	0.05	40.49
2017	9	1	3.32	1.82	0.06	34.72
2018	9	1	6.74	2.60	0.11	78.60
All Years	9	1	4.53	2.13	0.04	45.08

Table 4B. Summary statistics for the remote sensing trait flood field (RS\_FLTFLD) score by years and all years combined; Maximum (Max) RS\_FLTFLD score, Minimal (Min) RS\_FLTFLD score, RS\_FLTFLD variance, RS\_FLTFLD standard deviation (Std Dev), RS\_FLTFLD standard error (Std Err), and RS\_FLTFLD coefficient of variation (CV).

Analysis Statistics	RS_FLTFLD D (score) Max	RS_FLTFLD D (score) Min	RS_FLTFLD D (score) Variance	RS_FLTFLD D (score) Std Dev	RS_FLTFLD D (score) Std Err	RS_FLTFLD D (score) CV
2017	9	1	2.78	1.67	0.06	31.20
2018	9	1	6.46	2.54	0.11	67.57
All Years	9	1	4.87	2.21	0.06	46.89

Table 4C. Summary statistics for the remote sensing trait flood recovery (RS\_FLTRCV) score by years and all years combined; Maximum (Max) RS\_FLTRCV score, Minimal (Min) RS\_FLTRCV score, RS\_FLTRCV variance, RS\_FLTRCV standard deviation (Std Dev), RS\_FLTRCV standard error (Std Err), and RS\_FLTRCV coefficient of variation (CV).

Analysis Statistics	RS_FLTRCV (score) Max	RS_FLTRCV V (score) Min	RS_FLTRCV V (score) Variance	RS_FLTRCV V (score) Std Dev	RS_FLTRCV V (score) Std Err	RS_FLTRCV V (score) CV
2017	9	1	4.07	2.02	0.07	40.40
2018	9	1	5.04	2.24	0.10	43.98
All Years	9	1	4.42	2.10	0.06	41.79



Table 4D. Summary statistics for the remote sensing trait canopy cover variation (RS\_CANCVR) percent (pct) by years and all years combined; Maximum (Max) RS\_CANCVR pct, Minimal (Min) RS\_CANCVR pct, RS\_CANCVR variance, RS\_CANCVR standard deviation (Std Dev), RS\_CANCVR standard error (Std Err), and RS\_CANCVR coefficient of variation (CV).

Analysis Statistics	RS_CANC VR (pct) Max	RS_CANC VR (pct) Min	RS_CANC VR (pct) Variance	RS_CANC VR (pct) Std Dev	RS_CANC VR (pct) Std Err	RS_CANC VR (pct) CV
2017	66.15	14.62	52.65	7.26	0.26	18.97
2018	66.36	17.09	74.91	8.66	0.39	19.68
All Years	66.36	14.62	68.75	8.29	0.23	20.51

Table 4E. Summary statistics for the remote sensing trait canopy health variation (RS\_CANHLTH) percent (pct) by years and all years combined; Maximum (Max) RS\_CANHLTH pct, Minimal (Min) RS\_CANHLTH pct, RS\_CANHLTH variance, RS\_CANHLTH standard deviation (Std Dev), RS\_CANHLTH standard error (Std Err), and RS\_CANHLTH coefficient of variation (CV).

Analysis Statistics	RS_CANH LTH (pct) Max	RS_CANH LTH (pct) Min	RS_CANH LTH (pct) Variance	RS_CANH LTH (pct) Std Dev	RS_CANH LTH (pct) Std Err	RS_CANH LTH (pct) CV
2017	63.58	54.74	1.26	1.12	0.04	1.92
2018	66.40	53.69	4.86	2.20	0.10	3.65
All Years	66.40	53.69	3.60	1.90	0.05	3.21

Table 4F. Summary statistics for the remote sensing trait green hue variation (RS\_GRNHUE) percent (pct) by years and all years combined; Maximum (Max) RS\_GRNHUE pct, Minimal (Min) RS\_GRNHUE pct, RS\_GRNHUE variance, RS\_GRNHUE standard deviation (Std Dev), RS\_GRNHUE standard error (Std Err), and RS\_GRNHUE coefficient of variation (CV).

Analysis Statistics	RS_GRNH UE (pct) Max	RS_GRNH UE (pct) Min	RS_GRNH UE (pct) Variance	RS_GRNH UE (pct) Std Dev	RS_GRNH UE (pct) Std Err	RS_GRNH UE (pct) CV
2017	77.32	63.98	3.16	1.78	0.06	2.47
2018	70.78	56.24	3.27	1.81	0.08	2.78
All Years	77.32	56.24	14.05	3.75	0.10	5.42

Table 4G. Summary statistics for yield (bu/a 60#) by years and all years combined; Maximum (Max) yield (bu/a 60#), Minimal (Min) yield (bu/a 60#), yield (bu/a 60#) variance, yield (bu/a 60#) standard deviation (Std Dev), yield (bu/a 60#) standard error (Std Err), and yield (bu/a 60#) coefficient of variation (CV).

Analysis Statistics	YIELD (bu/a 60#) Max	YIELD (bu/a 60#) Min	YIELD (bu/a 60#) Variance	YIELD (bu/a 60#) Std Dev	YIELD (bu/a 60#) Std Err	YIELD (bu/a 60#) CV
2017	84.20	18.30	91.75	9.58	0.34	21.19
2018	74.10	4.60	151.46	12.31	0.66	50.39
All Years	84.20	4.60	202.95	14.25	0.42	36.80

Table 5. Location weather data collected during flooding treatment for each year; Daily Means for Maximum (Max) Temperature (Temp), Minimum (Min) Temperature (Temp), and Mean Monthly Rain Totals by month and three month totals.

Monthly Totals	2014	2015	2017	2018	
Mean Daily Max Temp (°F)	June	87.83	90.80	86.12	90.69
	July	85.82	91.62	89.93	91.16
	August	90.65	88.79	85.83	89.18
Mean Daily Min Temp (°F)	June	69.67	72.53	68.71	70.09
	July	67.18	74.49	71.79	71.94
	August	70.73	68.54	69.25	69.29
Mean Daily GDUs	June	27.48	29.20	26.77	28.02
	July	25.53	29.95	28.83	28.87
	August	28.23	26.93	26.75	27.38
Monthly Accumulative Precipitation (inches)	June	11.87	2.29	4.54	1.03
	July	1.65	5.19	3.81	3.27
	August	1.84	4.59	3.16	2.46
3 Month Mean Daily Max Temp	88.10	90.41	87.29	90.34	
3 Month Mean Daily Min Temp	69.19	71.86	69.92	70.44	
3 Month Mean Daily GDUs	27.08	28.69	27.45	28.09	
3 Month Accumulative Precipitation	15.36	12.07	11.51	6.76	

Temperature was measured in degrees Fahrenheit (°F), GDUs were calculated by subtracting the plant's lower base or threshold temperature of 50 °F from the average daily air temperature in °F. Average daily air temperature was calculated by averaging the daily maximum and minimum air temperatures measured in any 24-hour period (Iowa State University). Precipitation was measured in inches.

Table 6. Analysis of variance (ANOVA) of genotypes across years for the traits VS\_FLTFLD, RS\_FLTFLD, RS\_FLTRCV, RS\_CANCVR, RS\_CANHLTH, RS\_GRNHUE, and Yield

Trait	Source	DF	Sum of Squares	F Ratio	Prob > F
VS_FLTFLD (score)	Genotype	476	4992.67	3.21	<0.0001**
	Rep	4	742.7	56.85	<0.0001**
	Error	2833	9252.66		
	Total	3313	15004.37		
RS_FLTFLD (score)	Genotype	253	2137.11	2.87	<0.0001**
	Rep	3	1224.8	138.47	<0.0001**
	Error	1065	3139.95		
	Total	1321	6430.54		
RS_FLTRCV (score)	Genotype	253	2136.43	2.72	<0.0001**
	Rep	3	328.23	35.22	<0.0001**
	Error	992	3081.41		
	Total	1248	5521.65		
RS_CANCVR (pct)	Genotype	253	42957.54	4.36	<0.0001**
	Rep	3	5209.35	44.6	<0.0001**
	Error	1012	39399.43		
	Total	1268	87173.34		
RS_CANHLTH (pct)	Genotype	253	1801.32	2.77	<0.0001**
	Rep	3	194.31	25.17	<0.0001**
	Error	1027	2643.06		
	Total	1283	4613.13		
RS_GRNHUE (pct)	Genotype	253	8122.76	3.31	<0.0001**
	Rep	3	35.18	1.21	0.30507 <sup>ns</sup>
	Error	1047	10153.28		
	Total	1303	18312.58		
YIELD (bu/a 60#)	Genotype	325	352839.99	6.64	<0.0001**
	Rep	4	3898.18	5.96	0.0001**
	Error	1290	211076.01		
	Total	1619	582484.16		

\* Significant at the 0.05 probability level

\*\* Significant at the 0.01 probability level

ns Not significant at the 0.05 probability level

Table 7. Analysis of variance (ANOVA) of genotypes split by individual years for the traits VS\_FLTFLD, RS\_FLTFLD, RS\_FLTRCV, RS\_CANCVR, RS\_CANHLTH, RS\_GRNHUE, and Yield.

Year	Trait	Source	DF	Sum of Squares	F Ratio	Prob > F
2014	VS_FLTFLD	Genotype	131	1334.26	4.54	<.0001**
		Rep	4	32.78	3.65	0.01**
		Error	541	1213.1		
		Total	676	2563.12		
2015	VS_FLTFLD	Genotype	239	2024.8	3.69	<.0001**
		Rep	4	204.61	22.31	<.0001**
		Error	1071	2456.18		
		Total	1314	4682.09		
2017	VS_FLTFLD	Genotype	201	1651.31	5.46	<.0001**
		Rep	3	110.41	24.45	<.0001**
		Error	583	877.45		
		Total	787	2609.22		
2018	VS_FLTFLD	Genotype	129	876.5	2.01	<.0001**
		Rep	3	1382.36	136.6	<.0001**
		Error	401	1352.72		
		Total	533	3592.85		
2017	RS_FLTFLD	Genotype	201	1284.15	4.58	<.0001**
		Rep	3	126.3	30.19	<.0001**
		Error	583	812.97		
		Total	787	2188.11		
2018	RS_FLTFLD	Genotype	129	808.86	2.2	<.0001**
		Rep	3	1507.78	176.32	<.0001**
		Error	401	1143.05		
		Total	533	3444.8		
2017	RS_FLTRCV	Genotype	201	1579.88	2.88	<.0001**
		Rep	3	44.94	5.48	<.0001**
		Error	583	1592.32		
		Total	787	3201.95		
2018	RS_FLTRCV	Genotype	129	834.76	2.13	<.0001**
		Rep	3	509.28	55.99	<.0001**
		Error	328	994.44		
		Total	460	2316.21		
2017	RS_CANCVR	Genotype	201	26381.42	5.36	<.0001**
		Rep	3	1143.92	15.56	<.0001**

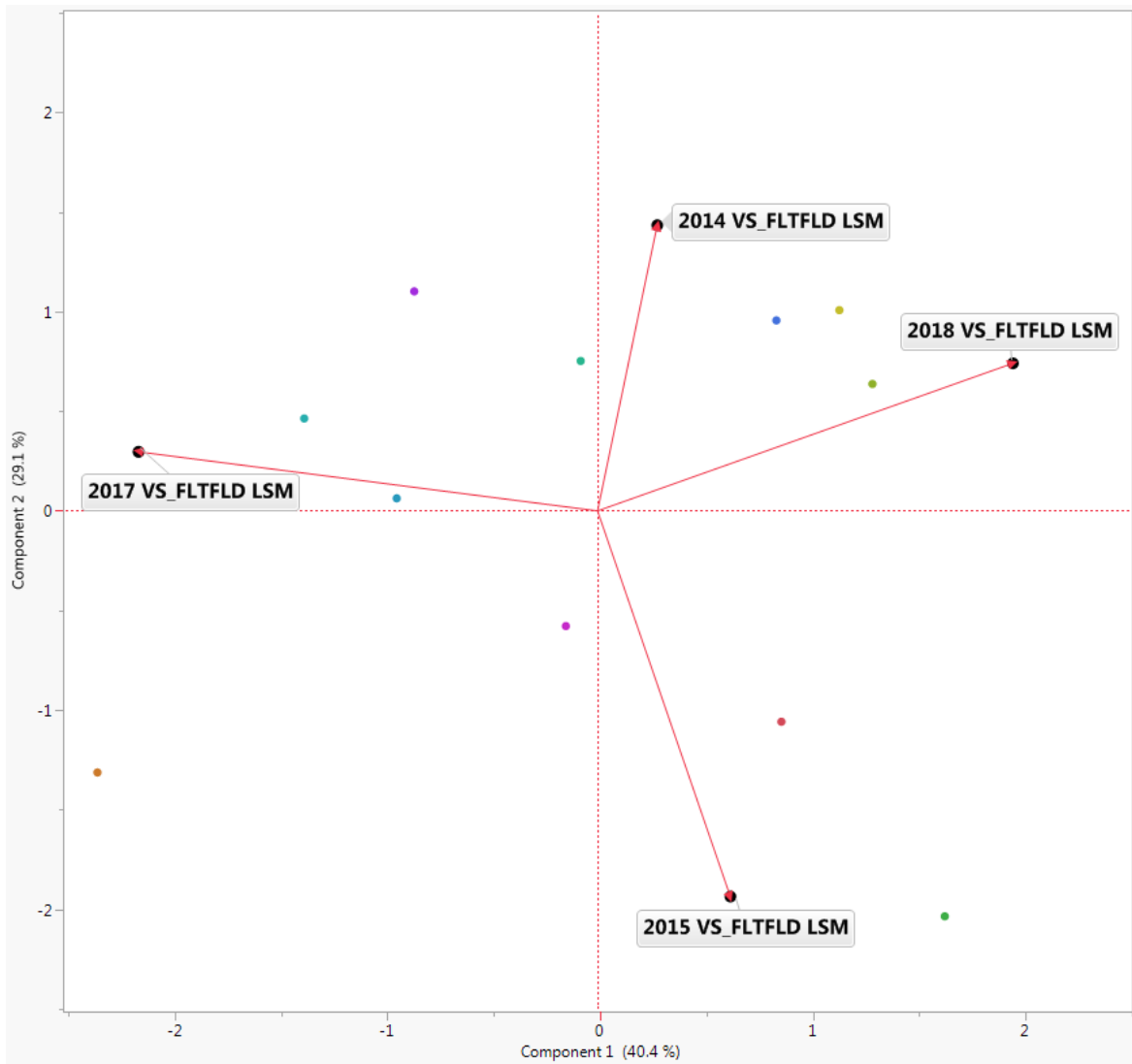
Table 7. Continued

Year	Trait	Source	DF	Sum of Squares	F Ratio	Prob > F
		Error	583	14284.48		
		Total	787	41433.22		
2018	RS_CANCVR	Genotype	129	13333.85	2.33	<.0001**
		Rep	3	7111.28	53.44	<.0001**
		Error	348	15436.82		
		Total	480	35957.01		
2017	RS_CANHLTH	Genotype	201	494.72	3.08	<.0001**
		Rep	3	36.94	15.42	<.0001**
		Error	583	465.47		
		Total	787	993.1		
2018	RS_CANHLTH	Genotype	129	752.35	1.96	<.0001**
		Rep	3	578.17	64.78	<.0001**
		Error	363	1079.88		
		Total	495	2406.22		
2017	RS_GRNHUE	Genotype	201	1281.16	3.19	<.0001**
		Rep	3	42.22	7.03	<.0001**
		Error	583	1166.66		
		Total	787	2483.61		
2018	RS_GRNHUE	Genotype	129	841.93	3.19	<.0001**
		Rep	3	61.53	10.04	<.0001**
		Error	383	782.51		
		Total	515	1685.33		
2017	YIELD (bu/a 60#)	Genotype	201	47055.99	5.79	<.0001**
		Rep	3	503.65	4.15	0.01**
		Error	569	23003.59		
		Total	773	70921.75		
2018	YIELD (bu/a 60#)	Genotype	108	25720.54	2.99	<.0001**
		Rep	3	10065.41	42.11	<.0001**
		Error	239	19040.58		
		Total	350	53011.98		

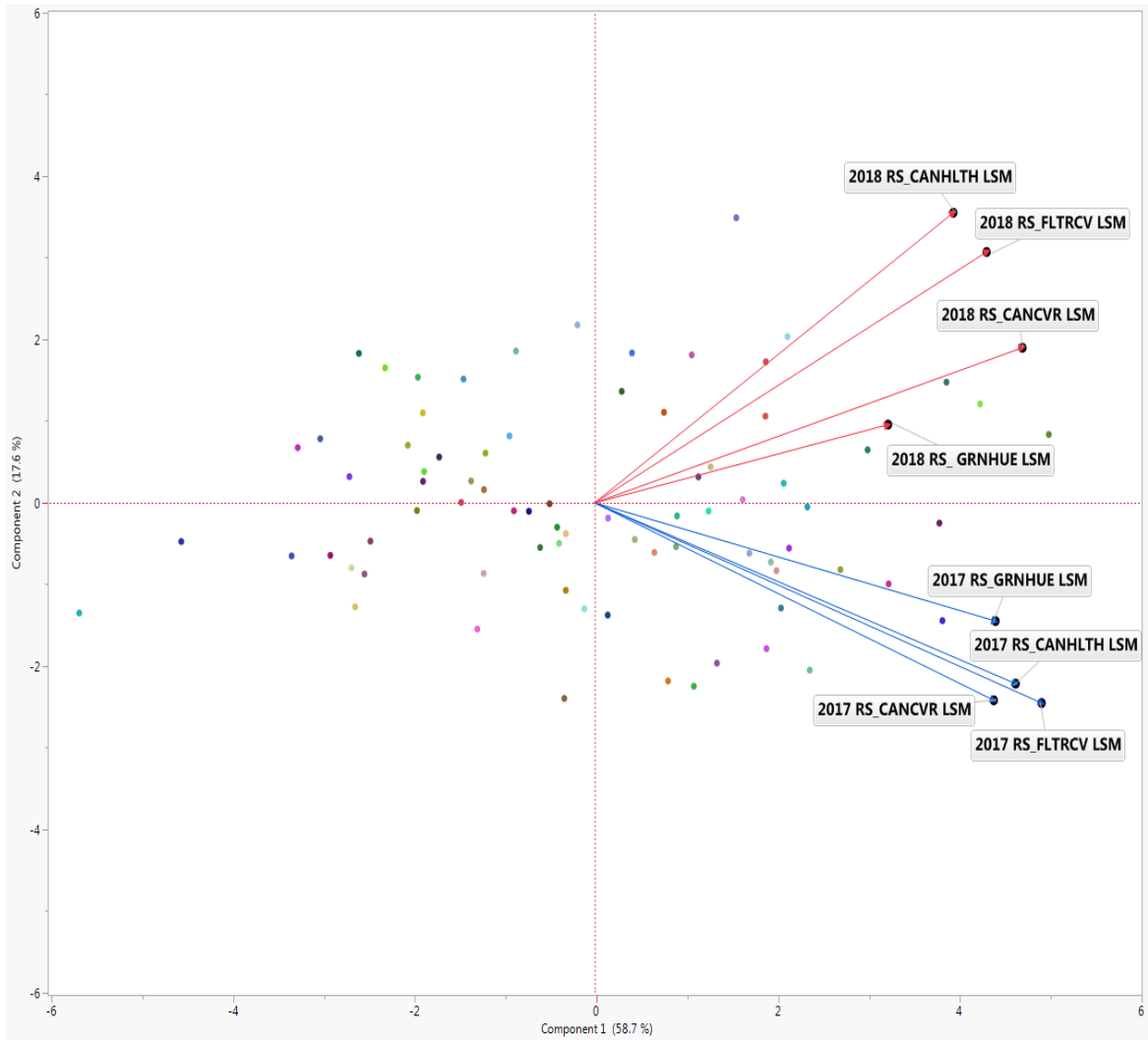
\* Significant at the 0.05 probability level

\*\* Significant at the 0.01 probability level

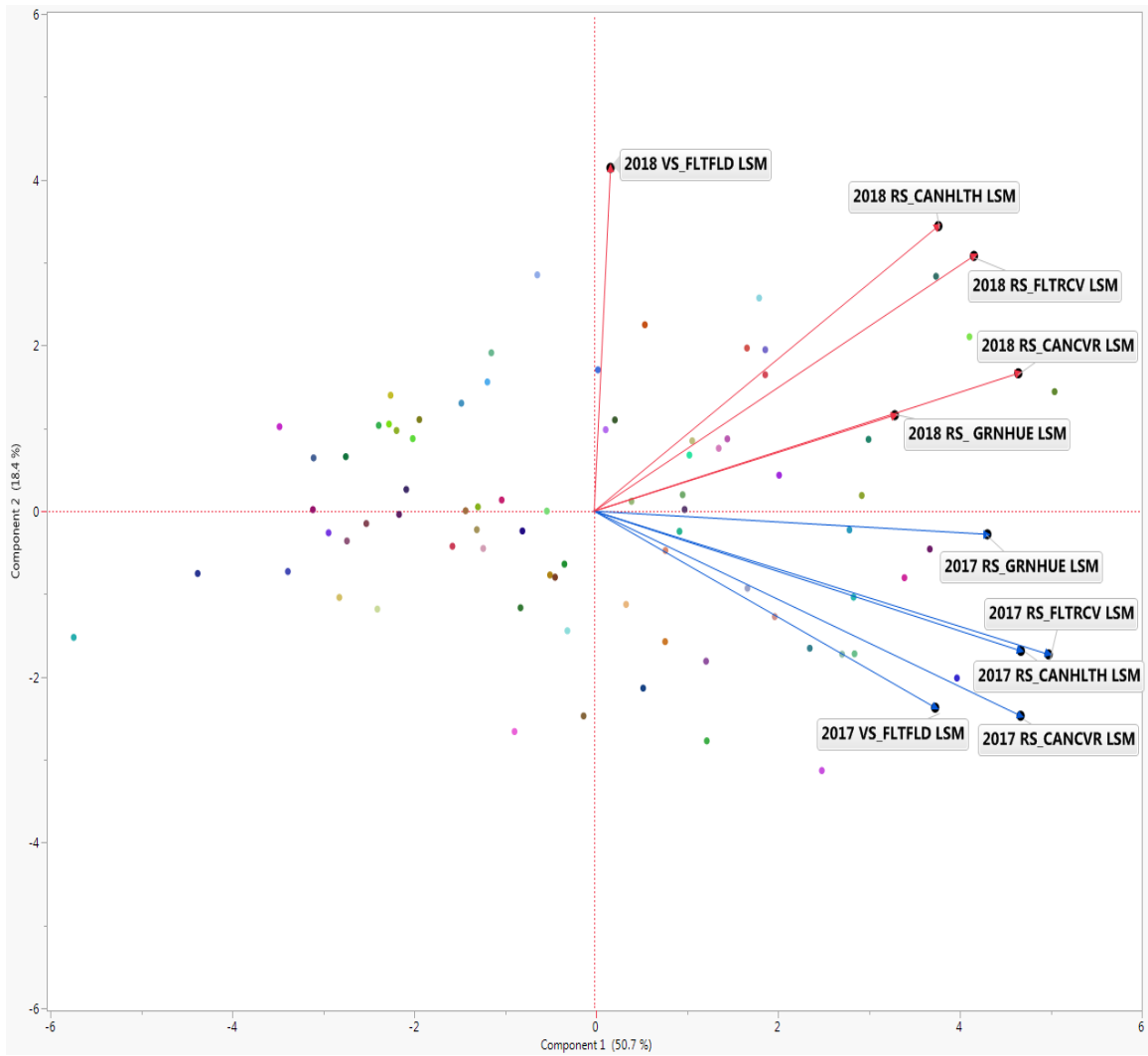
ns Not significant at the 0.05 probability level



**Figure 5. Biplot of the 2014, 2015, 2017, and 2018 visual flood tolerance field (VS\_FLTFLD) least square means using genotypes that repeated across years.**



**Figure 6. Biplot of the 2017 and 2018 remote sensing traits RS\_CANCVR, RS\_CANHLTH, RS\_GRNHUE, and RS\_FLTRCV least square means using genotypes that repeated across both years.**



**Figure 7. Biplot of the 2017 and 2018 VS\_FLTFLD, RS\_FLTRCV, and remote sensing traits least square means using genotypes that repeated across both years.**



Table 8. Trait correlations and probabilities for Yield (bu/a 60#), RS\_CANCVR (pct.), RS\_CANHLTH (pct.), RS\_GRNHUE (pct.), RS\_FLTRCV (score), RS\_FLTFLD (score), and VS\_FLTFLD (score) using 2017-2018 LSMeans by year and growth habit (GH).

Year	GH	Row	YIELD	RS_CAN CVR	RS_CAN HLTH	RS_GRN HUE	RS_FLT RCV	RS_FLT FLD	VS_FLT FLD
2017	DET	YIELD		<.0001	0.0003	<.0001	<.0001	<.0001	<.0001
2017	DET	RS_CANCVR	0.48****		<.0001	<.0001	<.0001	<.0001	<.0001
2017	DET	RS_CANHLTH	0.25***	0.66****		<.0001	<.0001	<.0001	<.0001
2017	DET	RS_GRNHUE	0.43****	0.66****	0.61****		<.0001	<.0001	<.0001
2017	DET	RS_FLTRCV	0.43****	0.85****	0.84****	0.78****		<.0001	<.0001
2017	DET	RS_FLTFLD	0.41****	0.87****	0.57****	0.68****	0.75****		<.0001
2017	DET	VS_FLTFLD	0.35****	0.70****	0.54****	0.67****	0.67****	0.67****	
2017	IND	YIELD		<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
2017	IND	RS_CANCVR	0.57****		<.0001	<.0001	<.0001	<.0001	<.0001
2017	IND	RS_CANHLTH	0.45****	0.53****		<.0001	<.0001	<.0001	<.0001
2017	IND	RS_GRNHUE	0.50****	0.49****	0.59****		<.0001	<.0001	<.0001
2017	IND	RS_FLTRCV	0.58****	0.83****	0.72****	0.70****		<.0001	<.0001
2017	IND	RS_FLTFLD	0.50****	0.84****	0.33****	0.41****	0.66****		<.0001
2017	IND	VS_FLTFLD	0.35****	0.74****	0.20****	0.34****	0.54****	0.76****	
2018	DET	YIELD		<.0001	<.0001	0.8691	<.0001	<.0001	<.0001
2018	DET	RS_CANCVR	0.62****		<.0001	0.7451	<.0001	<.0001	<.0001
2018	DET	RS_CANHLTH	0.64****	0.84****		0.1524	<.0001	<.0001	<.0001
2018	DET	RS_GRNHUE	0.02 <sup>NS</sup>	-0.02 <sup>NS</sup>	-0.11 <sup>NS</sup>		0.6238	0.8632	0.2104
2018	DET	RS_FLTRCV	0.64****	0.87****	0.90****	-0.04 <sup>NS</sup>		<.0001	<.0001
2018	DET	RS_FLTFLD	0.91****	0.62****	0.64****	0.01 <sup>NS</sup>	0.62****		<.0001

Table 8. Continued

Year	GH	Row	YIELD	RS_CAN CVR	RS_CAN HLTH	RS_GRN HUE	RS_FLT RCV	RS_FLT FLD	VS_FLT FLD
2018	DET	VS_FLTFLD	0.89****	0.60****	0.63****	0.09 <sup>NS</sup>	0.61****	0.97****	
2018	IND	YIELD		<.0001	<.0001	0.4392	<.0001	<.0001	<.0001
2018	IND	RS_CANCVR	0.41****		<.0001	0.0068	<.0001	<.0001	<.0001
2018	IND	RS_CANHLTH	0.47****	0.84****		0.0248	<.0001	<.0001	<.0001
2018	IND	RS_GRNHUE	_0.05 <sup>NS</sup>	0.16**	0.13*		0.0133	0.1677	0.7845
2018	IND	RS_FLTRCV	0.44****	0.86****	0.92****	0.14*		<.0001	<.0001
2018	IND	RS_FLTFLD	0.77****	0.50****	0.59****	_0.08 <sup>NS</sup>	0.55****		<.0001
2018	IND	VS_FLTFLD	0.75****	0.45****	0.56****	_0.01 <sup>NS</sup>	0.52****	0.95****	

p < .0001 "\*\*\*\*"; p < .001 "\*\*\*", p < .01 "\*\*", p < .05 "\*", and p > .05 "<sup>NS</sup>"



Table 9. Continued

Source	VS_FLTFLD		RS_FLTFLD		RS_FLTRCV		RS_CANCVR		RS_CANHLTH		RS_GRNHUE	
	$\sigma^2$	SE	$\sigma^2$	SE	$\sigma^2$	SE	$\sigma^2$	SE	$\sigma^2$	SE	$\sigma^2$	SE
2017												
Genotype	0.77	0.16	0.81	0.14	1.45	0.27	21.44	3.30	0.51	0.08	1.42	0.21
Environment	2.13	3.06	1.81	2.60	0.00	0.07	16.84	24.52	0.42	0.61	0.05	0.12
Genotype x Environment	0.08	0.13	0.05	0.11	0.03	0.20	1.33	2.08	0.00	0.06	0.00	0.13
Environment x Rep	0.02	0.02	0.04	0.04	0.03	0.04	0.22	0.29	0.06	0.06	0.15	0.15
Residual (error)	1.47	0.09	1.27	0.08	2.60	0.16	23.75	1.48	0.76	0.05	1.73	0.11
Repeatability	0.66		0.70		0.69		0.76		0.73		0.77	
Repeatability (SE)	0.07		0.06		0.06		0.05		0.05		0.05	
2018												
Genotype	0.63	0.23	0.72	0.20	1.28	0.25	20.21	3.78	0.87	0.21	1.14	0.22
Environment	4.98	7.07	5.38	7.62	0.94	1.58	22.82	35.99	1.21	1.96	0.21	0.33
Genotype x Environment	0.57	0.26	0.28	0.21	0.04	0.18	0.00	2.54	0.11	0.19	0.21	0.14
Environment x Rep	0.00	0.03	0.00	0.03	0.39	0.42	4.27	4.68	0.21	0.24	0.00	0.02
Residual (error)	2.83	0.23	2.55	0.21	2.50	0.20	37.31	3.05	2.57	0.21	1.70	0.14
Repeatability	0.39		0.48		0.66		0.68		0.55		0.68	
Repeatability (SE)	0.10		0.09		0.06		0.05		0.08		0.05	

pct. - percentage,  $\sigma^2$  – variance, SE – standard error, Environment represents the blocking factor for above and below the levee separating replications 1&2 from 3&4.

Table 10. 2017-2018 estimates of variance components, standard error (SE), and broad sense heritability ( $H^2$ ) for the traits; VS\_FLTFLD (score), RS\_FLTFLD (score), RS\_FLTRCV (score), RS\_CANCVR (pct.), RS\_CANHLTH (pct.), RS\_GRNHUE (pct.).

Source	VS_FLTFLD		RS_FLTFLD		RS_FLTRCV		RS_CANCVR		RS_CANHLTH		RS_GRNHUE	
	$\sigma^2$	SE	$\sigma^2$	SE	$\sigma^2$	SE	$\sigma^2$	SE	$\sigma^2$	SE	$\sigma^2$	SE
2017												
Additive	0.86	0.19	0.68	0.15	0.53	0.17	16.70	3.40	0.16	0.05	0.43	0.13
Dominance	1.87	0.89	1.31	0.71	3.36	1.31	24.02	13.46	0.28	0.22	3.03	1.09
Residual (error)	1.77	0.10	1.71	0.10	2.90	0.17	29.01	1.68	0.90	0.05	2.16	0.12
$H^2$	0.61		0.54		0.57		0.58		0.33		0.62	
$H^2$ (SE)	0.08		0.09		0.08		0.08		0.11		0.08	
2018												
Additive	0.28	0.16	0.26	0.15	0.71	0.21	13.66	3.77	0.45	0.17	0.45	0.16
Dominance	0.00	0.10	0.00	0.09	0.00	0.15	0.95	3.92	0.00	0.11	2.37	1.28
Residual (error)	6.14	0.41	5.85	0.39	3.71	0.25	55.22	3.77	3.83	0.26	2.25	0.16
$H^2$	0.04		0.04		0.16		0.21		0.11		0.56	
$H^2$ (SE)	0.03		0.03		0.05		0.06		0.04		0.11	

pct. - percentage,  $\sigma^2$  – variance, SE – standard error.

CHAPTER IV  
ACCURACY OF WHOLE GENOME PREDICTION FOR WATERLOGGING  
TOLERANCE IN SOYBEAN

**Introduction**

Soybean is an economically important crop around the world and is cultivated in many diverse environments; some of these environments are impacted by flooded conditions causing excess soil moisture in the roots and shoots of the soybean plant. This is termed waterlogging (Reyna et al., 2003) and later designated “partial waterlogging or soil flooding” at the 15th New Phytologist Workshop on Flooding Stress (Sasidharan et al., 2017). Soybean is severely distressed by flooding causing stunted growth, chlorosis of leaves, and even plant death. All these symptoms result in significant reductions in yield, with the greatest yield loss occurring during the reproductive phase of soybean.

Previously, breeders have identified numerous QTL conditioning increased flood tolerance using traditional RIL or NIL populations with the thought of pyramiding these QTL, thus significantly improving waterlogging tolerance in elite soybean cultivars (VanToai et al., 2001; Reyna et al., 2003; Cornelious et al., 2005; Githiri et al., 2006; Sayama et al., 2009; Nguyen et al., 2017; Ye et al., 2018). However, flood tolerance in soybean appears to be somewhat complex in its genetic architecture, a quantitative trait controlled by many genes, each accounting for a small percentage of the total genetic variance. This is further confounded by environmental conditions making significant

QTL, identified in specific populations, difficult to translate across various collections of germplasm, limiting the functionality these QTL have in a breeding program.

Several different quantitative traits, like waterlogging tolerance, utilized whole-genome predictions (WGP) and genomic selections (GS) have increased genetic gain for complex traits (Crossa et al., 2010; Heffner et al., 2001; Bao et al., 2015; Jarquin et al., 2016; Zhang et al., 2016). Genomic selection is a form of genetic marker based selection that exploits dense marker coverage across the genome, providing increased explanation of genetic variance, which has often been a limitation of marker assisted selection (MAS), and presents an improved method of selection. GS takes advantage of linkage disequilibrium (LD) among markers and quantitative trait loci (QTL) affecting traits of interests when computing estimates of genetic effects (Meuwissen et al., 2001). These effects, no matter how small, are calculated using a reference or training population containing both genomic and phenotypic data. This data is then entered in a model producing genomic predictions or genomic estimated breeding values (GEBV) for the trait of interest for each genotype within a validation or prediction population containing only genotypic information for each genotype (Meuwissen et al., 2001).

As next-generation sequencing technology progresses, the cost and speed of genotyping continues to experience momentous changes allowing high-density genotypic data to be readily available to researchers. Utilizing increased marker numbers was confirmed to bolster prediction accuracies in genotypes from validation populations that are unrelated to the training population (Hickey et al., 2014). This is because increased marker density results in greater LD between markers and causative QTL.

In North America, genetic diversity of soybean originates from a narrow germplasm base established from a small set of highly related individuals (Thompson and Nelson, 1998; Carter et al., 2004; Mikel et al., 2010). This, along with soybean's use of self-pollination as a means of reproduction, creates negligible amounts of outcrossing limiting recombination; which in turn naturally maintains higher levels of LD when compared to other crops like maize and rice, or close relatives like *G. soja* (Flint-Garcia et al., 2003; Bao et al., 2014). While high levels of LD should allow for complete genome coverage with few markers, Hyten et al. (2007) noted that there were variable patterns in specific chromosomal regions, requiring a larger number of markers than anticipated to conduct a whole-genome association analysis in soybean.

Waterlogging tolerance in soybean presents an opportunity for GS and increased genetic gain when evaluating factors such as trait complexity, environmental interactions, and number of reported QTL. The rationale of this study was to evaluate marker-based prediction accuracy and determine if genomic selection is effective in selecting waterlogged tolerant varieties in a breeding program focused on indeterminate maturity group IV genotypes. Marker effects were estimated for the soybean lines tested in the 2017 and 2018 flood screening experiments, and a tenfold cross-validation scheme was used to assess the prediction accuracy of the flood tolerant traits within each individual year. The 2017 dataset was then used as a training population to estimate marker effects for the 2018 genotypes (validation population) using BayesA and BayesB (Meuwissen et al., 2001) whole-genome regression methods for each of the flood



tolerant traits, determining which trait performed best when using datasets across years for implementation in a breeding program.

## **Materials and Methods**

### Plant Material

One-hundred and seventy-five different soybean genotypes representing maturity group (MG) IV were characterized for waterlogging tolerance in response to flooded field experiments in 2017 and 2018. One-hundred and twelve genotypes were characterized in 2017 and sixty-seven genotypes in 2018 with forty-three genotypes repeating both years. These genotypes were selected from various Corteva breeding programs across the Midwest, Midsouth, and Delta regions of the U.S. and represent entries from wide-area yield trials of elite soybean cultivars at various cycles of development. GS selected genotypes were all indeterminate growth habit (GH) and confirmed using a proprietary Corteva single nucleotide polymorphism (SNP) associated with growth habit in soybean. This was done to minimize maturity QTL that could influence flood tolerance predictions. During the flood tolerance screening, genotypes were added and dropped each year with selected genotypes repeating over multiple years based on advancement and discard decisions.

## Field Management and Data Collection

The 2-year field evaluations for soybean waterlogging tolerance were conducted at the Corteva Agriscience Research Station in Proctor, Arkansas (34.146°N, -90.321°W) on Sharkey silt clay (very-fine, smectitic, thermic Chromic Epiaquerts). These soils “consist of very deep poorly and very poorly drained, very slowly permeable soil that formed in the clayey alluvium” (<https://websoilsurvey.sc.egov.usda.gov/>, accessed 01/21/2019). Each flood treatment location contained experiments grown as randomized complete block design (RCBD) with 4 replications in 2017-2018. Plots were 7ft (2.13m) long single row and spaced 36 inches (0.91m) apart. The planting rate was 50 seeds per plot, or 7.14 seeds ft<sup>2</sup> not including alley spacing. The planting dates for the experimental locations were May 18, 2017; and May 14, 2018, respectively. A series of levees were constructed to separate different maturities with spill gates to accommodate timely flooding at the R1 growth stage. Water levels targeting 5-10cm above the soil were used during flooding, ensuring soil remained saturated during treatment (Ye et al., 2018). All plots were surrounded to prevent un-bordered edge effects from occurring. Once most of the plants reached R1 growth stage (beginning bloom), one open flower on any node on the main stem (Fehr et al., 1971), flood treatment was initiated. This level was maintained for a period of 9-12 days until flood stress symptomology began to develop (Wu et al., 2017). After flood treatment, plots were watered using furrow irrigation as needed.

A digital image was captured for each plot employing the unmanned aerial vehicle (UAV) or drone discussed in chapter three. Individual plot clips were produced

via ArcMap (Esri's ArcGIS suite of geospatial processing programs) allowing each plot to be analyzed independently. Digital red-green-blue (RGB) imagery was analyzed via proprietary Corteva script producing three separate remote sensing (RS) traits using RGB vegetation indices (VIs): Canopy Cover (RS\_CANCVR), Canopy Health (RS\_CANHLTH), and Green Hue (RS\_GRNHUE).

A single-time-point and a multi-time-point measurement, using an index of the three RS traits, was developed creating a remote sensing flood tolerance field (RS\_FLTFLD) and remote sensing flood tolerance recovery (RS\_FLTRCV) score respectively (Aguate et al., 2017), with the null hypothesis being that multi-time-point measurements will not perform as well as or better than single-time-point measurements. The scores for RS\_FLTFLD and RS\_FLTRCV were identical in scale to the visual score VS\_FLTFLD.

Again, plot maintenance was a critical component for enabling the drone to capture the highest quality images. Weeds within a plot are the number one reason for erroneous data and plots should be weed free prior to any flights. There were sixteen different flights in 2017, with the first flight commencing on June 21st (pre-flood treatment), eight separate flights during flooding treatment occurring June 26th - July 7th, and seven post flood treatment flights transpiring July 10th - 24th. In 2018, a total of ten flights were logged with the initial flight transpiring on June 29th (pre-flood treatment), four subsequent flights during flooding treatment occurring July 2nd - 12th, and five succeeding flood treatment flights transpiring July 17th - August 2nd.

## Genotypic Data Collection

All Corteva Agriscience lines grown in 2017-2018 were genotyped using DNA analysis. Each genotype was screened with genome-wide single-nucleotide polymorphism (SNP) markers proprietary to Corteva Agriscience. Genetic and physical positions of the proprietary SNP markers on the *Glycine max* Consensus 4.0 genetic map (Hyten et al., 2010) were estimated based on the Illumina Infinium BeadChip containing over 50,000 SNP markers published by Song et al. (2013). Marker density varied year to year with 2,012 and 5,581 markers for the years 2017 and 2018 respectively (Table 4, page 112). SNP markers used in this study are listed in Appendix A (page 112). This variation in marker numbers year to year was due to the addition and subtraction of genotypes in the waterlogging tolerance screening. Additionally, markers were excluded that had missing data among genotypes greater than 25% after imputation and when minor allele frequency was less than 5%. Numerical imputation was done via TASSEL (Trait Analysis by aSSociation, Evolution and Linkage) using k-nearest-neighbors with a default value of  $k = 5$  and distance type Euclidean. This imputation method compares missing genotypic data to that of other neighbors that are similar and uses an average of the neighbors to fill in the missing SNP data. This serves to provide a marker matrix with no missing data. The TASSEL software can be found at: <http://sourceforge.net/projects/tassel> (Bradbury et al., 2007).

## Genomic Prediction and Validation

To assess accuracy of genomic selection for each trait the LSMeans data for RS\_FLTFLD, RS\_FLTRCV, RS\_CANCVR, RS\_CANHLTH, and RS\_GRNHUE from the experiments grown in 2017 and 2018 were used as the phenotypic dataset for each year's training population. Marker effects were estimated using the entire MG4 indeterminate genotypic set within each year. A tenfold cross-validation study was conducted. For each round of validation, a random group of individuals were selected from the reference population (training set) consisting of approximately ten percent of the lines, creating a prediction population or testing set. This analysis was conducted using the R-package (R Development Core Team, 2018) Bayesian Linear Regression (BLR) (de los Campos and Perez, 2018), using the Bayesian LASSO (BL) method of Park and Casella (2008), with 6,000 iterations and the first 1,000 being discarded as burn in. The prior distribution of BL is a double exponential or Laplace prior with higher mass densities at zero and thicker tails than normal distribution, inducing a shrinkage of estimates dependent on the size of the effect (Gianola, 2013). Prediction accuracy was calculated as the pooled-correlations between the marker-base predictions and the observed phenotypes.

To evaluate model differences the 2017 dataset was used as a training population to estimate marker effects for the 2018 genotypes (validation population) using BayesA and BayesB (Meuwissen et al., 2001) whole-genome regression methods for each of the flood tolerant traits determining which trait performed best when using data sets across years. Whole-genome regression performance of BayesA and BayesB was evaluated

using estimates of the log-likelihood evaluated at the posterior mean of model unknowns ( $\bar{l}(\theta)$ ), the posterior mean of the log-likelihood ( $\bar{l}(\cdot)$ ), the estimated effective number of parameters (pD), and Deviance Information Criterion (DIC) measuring goodness of fit and model complexity conducted (Spiegelhalter et al., 2002; Perez et al., 2010). This analysis was conducted using the R-package (R Development Core Team, 2018) BGLR (Bayesian Generalized Linear Regression) (de los Campos and Perez, 2018). Parameters were set by inputting  $R^2$  values representing the calculated broad sense heritability for each of the flood traits in 2017. The BayesB “probIn” parameter was set to 0.1 and represents the prior probability of a marker having a non-null effect. Each method was run for 12,000 iterations with the first 2,000 being discarded as burn in.

## **Results and Discussion**

Using the BL model in the cross-validation analysis, the average prediction accuracy of the remote sensing traits characterizing flood tolerance was positive for both 2017 and 2018. For 2017, superior prediction accuracies resulted, with a mean accuracy of 0.57 for all remote sensing traits, compared to 0.27 for 2018 flood screening. The highest performing trait within 2017 was FLTRCV followed by RS\_CANHLTH, RS\_GRNHUE, RS\_CANCVR, and finally RS\_FLTFLD with prediction accuracies of 0.68, 0.64, 0.60, 0.50, and 0.36 respectively (Table 11, page 89). Prediction accuracies exhibited a significant decrease the following year and were 0.38, 0.27, 0.26, 0.25 and 0.20 for RS\_CANHLTH, RS\_FLTFLD, RS\_FLTRCV, RS\_GRNHUE, and RS\_CANCVR respectively (Table 12, page 90). Biplots using the pooled whole genome

predictions demonstrates that 2017's principle components 1 and 2 explains a greater percentage of the variation when compared to 2018's principle components 1 and 2, with 95.5% and 84.9% respectively (Figures 8 and 9, pages 87 and 88). This again illustrates the environmental influences seen in 2018 resulting in increased severity of waterlogging symptoms across all genotypes and rating fluctuations experienced by genotypes year to year during flood treatment. Model error variance for RS\_FLTFLD and RS\_FLTRCV was 0.47 and 0.48 respectively showing very little difference in 2017 (Table 11, page 89). However, these values differed dramatically in 2018, with RS\_FLTFLD and RS\_FLTRCV error variances of 0.45 and 1.08 respectively (Table 14, page 90). While the GxE effects in this research are hypothesized to be the primary influence in prediction correlations between 2017 and 2018, another possible influence could be differences in population sizes between years. It has been documented in other studies that reductions in training populations can negatively impact predictions (Heffner et al., 2011; Zhang et al., 2017). While the number of genotypes does differ between years, the same proportion, ninety percent, was utilized in each year's cross-validation analysis and included the forty-three genotypes tested in 2017 and 2018. Additionally, marker density in 2018 was nearly twice that of 2017, leading this author to believe that environmental effects and training set numbers play a larger role than marker density. This would suggest that an increase in number of genotypes and not marker density has the larger influence on prediction accuracy, additional study is needed to further optimize prediction accuracy year to year.

Prediction accuracy across years using two different methods was evaluated with the R-package (R Development Core Team, 2018) Bayesian Generalized Linear Regression (BGLR) (de los Campos and Perez, 2018) via the BayesA and BayesB methods of Meuwissen et al. (2001). The 2017 data was used as the training population, while the 2018 dataset was the validation population. Genotypes that were subjected to the waterlogged screening in both 2017 and 2018 were removed to avoid arbitrarily inflating prediction correlations. Neither of the two genomic models, BayesA or BayesB, exhibited significant discrepancies in predictions, even though each model estimates marker effects distinctly. Correlations of the BayesA and BayesB for each of the traits RS\_FLTFLD, RS\_FLTRCV, RS\_CANCVR, RS\_CANHLTH, and RS\_GRNHUE were 0.98 or higher. These results correspond with previous research, which revealed only minor differences in predictions using Bayesian models (Lorenzana and Bernardo, 2009; Zhong et al., 2009; Heffner et al., 2011). Model comparisons using estimates of the log-likelihood evaluated at the posterior mean of model unknowns ( $\bar{l}(\theta)$ ), the posterior mean of the log-likelihood ( $\bar{l}(\cdot)$ ), the estimated effective number of parameters (pD), and Deviance Information Criterion (DIC) measuring goodness of fit and model complexity (Spiegelhalter et al., 2002) show very little difference between the BayesA and BayesB (Table 13, page 91) (Perez et al., 2010). The remote sensing trait with the highest accuracy was RS\_FLTRCV with a correlation of 0.49 and 0.47, while the RS\_FLTFLD trait correlation was 0.16 and 0.21 for BayesA and BayesB respectively (Table 13, page 91). The three-other remote sensing flood traits, RS\_CANCVR, RS\_CANHLTH, and

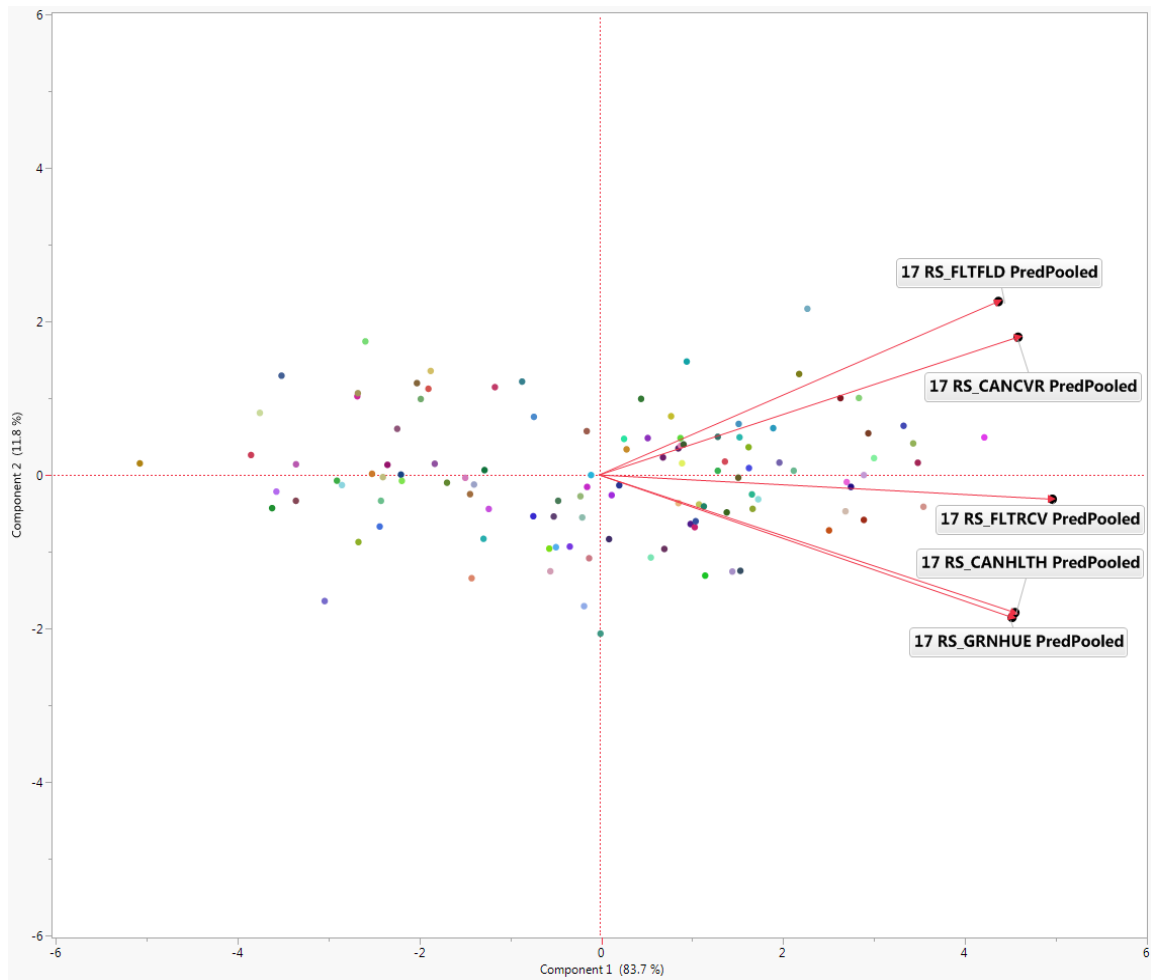


RS\_GRNHUE correlated 0.28, 0.46, and 0.21 for BayesA and 0.28, 0.49, 0.21 for BayesB respectively (Table 13, page 91, Figures 10 and 11, pages 92 and 93).

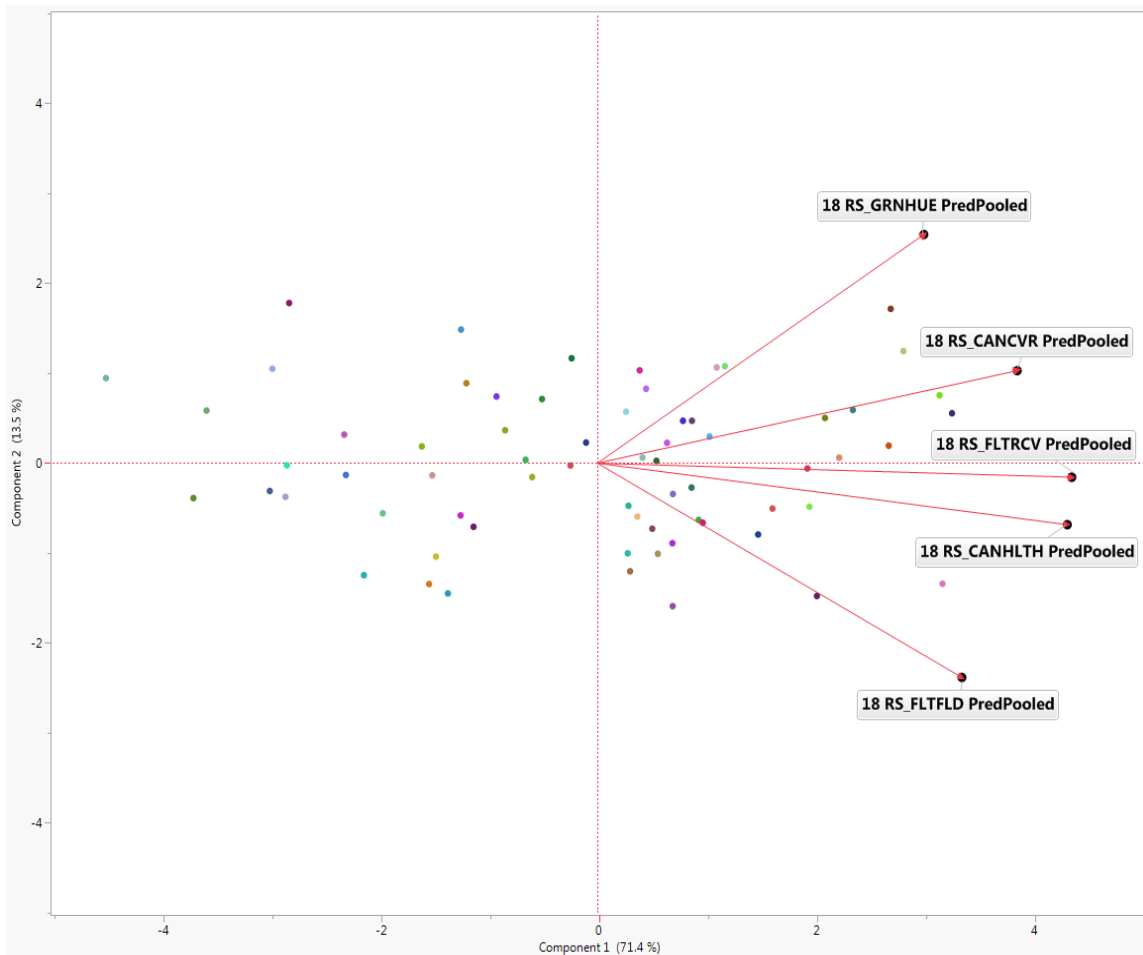
Breeders are not able to anticipate which year's testing will be the most predictive on a year by year basis and which will optimize future prediction accuracy in successive cycles. Therefore, multi-year training populations offer advantages over single-year training populations (Auinger et al., 2016; Bernal-Vasquez et al., 2017). Incorporating multiple cycles from a breeding program has many benefits: allowing for separation of the genotype-by-year effects, significantly increasing the size of the training population providing greater prediction accuracy, and improving kinship connecting related genotypes across years (Auinger et al., 2016; Bernal-Vasquez et al., 2017). Applying multiple years' worth of data into a training set mitigates the risk of poor phenotypic data from a single year driving erroneous predictions due to environmental factors like disease or weather.

Genomic selection via predictions can be a valuable tool for making flood tolerant selections in soybeans even when genotypes experience environmental influences. Despite the lower prediction accuracies for waterlogging tolerance in 2018, genetic gain was possible using genomic selection which outperform phenotypic selection by facilitating additional rounds of selection in earlier generations. GS also serves to enable selection on a greater number of genotypes without increased resources necessary for field plots; these resources could in turn be used to intensify genotyping across a wider array of germplasm, furthering genetic gain.

These results of this research suggest that genomic selection is a valuable tool for improving waterlogging tolerance in soybeans. The type of models used to produce whole-genome predictions mattered very little in this study, while other factors such as training population size and marker density play a larger role in prediction accuracy. Additional study of training population construction with regards to number of genotypes and kinship will help to enhance these approaches in a breeding program. Furthermore, as additional years of data become available, follow-up studies will be required to evaluate training populations encompassing multiple cycles.



**Figure 8. Biplot using the pooled whole genome predictions of the 2017 traits RS\_CANCVR, RS\_CANHLTH, RS\_GRNHUE, RS\_FLTRCV, and RS\_FLTFLD. Components 1 and 2 are explaining 83.7% and 11.8% of the variation respectively.**



**Figure 9. Biplot using the pooled whole genome predictions of the 2018 traits RS\_CANCVR, RS\_CANHLTH, RS\_GRNHUE, RS\_FLTRCV, and RS\_FLTFLD. Components 1 and 2 are explaining 71.4% and 13.5% of the variation respectively.**

Table 11. Prediction accuracy, using the pooled-correlations between the marker-base predictions and the observed phenotypes, with individual k-fold correlations, and model error variance from the 2017 cross-validation analysis using R-Package BLR and the method Bayesian LASSO for the traits: RS\_CANCVR, RS\_CANHLTH, RS\_GRNHUE, RS\_FLTRCV, and RS\_FLTFLD.

	RS_CANC VR	RS_CANHL TH	RS_GRNH UE	RS_FLTR CV	RS_FLTF LD
Pooled Correlations	<b>0.55</b>	<b>0.64</b>	<b>0.60</b>	<b>0.68</b>	<b>0.36</b>
Fold=1	0.20	0.69	0.75	0.51	0.02
Fold=2	0.73	0.56	0.46	0.73	0.56
Fold=3	0.64	0.85	0.79	0.84	0.53
Fold=4	<b>0.84</b>	0.59	<b>0.26</b>	<b>0.87</b>	<b>0.72</b>
Fold=5	0.42	0.54	0.68	0.60	0.25
Fold=6	<b>0.14</b>	<b>0.32</b>	0.33	<b>0.20</b>	<b>-0.21</b>
Fold=7	0.61	<b>0.79</b>	0.71	0.86	0.43
Fold=8	0.69	0.67	<b>0.85</b>	0.78	0.55
Fold=9	0.75	0.77	0.64	0.82	0.57
Fold=10	0.52	0.60	0.51	0.62	0.20
$Var_{\varepsilon}$	1.25	0.32	0.61	0.48	0.47

Maximum and minimum fold correlations are in bold italics

$Var_{\varepsilon}$  = model error variance

Table 12. Prediction accuracy, using the pooled-correlations between the marker-base predictions and the observed phenotypes, with individual k-fold correlations, and model error variance from the 2018 cross-validation analysis using R-Package BLR and the method Bayesian LASSO for the traits: RS\_CANCVR, RS\_CANHLTH, RS\_GRNHUE, RS\_FLTRCV, and RS\_FLTFLD.

	RS_CANC VR	RS_CANHL TH	RS_GRNH UE	RS_FLTR CV	RS_FLTF LD
Pooled Correlation	<b>0.20</b>	<b>0.38</b>	<b>0.25</b>	<b>0.26</b>	<b>0.27</b>
Fold=1	0.45	0.69	0.39	-0.03	-0.26
Fold=2	0.09	0.50	<b>0.83</b>	0.24	0.60
Fold=3	0.22	0.48	0.37	0.09	0.52
Fold=4	<b>-0.27</b>	-0.12	0.23	<b>-0.25</b>	<b>0.80</b>
Fold=5	0.39	0.21	-0.07	0.45	-0.19
Fold=6	0.31	<b>0.94</b>	<b>-0.24</b>	0.78	0.78
Fold=7	-0.36	-0.13	0.42	-0.22	<b>-0.30</b>
Fold=8	<b>0.61</b>	0.89	0.19	<b>0.87</b>	-0.01
Fold=9	0.31	0.57	0.51	0.55	0.59
Fold=10	0.28	<b>-0.19</b>	-0.08	0.09	0.19
$Var_{\varepsilon}$	9.81	0.74	0.82	1.08	0.45

Maximum and minimum fold correlations are in bold italics

$Var_{\varepsilon}$  = model error variance

Table 13. Prediction accuracy across years, using the correlations between the marker-base predictions and the observed phenotypes, with log-likelihood evaluated at the posterior mean of model unknowns, posterior mean of the log-likelihood, effective number of estimated parameters, deviance information criterion, and model error variance from the 2017-2018 multi-year analysis using R-Package BGLR and the methods BayesA and BayesB for the traits: RS\_CANCVR, RS\_CANHLTH, RS\_GRNHUE, RS\_FLTRCV, and RS\_FLTFLD.

	RS_CA NCVR BayesA	RS_CA NCVR BayesB	RS_CAN HLTH BayesA	RS_CAN HLTH BayesB	RS_GR NHUE BayesA	RS_GR NHUE BayesB	RS_FL TRCV BayesA	RS_FL TRCV BayesB	RS_FL TFLD BayesA	RS_FL TFLD BayesB
Pearson Correlations	<b>0.28</b>	<b>0.28</b>	<b>0.46</b>	<b>0.49</b>	<b>0.21</b>	<b>0.21</b>	<b>0.49</b>	<b>0.47</b>	<b>0.16</b>	<b>0.21</b>
$l(\bar{\theta})^\dagger$	-237.0	-237.2	-66.9	-69.3	-115.0	-117.5	-110.2	-111.1	-96.3	-98.7
$\bar{l}(\cdot)$	-251.2	-250.5	-77.2	-79.5	-124.6	-126.6	-123.1	-125.1	-110.3	-111.4
(pD)	28.4	26.6	20.5	20.4	19.1	18.2	25.9	26.3	27.2	25.4
DIC	530.8	527.6	174.8	179.4	268.2	271.5	271.1	275.4	247.7	248.3
$Var_\varepsilon$	14.17	13.86	0.32	0.33	0.88	0.91	0.87	0.90	0.65	0.67

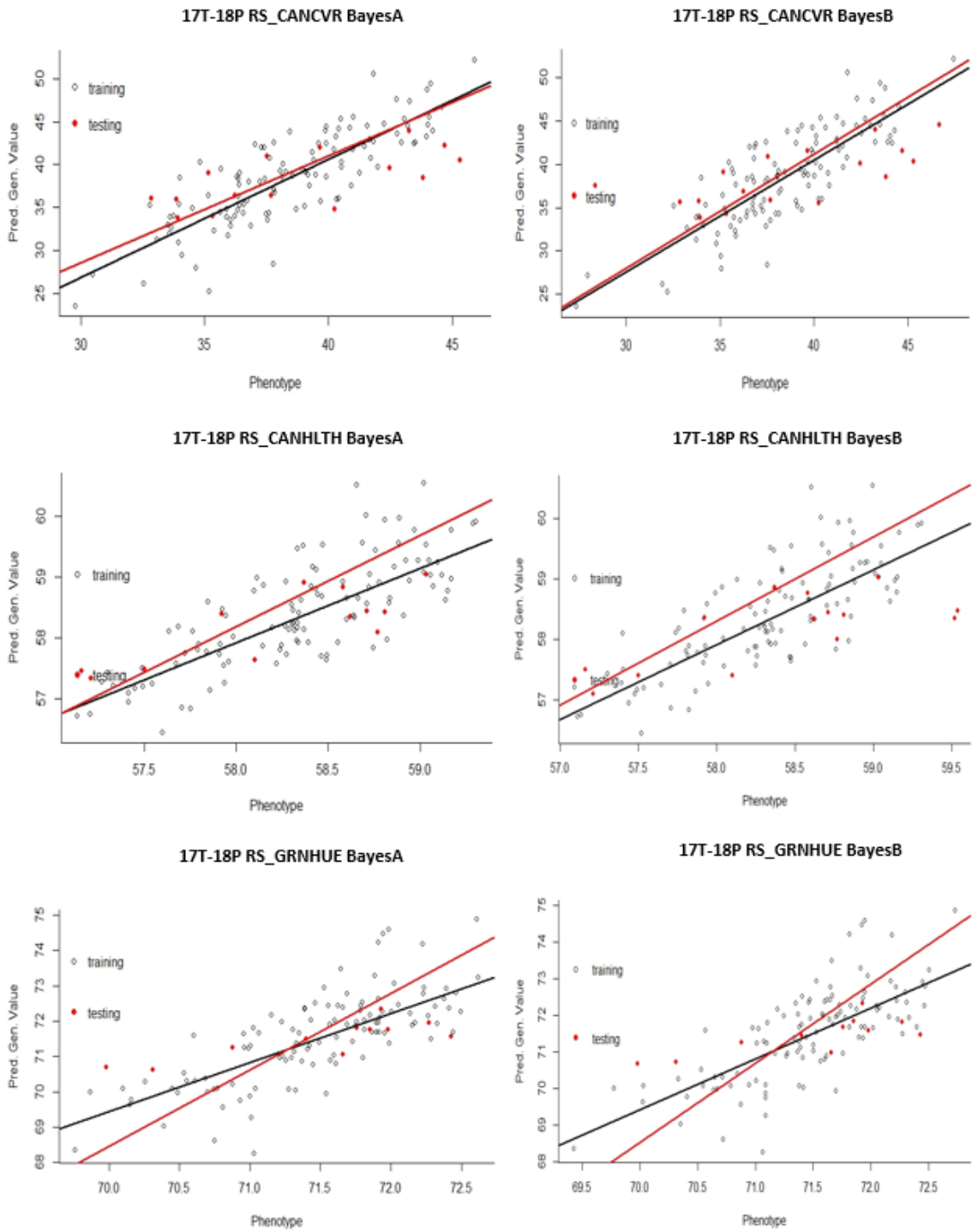
$l(\bar{\theta})^\dagger$  = likelihood evaluated at the posterior mean of model unknowns - less negative log-likelihood specifies better fit of data.

$\bar{l}(\cdot)$  = posterior mean of the log-likelihood - a less negative log-likelihood specifies better fit of data.

(pD) = estimated effective number of parameters (pD) - higher values will decrease the deviance.

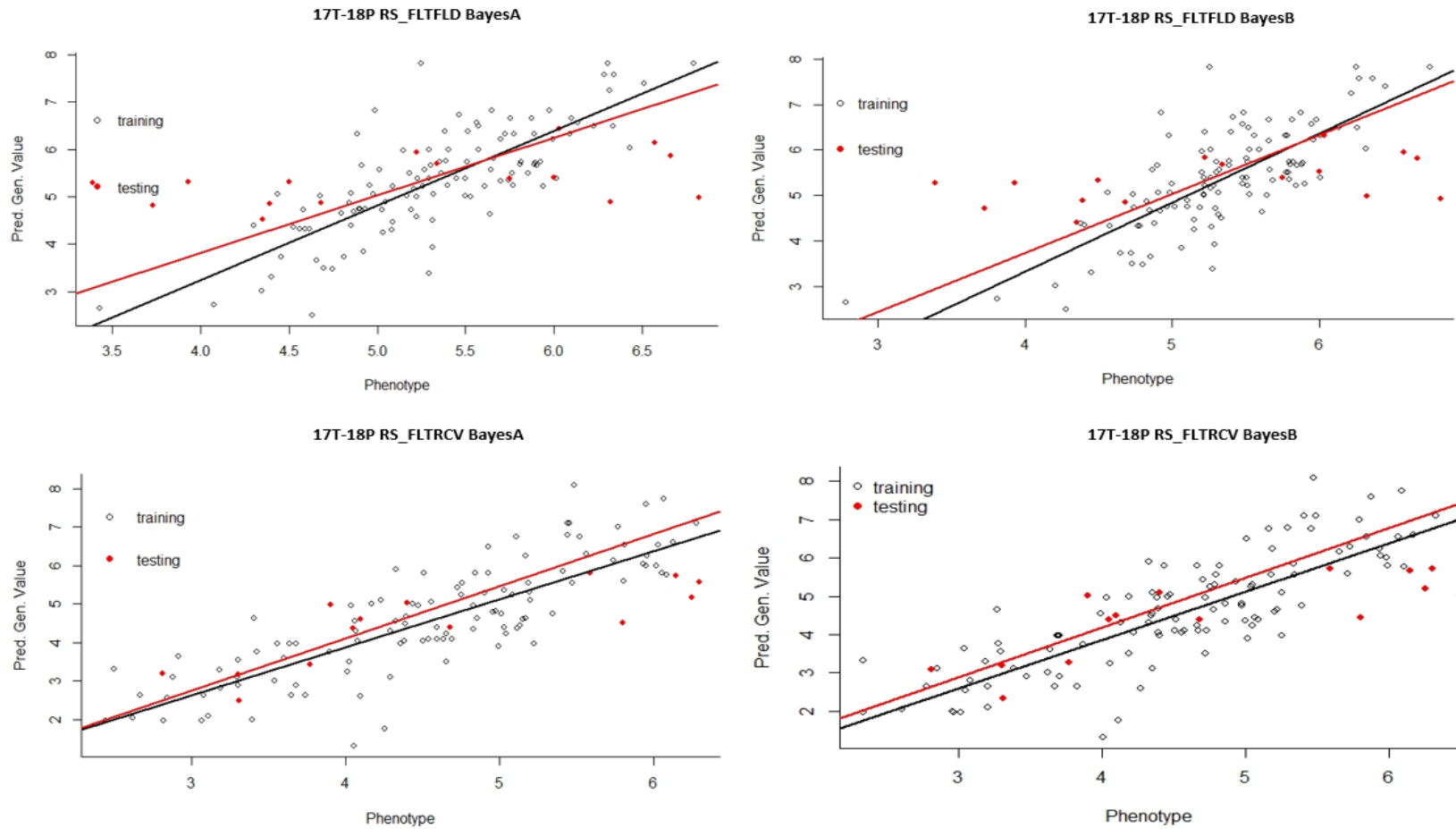
DIC = Deviance Information Criterion - lower DIC indicates a balance between goodness of fit and complexity like Akaike information criterion (AIC)

$Var_\varepsilon$  = model error variance.



**Figure 10. Estimated genetic values for the traits: RS\_CANCVR, RS\_CANHLTH, and RS\_GRNHUE utilizing the 2017 training and 2018 testing sets in the R-Package BGLR (Bayesian Generalized Linear Regression) for models BayesA and BayesB.**





**Figure 11. Estimated genetic values for the traits: RS\_FLTFLD and RS\_FLTRCV utilizing the 2017 training and 2018 testing sets in the R-Package BGLR (Bayesian Generalized Linear Regression) for models BayesA and BayesB.**

## CHAPTER V

### CONCLUSIONS

The objectives of this research were to: (1) investigate the flood screening process and contrast the traditional phenotyping using visual scores to those gathered using the UAS RGB digital imagery remote sensing traits. Analyze the various traits for successfully characterizing flood tolerance in a field setting while sustaining or even increasing accuracy. Compare the single-time-point score, RS\_FLTFLD, to the multi-time-point score, RS\_FLTRCV, and determine if using a multi-time-point score provides improved characterization of waterlogging tolerance in soybean flooded field conditions; (2) apply genomic selection techniques using whole-genome predictions for the remote sensing traits, RS\_FLTFLD, RS\_FLTRCV, RS\_CANCVR, RS\_CANHLTH, and RS\_GRNHUE, estimating each year of the 2017-2018 flood tolerance dataset using cross-validation measuring precision of the training population and testing population for each year independently. Then corroborate across year estimates using the 2017 dataset (training set) to generate predictions for the 2018 dataset (testing set) comparing two different Bayesian approaches, BayesA and BayesB, and then associate GEBV predictions to the observed flood tolerance traits.

Results from this study revealed varying degrees of response to the flooded field conditions, with the formation of aerenchyma and adventitious roots promptly observed in tolerant varieties in contrast to their susceptible counterparts. The years 2014, 2015, and 2017 had similar statistics, while 2018 deviated from the three previous years

demonstrating elevated measurements. This differentiation in 2018 was attributed to environmental factors: increase in temperatures and lack of precipitation, intensifying symptoms from waterlogging conditions. Additionally, several plots were suppressed that exhibited premature death prior to and during early flood treatment; this was attributed to an elevated occurrence of disease pressure.

Comparing LSMMeans from 2017-2018, overall values for VS\_FLTFLD, RS\_FLTFLD, and RS\_GRNHUE were depressed in 2018 in contrast to the previous year; the inverse was observed for the traits RS\_CANCVR and RS\_CANHLTH, with only moderate changes for the RS\_FLTRCV trait. This suggests that the multi-time-point measurement, RS\_FLTRCV, experienced only minor variation due to environmental influences when compared to the single-time-point measurements, VS\_FLTFLD and RS\_FLTFLD, providing a better-quality phenotypic characterization of waterlogging tolerance in soybean year to year.

Correlations of all traits in 2017 were significantly positive, with RS\_FLTRCV having the highest correlations to all three remote sensing traits, RS\_CANCVR, RS\_CANHLTH, and RS\_GRNHUE captured by the drone in 2017, with  $r$  values of 0.85, 0.84, and 0.78 for DET and 0.83, 0.72, and 0.70 for IND respectively. The visual scores (VS\_FLTFLD) also exhibited a positive correlation to the three remote sensing traits, RS\_CANCVR, RS\_CANHLTH, and RS\_GRNHUE with  $r$  values of 0.70, 0.54, and 0.67 for DET and 0.74, 0.20, 0.34 for IND respectively.

Variance components were analyzed and used to estimate repeatability and broad sense heritability values. Repeatability estimates were indeed higher than the broad

sense heritability estimate, which used molecular markers to create relationship matrices among the genotypes. Out of the three traits, VS\_FLTFLD, RS\_FLTFLD, RS\_FLTRCV, that utilized the 1-9 scoring scale, RS\_FLTRCV was the most consistent for both years 2017 and 2018, with estimates of 0.69 and 0.66 respectively. The traits VS\_FLTFLD and RS\_FLTFLD had greater fluctuations year to year. Broad sense heritability estimates for the three waterlogged tolerance scores and the three remote sensing traits in 2017 ranged from 0.33 to 0.62. This range corresponds to what others have reported in previous studies (Ye et al., 2018). Again, consistent with the repeatability results, 2018 confirmed a reduction in heritability estimate values; however, these were more pronounced and were attributed to the increase in residual (error) variance in 2018. This year to year deviation in heritability has been documented in other soybean traits. Jauregui et al. (2011) recognized a similar occurrence in soybean regarding food-grade traits, and prior soybean waterlogging tolerance research specified that variation of genotype injury scores and genotype x environment interactions can be highly significant for waterlogging injury (Conelious et al., 2006; Wu et al., 2017).

Comparisons of the remote sensing traits to traditional or “ground truth” phenotyping provides clear validation of high-throughput phenotyping using UAV imagery, illustrating that the UAVs using remote sensing devices (RGB cameras) can provide an accurate phenotypic characterization of waterlogging tolerance in soybean. Environmental factors such as temperature and disease can cause GxE interactions and play a significant role in the severity of waterlogging symptomology in a field setting. Environmental factors can be minimalized using a multi-time-point measurement,

instead of a single-time-point measurement, using an index of the three remote sensing traits. The remote sensing flood tolerance recovery (RS\_FLTRCV) trait was an improvement over the VS\_FLTFLD and RS\_FLTFLD traits in this study, capturing the actual changes exhibited in soybean during waterlogged field conditions. Additional evaluation is needed to confirm these findings and optimize further characterization.

Results from the genomic selection investigation using cross-validation analysis were positive for both 2017 and 2018, with the 2017 data demonstrating superior prediction accuracies with a mean accuracy of 0.57 for all remote sensing traits compared to 0.27 for 2018 flood screening. The highest performing trait within 2017 was FLTRCV followed by RS\_CANHLTH, RS\_GRNHUE, RS\_CANCVR, and finally RS\_FLTFLD with prediction accuracies of 0.68, 0.64, 0.60, 0.50, and 0.36 respectively. Prediction accuracies exhibited a significant decrease the following year and were 0.38, 0.27, 0.26, 0.25 and 0.20 for RS\_CANHLTH, RS\_FLTFLD, RS\_FLTRCV, RS\_GRNHUE, and RS\_CANCVR respectively. This again illustrates the environmental influences seen in 2018 resulting in increased severity of waterlogging symptoms across all genotypes and rating fluctuations experienced by genotypes year to year during flood treatment. RS\_FLTRCV was the only trait correlation in 2017 that was significant, at the  $p < .05$  level, for the cross-validation pooled predictions; all other trait correlations were not significant. None of the five remote sensing trait correlations were significant at the  $p < .05$  level in 2018. While the GxE effects in this research are hypothesized to be the primary influence in prediction correlation differences between 2017 and 2018, another possible influence could be differences in population sizes between years. It has been

reported in former studies that reductions in training populations can negatively impact predictions (Heffner et al., 2011; Zhang et al., 2017). While the number of genotypes does differ between years, the same proportion, ninety percent, was utilized in each year's cross-validation analysis and included the forty-three genotypes tested in 2017 and 2018. Further study is needed to determine what is truly influencing flood tolerance prediction accuracy year to year.

Evaluating prediction accuracy across years using the 2017 data as the training population and the 2018 dataset as the validation population for the two genomic models, BayesA and BayesB, demonstrated little differences between the two methods, even though each model estimates marker effects differently. Correlations of the BayesA and BayesB for each of the traits RS\_FLTFLD, RS\_FLTRCV, RS\_CANCVR, RS\_CANHLTH, and RS\_GRNHUE were 0.98 or higher. These results correspond with previous research, which revealed only minor differences in predictions using Bayesian models (Lorenzana and Bernardo, 2009; Zhong et al., 2009; Heffner et al., 2011). The remote sensing trait with the highest accuracy was RS\_FLTRCV with a correlation of 0.49 and 0.47, while the RS\_FLTFLD trait correlation was 0.16 and 0.21 for BayesA and BayesB respectively. The three-other remote sensing flood traits, RS\_CANCVR, RS\_CANHLTH, and RS\_GRNHUE correlations were 0.28, 0.46, and 0.21 for BayesA and 0.28, 0.49, 0.21 for BayesB respectively.

Anticipating which years' dataset will be the most predictive on a year by year basis and which will enhance future prediction accuracy in successive cycles is difficult for a breeder. Therefore, multi-year training populations offer benefits over single-year

training populations (Auinger et al., 2016; Bernal-Vasquez et al., 2017). Including multiple cycles from a breeding program has numerous benefits: permitting separation of the genotype-by-year effects, significantly increasing the numbers of the training population providing greater prediction accuracy, and improving kinship by connecting related genotypes across years (Auinger et al., 2016; Bernal-Vasquez et al., 2017). Inaccurate phenotypic data from a single year can create flawed predictions caused by environmental factors like incidence of disease or significant weather events; using multiple-years minimizes the influence of a single year, thus improving prediction accuracy.

Genomic selection via predictions may prove to be a valuable tool for making flood tolerant selections in soybeans even when genotypes experience environmental influences. Despite the lower prediction accuracies for waterlogging tolerance in 2018, genetic gain was possible using genomic selection and has the potential to outperform phenotypic selection by enabling additional rounds of selection in earlier generations where phenotypic selection alone cannot. GS also serves to enable selection on a larger number of genotypes without increased resources required for field plots; these resources could in turn be utilized to expand genotyping across a broader collection of germplasm, advancing genetic gain. While there may remain significant flood tolerant QTL in wild type and PI germplasm pools yet discovered, genomic selection provides a present method to leverage the existing waterlogging tolerance variation within elite germplasm improving genetic gain.

The results of this research suggest that high-throughput phenotyping using UAV imagery to create multi-time-point measurements in conjunction with genomic selection can be an influential tool for improving waterlogging tolerance in soybeans. The types of models used have little influence on prediction estimates, while factors such as reference population size and marker density play a larger role in prediction accuracy. Additional examination of training population construction with regards to number of genotypes, family structure among genotypes, and the inclusion of multiple years will help to enhance these approaches in a breeding program. Next steps will include modifications to the experiment design and improved agronomic methods, like the utilization of augmented blocks with increased replication and the application of seed treatment to all genotypes, with the goal of minimizing some of the environmental effects. Follow-up research will be needed to further each of these objectives, eventually providing information on how best to advance waterlogging tolerance in soybean.



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## APPENDIX

### LIST OF GENOME-WIDE MARKERS USED FOR EACH YEAR

Table A. Marker name, chromosome, public markers associated with proprietary Corteva Agriscience SNP markers, and year proprietary Corteva Agriscience SNP markers used in genotypes for 2014-2015 & 2017-2018 waterlogging tolerance screening.

Marker Name	Chromosome	Public Marker	Years
SNP1.120	1	BARC_1.01_Gm01_14097047_T_C	14,15,17,18
SNP1.043	1	BARC_1.01_Gm01_2928374_C_A	14,15,17,18
SNP1.052	1	BARC_1.01_Gm01_3537008_C_T	14,15,17,18
SNP1.203	1	BARC_1.01_Gm01_45165995_A_C	14,15,17,18
SNP1.233	1	BARC_1.01_Gm01_48362668_T_C	14,15,17,18
SNP1.071	1	BARC_1.01_Gm01_4841672_T_C	14,15
SNP1.238	1	BARC_1.01_Gm01_48565309_G_A	14
SNP1.248	1	BARC_1.01_Gm01_49101288_A_C	14,15
SNP1.263	1	BARC_1.01_Gm01_50008674_G_A	15,18
SNP1.282	1	BARC_1.01_Gm01_51398886_G_A	14,15,17,18
SNP1.286	1	BARC_1.01_Gm01_51764870_C_T	14,15
SNP1.306	1	BARC_1.01_Gm01_53862612_T_C	14,15,17,18
SNP1.335	1	BARC_1.01_Gm01_55751910_A_G	14,15,17,18
SNP1.001	1		14,15,17,18
SNP1.005	1		14,15,17,18
SNP1.007	1		14,15
SNP1.008	1		14,15,17,18
SNP1.010	1		14,15,17,18
SNP1.013	1		15,17,18
SNP1.015	1		14,15,17,18
SNP1.016	1		14,15,17,18
SNP1.017	1		14,15,17,18
SNP1.018	1		14,15,17,18
SNP1.019	1		15
SNP1.020	1		15,17,18
SNP1.021	1		14,15,17,18
SNP1.022	1		14,15,17,18
SNP1.023	1		14,15,17,18
SNP1.024	1		14,15,17,18
SNP1.025	1		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP1.027	1		14,15
SNP1.028	1		14,15,17,18
SNP1.033	1		14,15,17,18
SNP1.038	1		14,15,17,18
SNP1.045	1		14,15,17,18
SNP1.056	1		14,15,17,18
SNP1.060	1		14,15,17,18
SNP1.063	1		14,15,17,18
SNP1.065	1		14,15,17,18
SNP1.069	1		14,15
SNP1.072	1		14,15,17,18
SNP1.076	1		14,15,17
SNP1.078	1		14,15,17
SNP1.079	1		14,15
SNP1.081	1		14,15,17,18
SNP1.219	1		14,15,17,18
SNP1.208	1		14,15,17,18
SNP1.205	1		14,15,17,18
SNP1.198	1		14,15,17,18
SNP1.197	1		14,15,17,18
SNP1.196	1		14,15,17,18
SNP1.192	1		14,15,17,18
SNP1.191	1		14,15,17,18
SNP1.189	1		14,15
SNP1.188	1		14,15,17,18
SNP1.187	1		14,15,17,18
SNP1.186	1		14,15,17,18
SNP1.184	1		14,15,17,18
SNP1.181	1		14,15,17,18
SNP1.180	1		14,15,17,18
SNP1.182	1		14,15,18
SNP1.178	1		15,18
SNP1.176	1		14,15,17,18
SNP1.175	1		15,18
SNP1.172	1		14,15,17,18
SNP1.170	1		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP1.168	1		14,15,17,18
SNP1.167	1		14,15,17,18
SNP1.165	1		14,15,17
SNP1.163	1		14,15
SNP1.160	1		14,15,17,18
SNP1.157	1		14,15,17,18
SNP1.158	1		14,15,17,18
SNP1.153	1		14,15,17,18
SNP1.152	1		14,15
SNP1.151	1		14,15,17,18
SNP1.150	1		14,15,17,18
SNP1.144	1		14,15,17,18
SNP1.139	1		14,15,17,18
SNP1.131	1		14,15,17,18
SNP1.129	1		14,15,17,18
SNP1.115	1		14,15,17,18
SNP1.116	1		14,15,17,18
SNP1.112	1		14,15
SNP1.111	1		14,15,17,18
SNP1.105	1		14,15,17,18
SNP1.103	1		14,15,17,18
SNP1.123	1		14,15,17,18
SNP1.124	1		14,15,17,18
SNP1.092	1		14,15,17,18
SNP1.086	1		14,15,17
SNP1.083	1		14,15,17,18
SNP1.222	1		14,15,17,18
SNP1.225	1		14,15,17,18
SNP1.232	1		14,15,17,18
SNP1.234	1		14,15,17,18
SNP1.235	1		15,18
SNP1.236	1		14,15,17
SNP1.237	1		14,15,17,18
SNP1.240	1		14,15,17,18
SNP1.245	1		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP1.247	1		14,15,17,18
SNP1.249	1		14,15,17,18
SNP1.250	1		14,15,17,18
SNP1.252	1		15,17,18
SNP1.267	1		14,15,17,18
SNP1.272	1		14,15,17,18
SNP1.275	1		14,15,17,18
SNP1.276	1		14,15,17,18
SNP1.285	1		14,15
SNP1.287	1		14,15
SNP1.289	1		14,15,17,18
SNP1.294	1		14,15,17,18
SNP1.296	1		14,15,17,18
SNP1.302	1		14,15,17,18
SNP1.307	1		14,15,17,18
SNP1.312	1		14,15,17,18
SNP1.313	1		14,15,17,18
SNP1.316	1		14,15,17,18
SNP1.317	1		14,15
SNP1.334	1		14,15,17,18
SNP1.002	1		15,18
SNP1.003	1		15,18
SNP1.004	1		15,18
SNP1.006	1		15,18
SNP1.009	1		15,18
SNP1.011	1		15,18
SNP1.012	1		15,18
SNP1.014	1		15,18
SNP1.026	1		15,18
SNP1.029	1		15,18
SNP1.030	1		15,18
SNP1.031	1		15,18
SNP1.032	1		15,18
SNP1.034	1		15,18
SNP1.036	1		15,18
SNP1.037	1		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP1.040	1		15,18
SNP1.041	1		15,18
SNP1.042	1		15,18
SNP1.044	1		15,18
SNP1.048	1		15,18
SNP1.049	1		15,18
SNP1.050	1		15,18
SNP1.051	1		15
SNP1.053	1		15,18
SNP1.054	1		15,18
SNP1.055	1		15,18
SNP1.057	1		15,18
SNP1.058	1		15,18
SNP1.059	1		15,18
SNP1.061	1		15,18
SNP1.062	1		15,18
SNP1.064	1		15
SNP1.066	1		15,18
SNP1.067	1		15
SNP1.068	1		15,18
SNP1.070	1		15
SNP1.073	1		15,18
SNP1.074	1		15
SNP1.075	1		15
SNP1.077	1		15
SNP1.080	1		15,18
SNP1.082	1		15
SNP1.084	1		15,18
SNP1.085	1		15,18
SNP1.087	1		15,18
SNP1.088	1		15,18
SNP1.089	1		15,18
SNP1.093	1		15,18
SNP1.094	1		15,18
SNP1.095	1		15,18
SNP1.096	1		15,18



Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP1.098	1		15,18
SNP1.099	1		15,18
SNP1.100	1		15,18
SNP1.101	1		15,18
SNP1.102	1		15,18
SNP1.104	1		15,18
SNP1.106	1		15,18
SNP1.107	1		15,18
SNP1.108	1		15,18
SNP1.109	1		15,18
SNP1.110	1		15,18
SNP1.113	1		15
SNP1.114	1		15,18
SNP1.117	1		15,18
SNP1.118	1		15,18
SNP1.119	1		15,18
SNP1.121	1		15,18
SNP1.125	1		15,18
SNP1.126	1		15,18
SNP1.127	1		15
SNP1.128	1		15
SNP1.130	1		15,18
SNP1.132	1		15,18
SNP1.133	1		15,18
SNP1.134	1		15,18
SNP1.135	1		15,18
SNP1.136	1		15,18
SNP1.137	1		15,18
SNP1.138	1		15,18
SNP1.140	1		15,18
SNP1.141	1		15,18
SNP1.142	1		15,18
SNP1.143	1		15,18
SNP1.145	1		15,18
SNP1.146	1		15,18
SNP1.147	1		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP1.149	1		15,18
SNP1.154	1		15,18
SNP1.155	1		15,18
SNP1.156	1		15,18
SNP1.159	1		15,18
SNP1.161	1		15,18
SNP1.162	1		15,18
SNP1.164	1		15,18
SNP1.169	1		15,18
SNP1.171	1		15,18
SNP1.174	1		15,18
SNP1.177	1		15,18
SNP1.179	1		15,18
SNP1.183	1		15,18
SNP1.185	1		15,18
SNP1.190	1		15,18
SNP1.193	1		15,18
SNP1.194	1		15,18
SNP1.195	1		15,18
SNP1.199	1		15,18
SNP1.200	1		15,18
SNP1.201	1		15,18
SNP1.204	1		15,18
SNP1.206	1		15,18
SNP1.207	1		15,18
SNP1.209	1		15,18
SNP1.210	1		15,18
SNP1.211	1		15,18
SNP1.212	1		15,18
SNP1.213	1		15,18
SNP1.214	1		15,18
SNP1.215	1		15,18
SNP1.216	1		15,18
SNP1.217	1		15,18
SNP1.218	1		15,18
SNP1.220	1		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP1.223	1		15,18
SNP1.224	1		15,18
SNP1.226	1		15,18
SNP1.227	1		15
SNP1.228	1		15,18
SNP1.229	1		15,18
SNP1.230	1		15,18
SNP1.231	1		15,18
SNP1.239	1		15,18
SNP1.241	1		15,18
SNP1.242	1		15,18
SNP1.243	1		15,18
SNP1.244	1		15,18
SNP1.251	1		15
SNP1.253	1		15,18
SNP1.254	1		15,18
SNP1.255	1		15
SNP1.256	1		15
SNP1.257	1		15,18
SNP1.258	1		15,18
SNP1.259	1		15,18
SNP1.261	1		15,18
SNP1.262	1		15,18
SNP1.264	1		15,18
SNP1.265	1		15,18
SNP1.266	1		15,18
SNP1.268	1		15,18
SNP1.269	1		15,18
SNP1.270	1		15,18
SNP1.271	1		15,18
SNP1.273	1		15,18
SNP1.274	1		15,18
SNP1.277	1		15,18
SNP1.278	1		15,18
SNP1.279	1		15,18
SNP1.280	1		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP1.283	1		15,18
SNP1.284	1		15,18
SNP1.288	1		15,18
SNP1.290	1		15,18
SNP1.291	1		18
SNP1.292	1		18
SNP1.293	1		15,18
SNP1.295	1		15,18
SNP1.297	1		15,18
SNP1.298	1		15
SNP1.299	1		15,18
SNP1.300	1		18
SNP1.301	1		15
SNP1.303	1		15,18
SNP1.304	1		15,18
SNP1.305	1		15,18
SNP1.308	1		15,18
SNP1.309	1		15,18
SNP1.310	1		15,18
SNP1.311	1		15,18
SNP1.314	1		15,18
SNP1.315	1		15,18
SNP1.318	1		15,18
SNP1.319	1		15,18
SNP1.320	1		15,18
SNP1.321	1		15,18
SNP1.328	1		15,18
SNP1.329	1		15,18
SNP1.330	1		15,18
SNP1.331	1		15,18
SNP1.332	1		15,18
SNP2.156	2	BARC_1.01_Gm02_10354615_A_G	14,15,17,18
SNP2.174	2	BARC_1.01_Gm02_12043666_T_C	14,15
SNP2.185	2	BARC_1.01_Gm02_13535155_T_C	14,15,17,18
SNP2.212	2	BARC_1.01_Gm02_18024522_C_T	14,15,17,18
SNP2.035	2	BARC_1.01_Gm02_2454266_A_C	14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP2.041	2	BARC_1.01_Gm02_3091665_T_G	14,15,17,18
SNP2.307	2	BARC_1.01_Gm02_44109125_C_A	14,15,17,18
SNP2.317	2	BARC_1.01_Gm02_44500686_G_A	14,15
SNP2.335	2	BARC_1.01_Gm02_45811985_G_T	14
SNP2.341	2	BARC_1.01_Gm02_46165163_G_T	14,15,17,18
SNP2.399	2	BARC_1.01_Gm02_49608307_A_G	14,15,17,18
SNP2.412	2	BARC_1.01_Gm02_50529112_T_G	14,15,17,18
SNP2.077	2	BARC_1.01_Gm02_5325272_T_C	14,15
SNP2.078	2	BARC_1.01_Gm02_5382488_A_G	14,15,17,18
SNP2.086	2	BARC_1.01_Gm02_5846631_A_G	14,15,17,18
SNP2.087	2	BARC_1.01_Gm02_5900226_G_A	14,15,17,18
SNP2.141	2	BARC_1.01_Gm02_9591065_G_A	14,15,17,18
SNP2.144	2	BARC_1.01_Gm02_9714426_C_A	14,15,17,18
SNP2.002	2	BARC_1.01_Gm02_97985_T_C	14,15,17,18
SNP2.008	2		14,15
SNP2.010	2		14,15,17,18
SNP2.015	2		14,15,17
SNP2.017	2		14,15,17,18
SNP2.018	2		14,15,17,18
SNP2.019	2		14,15,17,18
SNP2.032	2		14,15,17,18
SNP2.033	2		14,15,17,18
SNP2.034	2		14,15,17,18
SNP2.047	2		15,17,18
SNP2.055	2		14,15,17,18
SNP2.056	2		14,15,17,18
SNP2.058	2		14,15,17,18
SNP2.063	2		14,15,17,18
SNP2.065	2		14,15,17
SNP2.070	2		14,15,17,18
SNP2.072	2		14,15,17,18
SNP2.073	2		14,15,17,18
SNP2.080	2		14,15,17,18
SNP2.082	2		14,15,17,18
SNP2.084	2		14,15,17,18
SNP2.093	2		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP2.105	2		14,15,17,18
SNP2.106	2		14,15
SNP2.111	2		14,15,17,18
SNP2.113	2		15,17,18
SNP2.114	2		15,17,18
SNP2.116	2		15,17,18
SNP2.120	2		15,17,18
SNP2.126	2		14,15,17,18
SNP2.132	2		14,15,17,18
SNP2.134	2		14,15,17,18
SNP2.135	2		14,15,17,18
SNP2.146	2		14,15,17,18
SNP2.148	2		14,15,17,18
SNP2.149	2		14,15,17,18
SNP2.157	2		14,15,17,18
SNP2.158	2		14,15,17,18
SNP2.169	2		14,15,17,18
SNP2.170	2		14,15,17,18
SNP2.173	2		14,15,17,18
SNP2.175	2		14,15,17,18
SNP2.176	2		14,15,17,18
SNP2.177	2		14,15,17,18
SNP2.178	2		14,15,17,18
SNP2.196	2		14
SNP2.200	2		14,15,17,18
SNP2.201	2		14,15
SNP2.204	2		14,15,17,18
SNP2.205	2		14,15
SNP2.208	2		14,15,17
SNP2.209	2		14,15,17
SNP2.210	2		14,15,17
SNP2.215	2		14,15,17
SNP2.224	2		14,15
SNP2.226	2		14,15,17,18
SNP2.229	2		14,15,17,18
SNP2.239	2		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP2.244	2		14,15
SNP2.246	2		14,15,17,18
SNP2.247	2		14,15,17,18
SNP2.248	2		14,15
SNP2.251	2		14,15,17,18
SNP2.253	2		14,15,17,18
SNP2.257	2		14,15,17,18
SNP2.260	2		14,15,17,18
SNP2.259	2		14,15,17,18
SNP2.263	2		14,15,17,18
SNP2.266	2		14,15,17,18
SNP2.268	2		14,15,17,18
SNP2.276	2		14,15,17,18
SNP2.277	2		14,15,17,18
SNP2.279	2		14,15,17,18
SNP2.285	2		14,15,17,18
SNP2.291	2		14,15
SNP2.296	2		14,15,17,18
SNP2.306	2		14,15,17,18
SNP2.310	2		14,15,17,18
SNP2.311	2		14,15,17,18
SNP2.312	2		14,15,17,18
SNP2.313	2		14,15,17,18
SNP2.314	2		14,15,17,18
SNP2.320	2		14,15,17,18
SNP2.326	2		14,15,17,18
SNP2.331	2		14,15,17,18
SNP2.332	2		14,15,17,18
SNP2.333	2		14,15,17,18
SNP2.338	2		14,15,17,18
SNP2.340	2		14,15
SNP2.342	2		14,15,17,18
SNP2.348	2		14,15,17,18
SNP2.354	2		14,15,17,18
SNP2.355	2		14,15,17,18
SNP2.356	2		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP2.360	2		14,15,17,18
SNP2.362	2		14,15
SNP2.363	2		14,15,17,18
SNP2.364	2		14,15,17,18
SNP2.365	2		14,15,17,18
SNP2.368	2		14,15,17,18
SNP2.370	2		15,18
SNP2.376	2		14,15,17,18
SNP2.378	2		14,15,17,18
SNP2.383	2		14,15,17,18
SNP2.388	2		14
SNP2.390	2		14,15,18
SNP2.395	2		14,15,17,18
SNP2.396	2		14,15,17,18
SNP2.397	2		14,15,17,18
SNP2.398	2		14,15,17,18
SNP2.403	2		14,15,18
SNP2.404	2		14,15,18
SNP2.406	2		14,15,17,18
SNP2.407	2		14,15,18
SNP2.408	2		14,15,18
SNP2.409	2		14,15,17,18
SNP2.411	2		14,15,18
SNP2.420	2		14,15,17,18
SNP2.421	2		14,15,17,18
SNP2.423	2		14,15,17,18
SNP2.426	2		14,15,17,18
SNP2.428	2		14,15,17,18
SNP2.429	2		14,15,17,18
SNP2.001	2		15,18
SNP2.003	2		15,18
SNP2.004	2		15,18
SNP2.005	2		15,18
SNP2.006	2		15,18
SNP2.007	2		15,18
SNP2.009	2		15,18



Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP2.012	2		15,18
SNP2.013	2		15,18
SNP2.014	2		15,18
SNP2.016	2		15,18
SNP2.029	2		15,18
SNP2.030	2		15,18
SNP2.031	2		15,18
SNP2.038	2		18
SNP2.040	2		15,18
SNP2.042	2		15,18
SNP2.046	2		15,18
SNP2.048	2		15,18
SNP2.049	2		15,18
SNP2.050	2		15,18
SNP2.051	2		15,18
SNP2.052	2		15,18
SNP2.053	2		15,18
SNP2.054	2		15,18
SNP2.057	2		18
SNP2.059	2		15,18
SNP2.061	2		15,18
SNP2.062	2		15,18
SNP2.064	2		15,18
SNP2.066	2		15,18
SNP2.068	2		15,18
SNP2.069	2		15,18
SNP2.071	2		15,18
SNP2.075	2		15,18
SNP2.076	2		15,18
SNP2.079	2		15,18
SNP2.081	2		15,18
SNP2.083	2		15,18
SNP2.085	2		15,18
SNP2.088	2		15,18
SNP2.091	2		15,18
SNP2.092	2		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP2.097	2		15,18
SNP2.102	2		15,18
SNP2.103	2		15,18
SNP2.104	2		15,18
SNP2.108	2		15,18
SNP2.112	2		15,18
SNP2.115	2		15,18
SNP2.118	2		15,18
SNP2.127	2		15,18
SNP2.128	2		15,18
SNP2.129	2		15,18
SNP2.130	2		15,18
SNP2.133	2		15,18
SNP2.136	2		15,18
SNP2.137	2		15,18
SNP2.138	2		15,18
SNP2.139	2		15,18
SNP2.140	2		15,18
SNP2.142	2		15,18
SNP2.143	2		15,18
SNP2.145	2		15,18
SNP2.147	2		15,18
SNP2.150	2		15,18
SNP2.152	2		15,18
SNP2.153	2		15
SNP2.154	2		15,18
SNP2.159	2		15,18
SNP2.160	2		15,18
SNP2.162	2		18
SNP2.163	2		18
SNP2.164	2		15,18
SNP2.166	2		18
SNP2.171	2		15,18
SNP2.172	2		15,18
SNP2.179	2		15,18
SNP2.180	2		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP2.183	2		15,18
SNP2.184	2		15,18
SNP2.186	2		15,18
SNP2.187	2		15,18
SNP2.188	2		15,18
SNP2.189	2		15
SNP2.190	2		15
SNP2.192	2		15,18
SNP2.193	2		15,18
SNP2.194	2		15,18
SNP2.195	2		15,18
SNP2.197	2		15,18
SNP2.198	2		15,18
SNP2.199	2		15,18
SNP2.202	2		15,18
SNP2.203	2		15,18
SNP2.207	2		15
SNP2.211	2		15
SNP2.213	2		15,18
SNP2.214	2		15,18
SNP2.216	2		15,18
SNP2.217	2		15,18
SNP2.218	2		15,18
SNP2.219	2		15,18
SNP2.220	2		15,18
SNP2.221	2		15
SNP2.222	2		15,18
SNP2.223	2		15,18
SNP2.225	2		15
SNP2.227	2		15,18
SNP2.228	2		15,18
SNP2.230	2		15,18
SNP2.231	2		15,18
SNP2.232	2		15,18
SNP2.233	2		15,18
SNP2.234	2		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP2.236	2		15,18
SNP2.237	2		15,18
SNP2.238	2		15,18
SNP2.240	2		15,18
SNP2.241	2		15,18
SNP2.243	2		15,18
SNP2.245	2		15,18
SNP2.249	2		15,18
SNP2.250	2		15,18
SNP2.252	2		15,18
SNP2.254	2		15,18
SNP2.255	2		15,18
SNP2.256	2		15,18
SNP2.258	2		15,18
SNP2.261	2		15,18
SNP2.262	2		15,18
SNP2.264	2		15,18
SNP2.265	2		15,18
SNP2.267	2		15,18
SNP2.269	2		15,18
SNP2.270	2		15,18
SNP2.271	2		15,18
SNP2.272	2		15,18
SNP2.273	2		15,18
SNP2.274	2		15,18
SNP2.275	2		15,18
SNP2.278	2		15,18
SNP2.280	2		15,18
SNP2.281	2		15,18
SNP2.282	2		15,18
SNP2.283	2		15,18
SNP2.284	2		15,18
SNP2.286	2		15,18
SNP2.287	2		15,18
SNP2.288	2		15,18
SNP2.289	2		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP2.292	2		15,18
SNP2.293	2		15,18
SNP2.294	2		15,18
SNP2.295	2		15,18
SNP2.297	2		15,18
SNP2.298	2		15,18
SNP2.299	2		15,18
SNP2.300	2		15,18
SNP2.303	2		15,18
SNP2.304	2		15,18
SNP2.305	2		15,18
SNP2.308	2		15,18
SNP2.309	2		15,18
SNP2.319	2		15
SNP2.321	2		15,18
SNP2.322	2		15,18
SNP2.323	2		15,18
SNP2.324	2		15
SNP2.325	2		15,18
SNP2.327	2		15,18
SNP2.328	2		15,18
SNP2.329	2		15,18
SNP2.330	2		15,18
SNP2.334	2		15,18
SNP2.336	2		15,18
SNP2.337	2		15,18
SNP2.339	2		15,18
SNP2.343	2		15,18
SNP2.344	2		15,18
SNP2.345	2		15,18
SNP2.346	2		15,18
SNP2.347	2		15,18
SNP2.349	2		15,18
SNP2.350	2		15,18
SNP2.351	2		15,18
SNP2.352	2		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP2.357	2		15,18
SNP2.358	2		18
SNP2.361	2		15,18
SNP2.366	2		15,18
SNP2.367	2		15,18
SNP2.369	2		15,18
SNP2.371	2		15,18
SNP2.377	2		15,18
SNP2.379	2		15,18
SNP2.380	2		15,18
SNP2.381	2		15,18
SNP2.382	2		15,18
SNP2.384	2		15,18
SNP2.385	2		15,18
SNP2.386	2		15,18
SNP2.387	2		15,18
SNP2.389	2		15,18
SNP2.391	2		15,18
SNP2.392	2		18
SNP2.393	2		15,18
SNP2.394	2		15,18
SNP2.400	2		15,18
SNP2.401	2		15,18
SNP2.405	2		15,18
SNP2.410	2		15,18
SNP2.413	2		15,18
SNP2.414	2		15,18
SNP2.415	2		15,18
SNP2.418	2		15,18
SNP2.419	2		18
SNP2.422	2		15,18
SNP2.424	2		15,18
SNP2.425	2		15,18
SNP2.427	2		15,18
SNP2.430	2		15,18
SNP3.015	3	BARC_1.01_Gm03_1118049_A_G	14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP3.046	3	BARC_1.01_Gm03_2993784_G_A	14,15,17,18
SNP3.050	3	BARC_1.01_Gm03_3299192_G_A	14,15,17,18
SNP3.054	3	BARC_1.01_Gm03_3390452_T_C	14,15,17,18
SNP3.055	3	BARC_1.01_Gm03_3454741_T_C	18
SNP3.189	3	BARC_1.01_Gm03_35318420_G_A	14,15,17,18
SNP3.190	3	BARC_1.01_Gm03_35349154_G_A	14,15,17,18
SNP3.211	3	BARC_1.01_Gm03_36454213_A_G	14,15,17,18
SNP3.234	3	BARC_1.01_Gm03_37828355_G_T	14,15,17,18
SNP3.238	3	BARC_1.01_Gm03_38076711_C_T	14,15,17,18
SNP3.308	3	BARC_1.01_Gm03_43838447_C_T	14,15,17,18
SNP3.315	3	BARC_1.01_Gm03_44510110_A_G	14,15
SNP3.326	3	BARC_1.01_Gm03_45338714_C_T	14,15,17,18
SNP3.341	3	BARC_1.01_Gm03_46454397_T_C	14,15,17,18
SNP3.349	3	BARC_1.01_Gm03_46888399_A_C	14,15,17,18
SNP3.009	3		14,15
SNP3.016	3		14,15,17,18
SNP3.027	3		14,15,17,18
SNP3.030	3		14,15,17,18
SNP3.035	3		14,15,17,18
SNP3.036	3		14,15,17,18
SNP3.039	3		14,15,17,18
SNP3.040	3		14,15,17,18
SNP3.041	3		14,15
SNP3.045	3		14,15
SNP3.049	3		17
SNP3.052	3		14,15,17,18
SNP3.053	3		14,15,17,18
SNP3.057	3		14,15,17,18
SNP3.060	3		14,15,17,18
SNP3.061	3		14,15,17,18
SNP3.063	3		14,15,17,18
SNP3.064	3		14,15,17,18
SNP3.067	3		14,15
SNP3.069	3		14,15,17,18
SNP3.070	3		14,15,17,18
SNP3.071	3		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP3.073	3		14,15,17,18
SNP3.074	3		14,15,17,18
SNP3.075	3		14,15,17,18
SNP3.080	3		14,15,17,18
SNP3.081	3		14,15,17,18
SNP3.085	3		14,15,17,18
SNP3.087	3		14,15,17,18
SNP3.092	3		15
SNP3.093	3		14,15,17,18
SNP3.094	3		14,15,17,18
SNP3.096	3		14,15,17,18
SNP3.097	3		14,15,17,18
SNP3.098	3		14,15,17,18
SNP3.099	3		14,15,17,18
SNP3.101	3		14,15
SNP3.104	3		14,15,17,18
SNP3.103	3		14,15,17,18
SNP3.105	3		14,15,17,18
SNP3.106	3		14,15,17,18
SNP3.107	3		14,15,17,18
SNP3.109	3		14,15,17,18
SNP3.110	3		14,15,17,18
SNP3.112	3		14,15,17,18
SNP3.113	3		14,15,17,18
SNP3.117	3		14,15,17,18
SNP3.116	3		14,15,17,18
SNP3.118	3		14,15,17,18
SNP3.121	3		14,15,17,18
SNP3.127	3		14,15,17,18
SNP3.129	3		14,15,17,18
SNP3.130	3		14,15,17,18
SNP3.150	3		14,15
SNP3.144	3		14,15
SNP3.143	3		14,15,17,18
SNP3.134	3		14,15,17,18
SNP3.124	3		14,15,17,18



Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP3.171	3		14,15,17,18
SNP3.173	3		14,15,17,18
SNP3.179	3		14,15,17,18
SNP3.180	3		14,15,17,18
SNP3.193	3		14,15,17,18
SNP3.200	3		14,15,17,18
SNP3.202	3		14,15
SNP3.203	3		14,15
SNP3.204	3		14,15,17,18
SNP3.205	3		14,15,17,18
SNP3.206	3		14,15,17,18
SNP3.207	3		14,15,17,18
SNP3.208	3		14,15
SNP3.209	3		14,15,17,18
SNP3.213	3		14,15
SNP3.214	3		14,15,17
SNP3.216	3		14,15,17
SNP3.219	3		14,15,17,18
SNP3.245	3		14,15
SNP3.247	3		14,15,17,18
SNP3.248	3		14,15,17,18
SNP3.250	3		14,15,17,18
SNP3.255	3		14
SNP3.257	3		14,15,17,18
SNP3.258	3		14,15,17,18
SNP3.259	3		14,15,17,18
SNP3.260	3		14,15,17,18
SNP3.261	3		14,15,17,18
SNP3.271	3		14,15,17,18
SNP3.273	3		14,15,17,18
SNP3.275	3		14,15,17,18
SNP3.276	3		14,15,17,18
SNP3.280	3		14,15,17,18
SNP3.283	3		14,15,17,18
SNP3.288	3		14,15,17,18
SNP3.292	3		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP3.304	3		14,15,17,18
SNP3.305	3		14,15,17,18
SNP3.307	3		14,15,17,18
SNP3.310	3		14,15,17,18
SNP3.311	3		14,15,17,18
SNP3.313	3		14,15,17,18
SNP3.316	3		14,15,17,18
SNP3.322	3		14,15
SNP3.333	3		14,15,17,18
SNP3.335	3		14,15
SNP3.336	3		14,15,17,18
SNP3.337	3		14,15,17,18
SNP3.345	3		14,15,17,18
SNP3.344	3		14,15,17,18
SNP3.347	3		14,15,17,18
SNP3.358	3		14,15,17,18
SNP3.360	3		14,15
SNP3.001	3		15,18
SNP3.002	3		15,18
SNP3.003	3		15,18
SNP3.004	3		15,18
SNP3.005	3		15,18
SNP3.006	3		14,15,17,18
SNP3.007	3		15,18
SNP3.008	3		14,15,17,18
SNP3.010	3		15,18
SNP3.011	3		15,18
SNP3.012	3		15,18
SNP3.013	3		15,18
SNP3.014	3		15,18
SNP3.017	3		15,18
SNP3.019	3		15,18
SNP3.020	3		15,18
SNP3.021	3		15,18
SNP3.022	3		15,18
SNP3.023	3		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP3.025	3		15,18
SNP3.026	3		15,18
SNP3.028	3		15,18
SNP3.029	3		15,18
SNP3.031	3		15,18
SNP3.032	3		15,18
SNP3.033	3		15,18
SNP3.034	3		15,18
SNP3.037	3		15,18
SNP3.038	3		15,18
SNP3.042	3		15,18
SNP3.043	3		15,18
SNP3.044	3		15,18
SNP3.047	3		15,18
SNP3.048	3		15,18
SNP3.051	3		15,17,18
SNP3.056	3		15,18
SNP3.059	3		15,18
SNP3.062	3		15,18
SNP3.065	3		14,15,17,18
SNP3.068	3		14,15,17,18
SNP3.076	3		15,18
SNP3.077	3		15,18
SNP3.078	3		15,18
SNP3.079	3		15,18
SNP3.082	3		15,18
SNP3.083	3		15
SNP3.084	3		15,18
SNP3.086	3		15,18
SNP3.088	3		15,18
SNP3.089	3		15,18
SNP3.090	3		15,18
SNP3.091	3		15,18
SNP3.095	3		15,18
SNP3.100	3		15
SNP3.108	3		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP3.115	3		15,18
SNP3.119	3		15,18
SNP3.120	3		15,18
SNP3.122	3		15,18
SNP3.123	3		15,18
SNP3.125	3		15,18
SNP3.126	3		15,18
SNP3.128	3		15,18
SNP3.131	3		15,18
SNP3.132	3		15,18
SNP3.133	3		15,18
SNP3.135	3		15,18
SNP3.136	3		15,18
SNP3.138	3		15,18
SNP3.139	3		15,18
SNP3.140	3		15,18
SNP3.141	3		15,18
SNP3.142	3		15,18
SNP3.145	3		15,18
SNP3.147	3		15,18
SNP3.148	3		15,18
SNP3.149	3		15,18
SNP3.151	3		15,18
SNP3.152	3		15,18
SNP3.153	3		15,18
SNP3.155	3		15,18
SNP3.162	3		18
SNP3.163	3		18
SNP3.164	3		18
SNP3.165	3		15,18
SNP3.166	3		18
SNP3.168	3		15,18
SNP3.169	3		15,18
SNP3.170	3		15,18
SNP3.172	3		15,18
SNP3.174	3		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP3.176	3		15,18
SNP3.177	3		15,18
SNP3.178	3		15,18
SNP3.182	3		15,18
SNP3.188	3		18
SNP3.191	3		15,18
SNP3.192	3		15,18
SNP3.194	3		15,18
SNP3.195	3		15,18
SNP3.196	3		15,18
SNP3.197	3		15,18
SNP3.198	3		15,18
SNP3.199	3		15,18
SNP3.201	3		15,18
SNP3.210	3		15,18
SNP3.212	3		15,18
SNP3.215	3		15,18
SNP3.217	3		15,18
SNP3.218	3		15,18
SNP3.223	3		18
SNP3.224	3		15,18
SNP3.225	3		15,18
SNP3.226	3		15,18
SNP3.227	3		15,18
SNP3.228	3		15,18
SNP3.229	3		15,18
SNP3.230	3		15,18
SNP3.231	3		15,18
SNP3.232	3		15,18
SNP3.233	3		15,18
SNP3.235	3		15,18
SNP3.237	3		15,18
SNP3.239	3		15,18
SNP3.249	3		15,18
SNP3.251	3		15,18
SNP3.252	3		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP3.256	3		15,18
SNP3.262	3		15,18
SNP3.263	3		15,18
SNP3.264	3		15,18
SNP3.265	3		15,18
SNP3.266	3		15,18
SNP3.267	3		15,18
SNP3.268	3		15,18
SNP3.269	3		15,18
SNP3.270	3		15,18
SNP3.272	3		15,18
SNP3.274	3		14,15,17,18
SNP3.277	3		15,18
SNP3.278	3		15
SNP3.279	3		15,18
SNP3.281	3		15,18
SNP3.282	3		15,18
SNP3.284	3		15,18
SNP3.285	3		15,18
SNP3.286	3		15,18
SNP3.290	3		15,18
SNP3.291	3		15,18
SNP3.293	3		15,18
SNP3.294	3		15,18
SNP3.296	3		15,18
SNP3.297	3		15,18
SNP3.298	3		15,18
SNP3.302	3		15,18
SNP3.306	3		15,18
SNP3.309	3		15,18
SNP3.312	3		15,18
SNP3.314	3		15,18
SNP3.317	3		15,18
SNP3.318	3		15,18
SNP3.319	3		15,18
SNP3.320	3		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP3.323	3		15,18
SNP3.324	3		15,18
SNP3.325	3		15,18
SNP3.327	3		15,18
SNP3.328	3		15,18
SNP3.329	3		15,18
SNP3.330	3		15,18
SNP3.331	3		15,18
SNP3.332	3		15,18
SNP3.334	3		15,18
SNP3.338	3		15,18
SNP3.339	3		15,18
SNP3.340	3		15,18
SNP3.342	3		15,18
SNP3.343	3		15,18
SNP3.346	3		15,18
SNP3.348	3		15,18
SNP3.350	3		15,18
SNP3.351	3		15,18
SNP3.352	3		15,18
SNP3.353	3		15,18
SNP3.354	3		15,18
SNP3.355	3		14,15,17,18
SNP3.356	3		14,15,17,18
SNP3.357	3		15,18
SNP4.030	4	BARC_1.01_Gm04_2045637_T_C	18
SNP4.246	4	BARC_1.01_Gm04_41667205_G_A	14,15
SNP4.260	4	BARC_1.01_Gm04_42935780_C_A	14,15,17,18
SNP4.270	4	BARC_1.01_Gm04_43566801_T_G	14,15,17,18
SNP4.287	4	BARC_1.01_Gm04_44394952_A_G	14,15,17,18
SNP4.290	4	BARC_1.01_Gm04_44751336_T_C	14,15,17,18
SNP4.294	4	BARC_1.01_Gm04_45123205_C_T	14,15,17,18
SNP4.295	4	BARC_1.01_Gm04_45147931_C_A	14,15,17,18
SNP4.310	4	BARC_1.01_Gm04_46062587_A_G	14,15,17,18
SNP4.321	4	BARC_1.01_Gm04_46639884_T_C	14,15,17,18
SNP4.327	4	BARC_1.01_Gm04_46966383_G_A	14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP4.001	4	BARC_1.01_Gm04_57542_C_A	14,15,17,18
SNP4.079	4	BARC_1.01_Gm04_5754268_T_C	15,18
SNP4.081	4	BARC_1.01_Gm04_6013342_A_C	14,15,17,18
SNP4.111	4	BARC_1.01_Gm04_8224272_G_A	14,15
SNP4.125	4	BARC_1.01_Gm04_9144856_G_T	14,15,17,18
SNP4.002	4		14,15,17,18
SNP4.012	4		14,15,17,18
SNP4.013	4		14,15,17
SNP4.014	4		14,15,17,18
SNP4.015	4		14,15,17
SNP4.028	4		15,17,18
SNP4.031	4		17,18
SNP4.036	4		14,15
SNP4.072	4		14,15,17,18
SNP4.082	4		14,15,17,18
SNP4.083	4		14,15,17,18
SNP4.084	4		14,15,17,18
SNP4.086	4		14,15,17,18
SNP4.089	4		14,15,17,18
SNP4.091	4		14,15,17,18
SNP4.092	4		15,18
SNP4.093	4		14,15,17,18
SNP4.096	4		14,15,17,18
SNP4.097	4		14,15,17,18
SNP4.098	4		14,15,17,18
SNP4.105	4		14,15,17,18
SNP4.108	4		14,15,17,18
SNP4.112	4		14,15,17,18
SNP4.114	4		14,15,17,18
SNP4.121	4		14,15,17,18
SNP4.122	4		14,15,17,18
SNP4.127	4		14,15,17,18
SNP4.126	4		14,15,17,18
SNP4.130	4		14,15,17,18
SNP4.133	4		14,15,17,18
SNP4.135	4		14,15



Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP4.144	4		14,15
SNP4.145	4		14,15,17,18
SNP4.151	4		15
SNP4.153	4		14,15,17,18
SNP4.155	4		14,15,17,18
SNP4.159	4		14,15,17,18
SNP4.170	4		14,15,17,18
SNP4.171	4		14,15,17,18
SNP4.173	4		14,15
SNP4.200	4		14,15,17,18
SNP4.185	4		14,15
SNP4.218	4		14,15,17,18
SNP4.224	4		14,15,17,18
SNP4.226	4		14,15,17,18
SNP4.225	4		14,15,17,18
SNP4.228	4		14,15
SNP4.232	4		14,15,17,18
SNP4.236	4		15
SNP4.247	4		14,15,17,18
SNP4.249	4		14,15,17,18
SNP4.251	4		14,15,17,18
SNP4.264	4		15,17
SNP4.271	4		14,15,17,18
SNP4.274	4		14,15,17,18
SNP4.276	4		14,15,17,18
SNP4.277	4		14,15,18
SNP4.279	4		14,15,17,18
SNP4.280	4		14,15,17,18
SNP4.281	4		14,15,17,18
SNP4.282	4		14,15,17,18
SNP4.283	4		14,15,17,18
SNP4.285	4		14,15,17,18
SNP4.296	4		14,15,17,18
SNP4.297	4		14,15,17,18
SNP4.298	4		14,15,17,18
SNP4.299	4		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP4.311	4		14,15,17,18
SNP4.313	4		14,15,17,18
SNP4.316	4		14,15,17,18
SNP4.317	4		14,15,17,18
SNP4.323	4		14,15,17,18
SNP4.326	4		14,15,17,18
SNP4.330	4		14,15,17,18
SNP4.334	4		14,15,17,18
SNP4.336	4		14,15,17,18
SNP4.343	4		14,15,17,18
SNP4.353	4		14,15
SNP4.358	4		14,15,17,18
SNP4.003	4		15,18
SNP4.006	4		15
SNP4.007	4		15
SNP4.008	4		15,18
SNP4.009	4		15,18
SNP4.010	4		15,18
SNP4.011	4		15,18
SNP4.025	4		15,18
SNP4.033	4		15,18
SNP4.035	4		18
SNP4.037	4		15,18
SNP4.038	4		15,18
SNP4.039	4		15,18
SNP4.040	4		15,18
SNP4.041	4		15,18
SNP4.042	4		15,18
SNP4.046	4		18
SNP4.047	4		18
SNP4.048	4		18
SNP4.049	4		18
SNP4.050	4		18
SNP4.051	4		18
SNP4.052	4		18
SNP4.071	4		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP4.074	4		18
SNP4.075	4		15,18
SNP4.076	4		18
SNP4.077	4		18
SNP4.078	4		15,18
SNP4.080	4		15,18
SNP4.085	4		15,18
SNP4.087	4		15,18
SNP4.088	4		15,18
SNP4.094	4		15,18
SNP4.095	4		15,18
SNP4.100	4		15,18
SNP4.101	4		15,18
SNP4.102	4		15,18
SNP4.104	4		15,18
SNP4.106	4		15,18
SNP4.107	4		15,18
SNP4.109	4		15,18
SNP4.110	4		15,18
SNP4.113	4		15,18
SNP4.115	4		15,18
SNP4.116	4		15,18
SNP4.117	4		15,18
SNP4.119	4		15,18
SNP4.120	4		15,18
SNP4.124	4		15,18
SNP4.129	4		15,18
SNP4.131	4		15,18
SNP4.134	4		15,18
SNP4.136	4		15,18
SNP4.137	4		15,18
SNP4.138	4		15,18
SNP4.139	4		15,18
SNP4.140	4		15,18
SNP4.142	4		15
SNP4.143	4		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP4.147	4		15,18
SNP4.148	4		15,18
SNP4.149	4		15
SNP4.150	4		15
SNP4.152	4		15,18
SNP4.154	4		15,18
SNP4.156	4		15,18
SNP4.157	4		15
SNP4.158	4		15,18
SNP4.160	4		15,18
SNP4.162	4		15,18
SNP4.164	4		15,18
SNP4.165	4		15,18
SNP4.166	4		15,18
SNP4.169	4		15,18
SNP4.172	4		15,18
SNP4.175	4		15,18
SNP4.176	4		15,18
SNP4.177	4		15,18
SNP4.178	4		15,18
SNP4.179	4		15,18
SNP4.180	4		15,18
SNP4.181	4		15,18
SNP4.182	4		15,18
SNP4.183	4		15,18
SNP4.184	4		15,18
SNP4.186	4		15,18
SNP4.188	4		15,18
SNP4.189	4		15,18
SNP4.190	4		15,18
SNP4.191	4		15,18
SNP4.192	4		15,18
SNP4.193	4		15,18
SNP4.194	4		15,18
SNP4.195	4		15,18
SNP4.196	4		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP4.199	4		15,18
SNP4.202	4		15,18
SNP4.203	4		15,18
SNP4.205	4		15,18
SNP4.206	4		15,18
SNP4.207	4		15,18
SNP4.208	4		15,18
SNP4.209	4		15,18
SNP4.213	4		15,18
SNP4.214	4		15,18
SNP4.215	4		15,18
SNP4.219	4		15,18
SNP4.220	4		15,18
SNP4.221	4		15,17,18
SNP4.222	4		15,18
SNP4.223	4		15,18
SNP4.229	4		15,18
SNP4.230	4		15,18
SNP4.231	4		15,18
SNP4.233	4		15,18
SNP4.235	4		15,18
SNP4.237	4		15,18
SNP4.240	4		15,18
SNP4.241	4		15,18
SNP4.242	4		15,18
SNP4.243	4		15,18
SNP4.244	4		15,18
SNP4.245	4		15,18
SNP4.248	4		15,18
SNP4.250	4		15,18
SNP4.252	4		15,18
SNP4.254	4		15,18
SNP4.255	4		15,18
SNP4.256	4		15,18
SNP4.257	4		15,18
SNP4.258	4		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP4.262	4		15,18
SNP4.263	4		15,18
SNP4.265	4		15,18
SNP4.266	4		14,15,17,18
SNP4.267	4		15,18
SNP4.268	4		14,15,18
SNP4.269	4		15,18
SNP4.272	4		15,18
SNP4.275	4		14,15,18
SNP4.278	4		15,18
SNP4.284	4		15,18
SNP4.286	4		15,18
SNP4.289	4		15,18
SNP4.292	4		15,18
SNP4.293	4		15,18
SNP4.301	4		15,18
SNP4.302	4		15,18
SNP4.304	4		15,18
SNP4.305	4		15,18
SNP4.307	4		15,18
SNP4.308	4		15,18
SNP4.309	4		15,18
SNP4.312	4		15,18
SNP4.314	4		15,18
SNP4.315	4		15,18
SNP4.318	4		15,18
SNP4.319	4		15,18
SNP4.320	4		15,18
SNP4.322	4		15,18
SNP4.324	4		15,18
SNP4.325	4		15,18
SNP4.328	4		18
SNP4.329	4		18
SNP4.331	4		15,18
SNP4.332	4		15,18
SNP4.333	4		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP4.337	4		18
SNP4.338	4		15,18
SNP4.339	4		15,18
SNP4.340	4		15,18
SNP4.341	4		15,18
SNP4.342	4		15,18
SNP4.345	4		15,18
SNP4.346	4		15,18
SNP4.347	4		15,18
SNP4.348	4		15,18
SNP4.351	4		15,18
SNP4.352	4		15,18
SNP4.356	4		15,18
SNP4.357	4		15,18
SNP4.360	4		15,18
SNP4.361	4		15,18
SNP4.362	4		15,18
SNP5.054	5	BARC_1.01_Gm05_1465819_C_A	14,15,17,18
SNP5.064	5	BARC_1.01_Gm05_2012649_T_C	14,15,17,18
SNP5.033	5	BARC_1.01_Gm05_266891_G_A	17,18
SNP5.127	5	BARC_1.01_Gm05_27637251_A_G	14,15,17,18
SNP5.173	5	BARC_1.01_Gm05_32654943_T_C	15,18
SNP5.211	5	BARC_1.01_Gm05_35086975_T_G	14,15,17,18
SNP5.242	5	BARC_1.01_Gm05_37084236_A_G	14,15,17,18
SNP5.253	5	BARC_1.01_Gm05_37781995_T_G	14,15,17,18
SNP5.257	5	BARC_1.01_Gm05_37964167_G_T	14,15,17,18
SNP5.313	5	BARC_1.01_Gm05_39083568_A_G	14,15,17,18
SNP5.298	5	BARC_1.01_Gm05_40036925_C_T	14,15,17,18
SNP5.289	5	BARC_1.01_Gm05_40421702_T_G	14,15,17,18
SNP5.094	5	BARC_1.01_Gm05_4043899_C_T	18
SNP5.018	5	BARC_1.01_Gm05_7943632_T_G	14,15,17,18
SNP5.001	5	BARC_1.01_Gm05_9097414_G_A	14,15,17,18
SNP5.028	5		14,15,17,18
SNP5.030	5		18
SNP5.035	5		14,15,17,18
SNP5.038	5		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP5.051	5		14,15,17,18
SNP5.052	5		14,15,17,18
SNP5.053	5		14,15
SNP5.056	5		14,15,17,18
SNP5.059	5		14,15,17,18
SNP5.066	5		14,15,17,18
SNP5.070	5		14,15,17,18
SNP5.071	5		14,15,17,18
SNP5.072	5		14,15,17,18
SNP5.073	5		15
SNP5.074	5		14,15,17,18
SNP5.078	5		14,15,17,18
SNP5.082	5		14,15,17,18
SNP5.083	5		14,15,17,18
SNP5.084	5		14,15,17,18
SNP5.090	5		14,15,17,18
SNP5.091	5		14,15,17,18
SNP5.095	5		14,15,17,18
SNP5.097	5		14,15
SNP5.098	5		14,15,17,18
SNP5.099	5		14,15,17,18
SNP5.017	5		14,15,17,18
SNP5.015	5		14,15,17,18
SNP5.010	5		14,15,17,18
SNP5.009	5		14,15,17,18
SNP5.007	5		14,15,17,18
SNP5.005	5		14,15,17,18
SNP5.003	5		14,15,17,18
SNP5.104	5		14,15,17,18
SNP5.102	5		14,15,17,18
SNP5.114	5		14,15,17,18
SNP5.117	5		15
SNP5.118	5		14,15,17
SNP5.128	5		14,15,17,18
SNP5.131	5		14,15,17,18
SNP5.132	5		14,15,17,18



Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP5.142	5		14,15,17,18
SNP5.147	5		14,15,17,18
SNP5.149	5		14,15,17,18
SNP5.153	5		14,15,17,18
SNP5.157	5		14,15
SNP5.159	5		18
SNP5.160	5		14,15,17,18
SNP5.161	5		14,15,17,18
SNP5.162	5		14,15,17,18
SNP5.165	5		14,15,17,18
SNP5.166	5		14,15,17,18
SNP5.167	5		14,15,17,18
SNP5.168	5		14,15,17,18
SNP5.169	5		14,15,17,18
SNP5.172	5		14,15,17,18
SNP5.174	5		14,15
SNP5.175	5		14,15
SNP5.176	5		14,15,17,18
SNP5.177	5		14,15,17,18
SNP5.178	5		14,17,18
SNP5.180	5		14,15
SNP5.184	5		14,15,17,18
SNP5.186	5		14,15,17,18
SNP5.187	5		14,15,17,18
SNP5.188	5		14,15,17,18
SNP5.189	5		14,15,17,18
SNP5.190	5		14,15,17,18
SNP5.191	5		14,15,17,18
SNP5.193	5		14,15,17,18
SNP5.194	5		14,15,17,18
SNP5.195	5		14,15,17,18
SNP5.197	5		14,15,17,18
SNP5.201	5		14,15,17,18
SNP5.202	5		14,15,17,18
SNP5.203	5		14,15,17,18
SNP5.217	5		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP5.219	5		14,15,17,18
SNP5.223	5		14,15,17,18
SNP5.224	5		14,15,17,18
SNP5.228	5		14,15,17,18
SNP5.229	5		14,15,17,18
SNP5.237	5		14,15,17,18
SNP5.238	5		14,15,17,18
SNP5.239	5		14
SNP5.252	5		14,15,18
SNP5.255	5		14,15,17,18
SNP5.256	5		14,15,18
SNP5.259	5		14,15
SNP5.321	5		14,15,17,18
SNP5.322	5		14,15,17,18
SNP5.320	5		14,15
SNP5.319	5		15,18
SNP5.318	5		14,15,17,18
SNP5.311	5		14,15
SNP5.310	5		14,15
SNP5.308	5		14,15
SNP5.301	5		14,15,17,18
SNP5.297	5		14,15,17,18
SNP5.296	5		14,15,17,18
SNP5.295	5		14,15,17,18
SNP5.293	5		14,15,17,18
SNP5.291	5		14,15,17,18
SNP5.290	5		14,15,17,18
SNP5.288	5		14,15
SNP5.284	5		14,15,17,18
SNP5.281	5		14,15,17,18
SNP5.280	5		14,15,17,18
SNP5.278	5		14,15,17,18
SNP5.277	5		14,15,17,18
SNP5.276	5		14,15,17,18
SNP5.275	5		14,15,17,18
SNP5.274	5		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP5.272	5		14,15,17,18
SNP5.270	5		14,15
SNP5.269	5		14,15
SNP5.264	5		14,15
SNP5.263	5		14,15
SNP5.262	5		14,15,17,18
SNP5.002	5		14,15,17,18
SNP5.004	5		15,18
SNP5.006	5		15
SNP5.008	5		17,18
SNP5.011	5		18
SNP5.013	5		15,18
SNP5.014	5		15,18
SNP5.019	5		15,18
SNP5.020	5		15,18
SNP5.021	5		15,18
SNP5.022	5		15,18
SNP5.023	5		15,18
SNP5.025	5		15,18
SNP5.027	5		15,18
SNP5.029	5		15,18
SNP5.031	5		15,18
SNP5.032	5		18
SNP5.034	5		15,18
SNP5.036	5		14,15,17,18
SNP5.040	5		15,18
SNP5.041	5		15,18
SNP5.042	5		15,18
SNP5.043	5		14,15,17,18
SNP5.044	5		14,15,17,18
SNP5.047	5		18
SNP5.048	5		15,18
SNP5.050	5		15
SNP5.055	5		15,18
SNP5.057	5		15,18
SNP5.058	5		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP5.061	5		15,18
SNP5.065	5		15,18
SNP5.075	5		15,18
SNP5.076	5		18
SNP5.077	5		15,18
SNP5.079	5		15,18
SNP5.080	5		15,18
SNP5.081	5		15,18
SNP5.085	5		18
SNP5.086	5		18
SNP5.087	5		18
SNP5.088	5		18
SNP5.089	5		18
SNP5.092	5		18
SNP5.093	5		18
SNP5.096	5		15,18
SNP5.101	5		15,18
SNP5.105	5		15
SNP5.107	5		15
SNP5.108	5		15
SNP5.109	5		15
SNP5.110	5		15,18
SNP5.111	5		15
SNP5.112	5		15,18
SNP5.113	5		15,18
SNP5.115	5		15
SNP5.116	5		15,18
SNP5.119	5		15
SNP5.120	5		15
SNP5.121	5		15,18
SNP5.122	5		15,18
SNP5.123	5		15,18
SNP5.124	5		15,18
SNP5.125	5		15,18
SNP5.126	5		15,18
SNP5.129	5		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP5.134	5		15
SNP5.135	5		15
SNP5.136	5		15
SNP5.137	5		15
SNP5.140	5		15,18
SNP5.141	5		15,18
SNP5.143	5		15,18
SNP5.145	5		15,18
SNP5.151	5		15,18
SNP5.152	5		15,18
SNP5.154	5		18
SNP5.156	5		15,18
SNP5.158	5		18
SNP5.171	5		15,18
SNP5.179	5		18
SNP5.181	5		18
SNP5.182	5		18
SNP5.183	5		15,18
SNP5.196	5		15,18
SNP5.199	5		15,18
SNP5.200	5		15,18
SNP5.205	5		15,18
SNP5.206	5		15,18
SNP5.207	5		15,18
SNP5.208	5		15,18
SNP5.209	5		18
SNP5.210	5		15,18
SNP5.212	5		15,18
SNP5.214	5		18
SNP5.215	5		18
SNP5.216	5		15,18
SNP5.220	5		15,18
SNP5.222	5		15,18
SNP5.231	5		15,18
SNP5.232	5		15,18
SNP5.233	5		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP5.236	5		15,18
SNP5.240	5		15,18
SNP5.243	5		15,18
SNP5.244	5		15
SNP5.245	5		15,18
SNP5.246	5		15,18
SNP5.248	5		15,18
SNP5.249	5		15,18
SNP5.250	5		15,18
SNP5.251	5		15,18
SNP5.260	5		15,18
SNP5.261	5		15,18
SNP5.265	5		15
SNP5.266	5		15
SNP5.267	5		15
SNP5.268	5		15
SNP5.273	5		15,18
SNP5.279	5		15,18
SNP5.282	5		15,18
SNP5.283	5		15,18
SNP5.285	5		15,18
SNP5.287	5		15,18
SNP5.292	5		15,18
SNP5.294	5		15,18
SNP5.302	5		15,18
SNP5.304	5		15,18
SNP5.307	5		15
SNP5.309	5		15,18
SNP5.312	5		15,18
SNP5.314	5		15
SNP5.315	5		15
SNP5.316	5		15
SNP5.317	5		15
SNP6.129	6	BARC_1.01_Gm06_11337170_C_T	14,15,17,18
SNP6.132	6	BARC_1.01_Gm06_11659627_A_G	14,15,17,18
SNP6.165	6	BARC_1.01_Gm06_13697072_T_C	14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP6.179	6	BARC_1.01_Gm06_14247209_T_G	14,15,18
SNP6.191	6	BARC_1.01_Gm06_14849154_A_C	14,15,17,18
SNP6.218	6	BARC_1.01_Gm06_16391391_G_A	14,15,17,18
SNP6.219	6	BARC_1.01_Gm06_16407652_T_C	14,15,17,18
SNP6.055	6	BARC_1.01_Gm06_4422517_A_G	14,15,17,18
SNP6.360	6	BARC_1.01_Gm06_46980915_T_G	14,15,17,18
SNP6.386	6	BARC_1.01_Gm06_48475049_C_T	14,15
SNP6.393	6	BARC_1.01_Gm06_48737145_A_G	14,15,17
SNP6.396	6	BARC_1.01_Gm06_48940023_G_A	14,15,18
SNP6.398	6	BARC_1.01_Gm06_49064024_G_T	14,15,17
SNP6.082	6	BARC_1.01_Gm06_7003339_A_C	14,15,17,18
SNP6.009	6	BARC_1.01_Gm06_825788_G_T	14,15,17,18
SNP6.002	6		15,17,18
SNP6.014	6		14,15,17,18
SNP6.016	6		14,15
SNP6.019	6		14,15,17,18
SNP6.023	6		14,15
SNP6.030	6		14,15,17,18
SNP6.031	6		14,15,17,18
SNP6.033	6		14,15,17,18
SNP6.037	6		14,15
SNP6.042	6		14,15,17,18
SNP6.058	6		14,15,17,18
SNP6.062	6		14,15
SNP6.063	6		14,15,17,18
SNP6.067	6		14,15,17,18
SNP6.072	6		14,15,17,18
SNP6.074	6		14,15,17,18
SNP6.079	6		14,15,17,18
SNP6.086	6		15
SNP6.090	6		15
SNP6.091	6		14,15,17,18
SNP6.095	6		14,15,17,18
SNP6.100	6		14,15
SNP6.102	6		14,15,17,18
SNP6.103	6		14,15

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP6.109	6		14,15,17,18
SNP6.113	6		14,15,17,18
SNP6.114	6		14,15,17,18
SNP6.115	6		14,15
SNP6.116	6		14,15,17,18
SNP6.117	6		14,15
SNP6.121	6		14,15,17,18
SNP6.122	6		14,15,17,18
SNP6.125	6		14,15,17,18
SNP6.128	6		14,15,17,18
SNP6.130	6		14,15,17,18
SNP6.133	6		14,15,17,18
SNP6.137	6		14,15,17,18
SNP6.139	6		14,15,17,18
SNP6.143	6		14,15,17,18
SNP6.157	6		14,15,17,18
SNP6.162	6		14,15,17,18
SNP6.167	6		14,15,17,18
SNP6.172	6		14,15,17,18
SNP6.174	6		14,15,17,18
SNP6.176	6		14,17
SNP6.192	6		14,15,17,18
SNP6.206	6		15,18
SNP6.208	6		14,15
SNP6.212	6		15,18
SNP6.213	6		14,15,17,18
SNP6.214	6		14,15,17,18
SNP6.215	6		14,15,17,18
SNP6.217	6		15,18
SNP6.220	6		14,15,17,18
SNP6.221	6		14,15,17,18
SNP6.222	6		14,15,17,18
SNP6.223	6		14,15,17,18
SNP6.224	6		14,15,17,18
SNP6.225	6		14,15,17,18
SNP6.226	6		14,15,17,18



Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP6.228	6		14,15
SNP6.229	6		14,15,17,18
SNP6.235	6		14,15,17,18
SNP6.238	6		14,15,17,18
SNP6.240	6		14,15,17,18
SNP6.246	6		14,15,17,18
SNP6.247	6		14,15,17,18
SNP6.260	6		14,15,17,18
SNP6.264	6		14,15,17,18
SNP6.268	6		14,15,17,18
SNP6.272	6		14,15,17,18
SNP6.276	6		14,15,17,18
SNP6.277	6		14,15,17,18
SNP6.279	6		14,15,17,18
SNP6.290	6		14,15,17,18
SNP6.293	6		14,15,17,18
SNP6.296	6		14,15,17,18
SNP6.297	6		17,18
SNP6.312	6		14,15,17,18
SNP6.321	6		14,15,17,18
SNP6.326	6		14,15,17,18
SNP6.334	6		14,15,17,18
SNP6.343	6		14,15,17,18
SNP6.346	6		14,15,17,18
SNP6.351	6		14,15
SNP6.352	6		14,15,17,18
SNP6.354	6		14,15
SNP6.356	6		14,15,17
SNP6.358	6		14,15,17
SNP6.359	6		14,15,17
SNP6.361	6		14,15,17,18
SNP6.368	6		14,15
SNP6.369	6		14,15,17,18
SNP6.370	6		14,15,17,18
SNP6.371	6		14,15,17,18
SNP6.381	6		14,15,17

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP6.392	6		14,15,17
SNP6.394	6		17,18
SNP6.397	6		14,15,17
SNP6.399	6		15,18
SNP6.401	6		14,15,17,18
SNP6.403	6		14,15
SNP6.411	6		15,17,18
SNP6.413	6		15,18
SNP6.414	6		14,15,17,18
SNP6.003	6		15,18
SNP6.004	6		15,18
SNP6.005	6		15,18
SNP6.006	6		15,18
SNP6.007	6		15,18
SNP6.008	6		15,18
SNP6.010	6		15,18
SNP6.011	6		15,18
SNP6.012	6		15,18
SNP6.013	6		15,18
SNP6.015	6		15,18
SNP6.017	6		15,18
SNP6.018	6		15,18
SNP6.020	6		15,18
SNP6.021	6		15,18
SNP6.024	6		15,18
SNP6.025	6		15,18
SNP6.028	6		15,18
SNP6.029	6		15,18
SNP6.040	6		15,18
SNP6.041	6		15,18
SNP6.043	6		15,18
SNP6.044	6		15,18
SNP6.045	6		15,18
SNP6.046	6		15,18
SNP6.048	6		15,18
SNP6.049	6		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP6.051	6		15,18
SNP6.056	6		15,18
SNP6.057	6		15,18
SNP6.059	6		15,18
SNP6.061	6		15,18
SNP6.066	6		15,18
SNP6.068	6		15,18
SNP6.071	6		15,18
SNP6.073	6		15,18
SNP6.075	6		15,18
SNP6.076	6		15,18
SNP6.080	6		15,18
SNP6.081	6		15,18
SNP6.083	6		15,18
SNP6.084	6		15,18
SNP6.085	6		15,18
SNP6.087	6		15
SNP6.088	6		15
SNP6.089	6		15
SNP6.092	6		15,18
SNP6.093	6		15,18
SNP6.094	6		15,18
SNP6.096	6		15,18
SNP6.099	6		15,18
SNP6.101	6		15,18
SNP6.104	6		15,18
SNP6.106	6		15,18
SNP6.107	6		15,18
SNP6.108	6		15,18
SNP6.110	6		15,18
SNP6.111	6		15,18
SNP6.112	6		15,18
SNP6.123	6		15,18
SNP6.124	6		15,18
SNP6.126	6		15,18
SNP6.127	6		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP6.134	6		15,18
SNP6.135	6		15,18
SNP6.136	6		15,18
SNP6.138	6		15,18
SNP6.140	6		15,18
SNP6.141	6		15,18
SNP6.144	6		15,18
SNP6.146	6		15,18
SNP6.147	6		15,18
SNP6.148	6		15,18
SNP6.149	6		15,18
SNP6.150	6		15,18
SNP6.151	6		15,18
SNP6.152	6		15,18
SNP6.154	6		15,18
SNP6.155	6		15,18
SNP6.156	6		15,18
SNP6.158	6		15,18
SNP6.159	6		15,18
SNP6.160	6		15,18
SNP6.161	6		15,18
SNP6.163	6		15,18
SNP6.164	6		14,15,18
SNP6.166	6		15,18
SNP6.168	6		14,15,18
SNP6.169	6		14,15,18
SNP6.170	6		15,18
SNP6.171	6		14,15,18
SNP6.173	6		14,15,18
SNP6.175	6		15,18
SNP6.178	6		14,15,18
SNP6.180	6		14,15,18
SNP6.181	6		14,15,18
SNP6.182	6		15,18
SNP6.183	6		15,18
SNP6.184	6		14,15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP6.186	6		15,18
SNP6.187	6		15,18
SNP6.188	6		15,18
SNP6.189	6		15,18
SNP6.190	6		15,18
SNP6.193	6		15,18
SNP6.194	6		15,18
SNP6.195	6		15
SNP6.198	6		15,18
SNP6.199	6		15
SNP6.200	6		15,18
SNP6.201	6		15,18
SNP6.202	6		18
SNP6.204	6		18
SNP6.205	6		18
SNP6.207	6		15,18
SNP6.209	6		15,18
SNP6.211	6		15,18
SNP6.216	6		15,18
SNP6.230	6		15,18
SNP6.232	6		15,18
SNP6.236	6		15,18
SNP6.237	6		15,18
SNP6.239	6		15,18
SNP6.241	6		15,18
SNP6.242	6		15,18
SNP6.243	6		15,18
SNP6.244	6		15,18
SNP6.245	6		15,18
SNP6.248	6		15,18
SNP6.249	6		15,18
SNP6.250	6		15,18
SNP6.251	6		15,18
SNP6.252	6		15,18
SNP6.253	6		15,18
SNP6.254	6		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP6.256	6		15,18
SNP6.257	6		15,18
SNP6.259	6		14,15,17,18
SNP6.261	6		15,18
SNP6.263	6		15,18
SNP6.265	6		15,18
SNP6.267	6		15,18
SNP6.269	6		15,18
SNP6.270	6		15,18
SNP6.271	6		15,18
SNP6.273	6		15,18
SNP6.275	6		15,18
SNP6.278	6		15,18
SNP6.280	6		15,18
SNP6.281	6		15,18
SNP6.282	6		15,18
SNP6.283	6		15,18
SNP6.284	6		15,18
SNP6.285	6		15,18
SNP6.286	6		15
SNP6.287	6		15,18
SNP6.288	6		15,18
SNP6.289	6		15,18
SNP6.291	6		15,18
SNP6.292	6		15,18
SNP6.294	6		15,18
SNP6.295	6		15,18
SNP6.298	6		15,18
SNP6.299	6		15,18
SNP6.300	6		15,18
SNP6.301	6		15,18
SNP6.302	6		15,18
SNP6.303	6		15,18
SNP6.304	6		15,18
SNP6.305	6		15,18
SNP6.306	6		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP6.308	6		15,18
SNP6.309	6		15,18
SNP6.310	6		15,18
SNP6.311	6		15,18
SNP6.313	6		15,18
SNP6.314	6		15,18
SNP6.315	6		15,18
SNP6.316	6		15,18
SNP6.317	6		15,18
SNP6.318	6		15,18
SNP6.319	6		15,18
SNP6.320	6		15,18
SNP6.322	6		15,18
SNP6.323	6		15,18
SNP6.324	6		15,18
SNP6.325	6		15,18
SNP6.327	6		15,18
SNP6.328	6		15,18
SNP6.329	6		15,18
SNP6.330	6		15,18
SNP6.331	6		15,18
SNP6.332	6		15,18
SNP6.333	6		15,18
SNP6.335	6		15,18
SNP6.336	6		15,18
SNP6.337	6		15,18
SNP6.338	6		15,18
SNP6.339	6		15,18
SNP6.340	6		15,18
SNP6.341	6		15
SNP6.342	6		15,18
SNP6.344	6		15,18
SNP6.345	6		15,18
SNP6.347	6		15,18
SNP6.348	6		15
SNP6.349	6		15

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP6.353	6		15,18
SNP6.355	6		15,18
SNP6.362	6		15,18
SNP6.363	6		15
SNP6.364	6		15,18
SNP6.365	6		15,18
SNP6.366	6		15
SNP6.367	6		15,18
SNP6.372	6		15,18
SNP6.373	6		15,18
SNP6.374	6		15,18
SNP6.375	6		15
SNP6.376	6		15,18
SNP6.377	6		15,18
SNP6.378	6		15
SNP6.379	6		15
SNP6.380	6		15
SNP6.382	6		15
SNP6.384	6		15,18
SNP6.385	6		15
SNP6.387	6		15
SNP6.390	6		15
SNP6.395	6		15,18
SNP6.400	6		15,18
SNP6.406	6		15,18
SNP6.407	6		15,18
SNP6.408	6		15,18
SNP6.412	6		15,18
SNP6.415	6		15,18
SNP6.416	6		15
SNP6.417	6		15,18
SNP6.418	6		15,18
SNP6.419	6		15,18
SNP6.420	6		15,18
SNP6.421	6		15,18
SNP6.422	6		15,18



Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP7.154	7	BARC_1.01_Gm07_10193199_G_A	14,15,17,18
SNP7.166	7	BARC_1.01_Gm07_13848426_A_G	14,15
SNP7.239	7	BARC_1.01_Gm07_19797313_A_G	18
SNP7.037	7	BARC_1.01_Gm07_3009018_G_A	14,15,17,18
SNP7.312	7	BARC_1.01_Gm07_36774827_C_T	15,17
SNP7.317	7	BARC_1.01_Gm07_36942235_C_T	14,15,17,18
SNP7.326	7	BARC_1.01_Gm07_37250989_T_C	14,15,17
SNP7.342	7	BARC_1.01_Gm07_38095213_G_A	14,15,17,18
SNP7.379	7	BARC_1.01_Gm07_42101622_A_G	15,18
SNP7.391	7	BARC_1.01_Gm07_42923420_G_A	14,15,17,18
SNP7.074	7	BARC_1.01_Gm07_5602544_A_G	14,15,17,18
SNP7.112	7	BARC_1.01_Gm07_7653599_C_T	14,15,18
SNP7.009	7		15,17,18
SNP7.015	7		14,15,17,18
SNP7.024	7		15,17
SNP7.031	7		14,15,17,18
SNP7.036	7		14,15,17,18
SNP7.038	7		14,15,17,18
SNP7.039	7		14,15,17,18
SNP7.040	7		14,15,17,18
SNP7.041	7		14,15,17,18
SNP7.043	7		14,15
SNP7.046	7		14,15,17,18
SNP7.047	7		14,15
SNP7.050	7		14,15,17,18
SNP7.057	7		14,15,17,18
SNP7.060	7		14,15,17,18
SNP7.067	7		14,15
SNP7.069	7		14,15,17,18
SNP7.071	7		14,15
SNP7.072	7		14,15,17,18
SNP7.080	7		14,15,17,18
SNP7.082	7		14,15,17,18
SNP7.083	7		14,15,17,18
SNP7.087	7		14,15,17,18
SNP7.093	7		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP7.103	7		14,15,17,18
SNP7.105	7		14,17,18
SNP7.107	7		14,15,17,18
SNP7.114	7		14,15,17,18
SNP7.123	7		14,15
SNP7.124	7		14,15,17,18
SNP7.125	7		14,15,17,18
SNP7.129	7		14,15,17,18
SNP7.133	7		14,15,17,18
SNP7.141	7		14,15,17,18
SNP7.144	7		14,15,17,18
SNP7.148	7		14,15,17,18
SNP7.149	7		14,15,17,18
SNP7.151	7		14,15,17,18
SNP7.162	7		14,15,17,18
SNP7.164	7		14,15,17,18
SNP7.167	7		14,15
SNP7.169	7		15
SNP7.176	7		14,15,17,18
SNP7.182	7		17,18
SNP7.190	7		14,15,17,18
SNP7.208	7		14,15,17,18
SNP7.209	7		14,15,17,18
SNP7.210	7		14,15,17,18
SNP7.216	7		14,15,17,18
SNP7.221	7		14,15,17,18
SNP7.235	7		14,15,17,18
SNP7.240	7		14,15,17,18
SNP7.241	7		14,15,17,18
SNP7.243	7		18
SNP7.247	7		18
SNP7.251	7		14,15,17,18
SNP7.262	7		14,15,17,18
SNP7.269	7		14,15,17,18
SNP7.272	7		14,15,17,18
SNP7.276	7		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP7.279	7		14,15,17,18
SNP7.290	7		14,15,17,18
SNP7.297	7		14,15,17,18
SNP7.314	7		15,17
SNP7.315	7		14,15,17,18
SNP7.316	7		14,15,17,18
SNP7.318	7		14,15,17,18
SNP7.319	7		14,15,17,18
SNP7.322	7		14,15
SNP7.323	7		14,15
SNP7.324	7		14,15,17
SNP7.325	7		14,15,17
SNP7.327	7		14,15,17,18
SNP7.328	7		14,15
SNP7.329	7		14,15,17
SNP7.330	7		14,15,17
SNP7.331	7		14,15,17,18
SNP7.333	7		14,15,17,18
SNP7.336	7		15,18
SNP7.337	7		14,15,17,18
SNP7.348	7		14,15,17,18
SNP7.356	7		14,15,17,18
SNP7.357	7		14,15,17
SNP7.358	7		14,15,17
SNP7.360	7		14,15,17,18
SNP7.362	7		14,15,17,18
SNP7.363	7		14,15,17,18
SNP7.368	7		14,15,17,18
SNP7.371	7		14,15,17,18
SNP7.372	7		14,15,17,18
SNP7.374	7		14,15,17,18
SNP7.377	7		14,15,17,18
SNP7.378	7		14,15,17,18
SNP7.380	7		14,15,17,18
SNP7.383	7		14,15,17,18
SNP7.386	7		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP7.388	7		14,15,17,18
SNP7.394	7		14,15,17,18
SNP7.399	7		14,15,17,18
SNP7.400	7		14,15,17,18
SNP7.401	7		14,15,17,18
SNP7.402	7		14,15,17,18
SNP7.404	7		14,15,17,18
SNP7.004	7		15,18
SNP7.005	7		15,18
SNP7.008	7		15,18
SNP7.011	7		18
SNP7.016	7		15,18
SNP7.017	7		15,18
SNP7.018	7		15,18
SNP7.020	7		18
SNP7.027	7		15,18
SNP7.032	7		15,18
SNP7.033	7		15,18
SNP7.034	7		15,18
SNP7.035	7		15,18
SNP7.042	7		15,18
SNP7.045	7		15,18
SNP7.048	7		15,18
SNP7.049	7		15,18
SNP7.052	7		14,15,17,18
SNP7.056	7		15,18
SNP7.058	7		15,18
SNP7.059	7		15,18
SNP7.061	7		15,18
SNP7.062	7		15
SNP7.064	7		15
SNP7.065	7		15
SNP7.066	7		15
SNP7.078	7		15,18
SNP7.079	7		15,18
SNP7.081	7		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP7.085	7		15,18
SNP7.086	7		15,18
SNP7.088	7		15,18
SNP7.089	7		15,18
SNP7.090	7		15,18
SNP7.091	7		15,18
SNP7.092	7		15,18
SNP7.094	7		15,18
SNP7.096	7		18
SNP7.097	7		15,18
SNP7.098	7		15,18
SNP7.099	7		15
SNP7.100	7		18
SNP7.101	7		15,18
SNP7.104	7		15,18
SNP7.106	7		15,18
SNP7.108	7		15,18
SNP7.110	7		15,18
SNP7.111	7		15,18
SNP7.113	7		15,18
SNP7.115	7		18
SNP7.116	7		15,18
SNP7.117	7		15,18
SNP7.118	7		15,18
SNP7.119	7		15,18
SNP7.120	7		15,18
SNP7.121	7		15,18
SNP7.122	7		15,18
SNP7.126	7		15,18
SNP7.127	7		15,18
SNP7.128	7		15,18
SNP7.130	7		15,18
SNP7.131	7		15,18
SNP7.132	7		15,18
SNP7.134	7		15,18
SNP7.135	7		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP7.137	7		15,18
SNP7.138	7		15,18
SNP7.140	7		18
SNP7.142	7		15,18
SNP7.143	7		15,18
SNP7.145	7		15,18
SNP7.146	7		15,18
SNP7.147	7		15,18
SNP7.150	7		15,18
SNP7.155	7		15,18
SNP7.156	7		15,18
SNP7.157	7		15,18
SNP7.158	7		15,18
SNP7.159	7		15,18
SNP7.160	7		15,18
SNP7.161	7		15,18
SNP7.163	7		15,18
SNP7.168	7		15,18
SNP7.170	7		18
SNP7.171	7		18
SNP7.172	7		18
SNP7.173	7		18
SNP7.174	7		18
SNP7.175	7		18
SNP7.177	7		18
SNP7.178	7		18
SNP7.179	7		18
SNP7.180	7		18
SNP7.181	7		18
SNP7.183	7		18
SNP7.184	7		18
SNP7.185	7		18
SNP7.187	7		18
SNP7.188	7		15,18
SNP7.189	7		15,18
SNP7.199	7		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP7.201	7		18
SNP7.203	7		15,18
SNP7.204	7		15
SNP7.205	7		15
SNP7.206	7		15,18
SNP7.207	7		15,18
SNP7.212	7		15,18
SNP7.213	7		15,18
SNP7.214	7		15,18
SNP7.215	7		15,18
SNP7.218	7		15,18
SNP7.219	7		15,18
SNP7.220	7		15,18
SNP7.222	7		15,18
SNP7.224	7		15,18
SNP7.225	7		15,18
SNP7.226	7		15,18
SNP7.227	7		15,18
SNP7.228	7		15,18
SNP7.229	7		15,18
SNP7.230	7		15,18
SNP7.231	7		15,18
SNP7.232	7		15,18
SNP7.233	7		15,18
SNP7.234	7		15,18
SNP7.236	7		15,18
SNP7.237	7		15,18
SNP7.238	7		18
SNP7.242	7		18
SNP7.244	7		18
SNP7.245	7		18
SNP7.248	7		18
SNP7.249	7		18
SNP7.250	7		18
SNP7.252	7		18
SNP7.253	7		18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP7.255	7		18
SNP7.256	7		18
SNP7.257	7		18
SNP7.258	7		18
SNP7.259	7		18
SNP7.260	7		18
SNP7.261	7		18
SNP7.263	7		18
SNP7.265	7		18
SNP7.267	7		18
SNP7.268	7		18
SNP7.270	7		18
SNP7.273	7		18
SNP7.274	7		15,18
SNP7.275	7		15,18
SNP7.278	7		15,18
SNP7.280	7		15,18
SNP7.281	7		15,18
SNP7.282	7		15,18
SNP7.283	7		15,18
SNP7.284	7		15,18
SNP7.285	7		15,18
SNP7.286	7		15,18
SNP7.287	7		15,18
SNP7.288	7		15,18
SNP7.289	7		15,18
SNP7.291	7		15,18
SNP7.292	7		15,18
SNP7.293	7		15,18
SNP7.294	7		15,18
SNP7.295	7		15,18
SNP7.296	7		15,18
SNP7.304	7		15
SNP7.306	7		15,18
SNP7.310	7		15
SNP7.320	7		15



Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP7.340	7		15,18
SNP7.343	7		15,18
SNP7.345	7		15,18
SNP7.346	7		15,18
SNP7.347	7		15,18
SNP7.353	7		15,18
SNP7.354	7		15,18
SNP7.359	7		15,18
SNP7.361	7		15,18
SNP7.364	7		15,18
SNP7.365	7		18
SNP7.366	7		15,18
SNP7.369	7		15,18
SNP7.370	7		15,18
SNP7.373	7		15,18
SNP7.375	7		18
SNP7.376	7		18
SNP7.384	7		15
SNP7.385	7		15,18
SNP7.389	7		15,18
SNP7.390	7		15,18
SNP7.393	7		15,18
SNP7.395	7		15,18
SNP7.396	7		15,18
SNP7.398	7		15,18
SNP7.403	7		15,18
SNP8.097	8	BARC_1.01_Gm08_10303031_C_T	14,15,17,18
SNP8.101	8	BARC_1.01_Gm08_10507567_A_G	15,18
SNP8.116	8	BARC_1.01_Gm08_11922354_T_C	14,15,17,18
SNP8.117	8	BARC_1.01_Gm08_12022663_C_T	14,15
SNP8.136	8	BARC_1.01_Gm08_13509852_T_G	14,15
SNP8.169	8	BARC_1.01_Gm08_16839374_G_T	14,15,17,18
SNP8.288	8	BARC_1.01_Gm08_37464144_A_G	17,18
SNP8.039	8	BARC_1.01_Gm08_3985008_T_C	14,15,17,18
SNP8.318	8	BARC_1.01_Gm08_42542473_G_A	14,15,17,18
SNP8.344	8	BARC_1.01_Gm08_44514044_C_A	14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP8.369	8	BARC_1.01_Gm08_46236506_A_C	14,15
SNP8.004	8		14,15,17,18
SNP8.008	8		14,15,17,18
SNP8.009	8		14,15,17,18
SNP8.010	8		14,15,17,18
SNP8.012	8		15,18
SNP8.027	8		14,15,17,18
SNP8.031	8		14,15,17,18
SNP8.034	8		14
SNP8.045	8		14,15,17,18
SNP8.051	8		14,15,17,18
SNP8.053	8		14,15
SNP8.054	8		14,15,17,18
SNP8.055	8		14,15,17,18
SNP8.057	8		14,15,17,18
SNP8.074	8		18
SNP8.105	8		14,15,17,18
SNP8.106	8		14
SNP8.107	8		14
SNP8.123	8		14,15,17,18
SNP8.124	8		14,15,17,18
SNP8.127	8		14,15
SNP8.128	8		14,15,17,18
SNP8.141	8		14,15,17,18
SNP8.147	8		14,15,17,18
SNP8.150	8		14,15,17,18
SNP8.151	8		14,15
SNP8.154	8		14,15,17,18
SNP8.155	8		14,15
SNP8.156	8		18
SNP8.159	8		14,15,17,18
SNP8.162	8		14,15
SNP8.163	8		14,15,17,18
SNP8.166	8		14,15,17,18
SNP8.176	8		14,15
SNP8.180	8		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP8.185	8		14,15,18
SNP8.187	8		14,15,17,18
SNP8.189	8		14,15
SNP8.190	8		14,15,17,18
SNP8.191	8		14,15,17,18
SNP8.192	8		14,15,17,18
SNP8.195	8		14,15,17,18
SNP8.196	8		14,15,17,18
SNP8.211	8		14,15,17,18
SNP8.213	8		14,15,17,18
SNP8.217	8		14,15,17,18
SNP8.220	8		14,15,17,18
SNP8.221	8		14,15,17,18
SNP8.224	8		14,15,17,18
SNP8.227	8		14,15,17,18
SNP8.232	8		14,15,17,18
SNP8.234	8		14,15,17,18
SNP8.242	8		14,15,17,18
SNP8.247	8		14,15,17,18
SNP8.252	8		14,15,17,18
SNP8.253	8		14,15,17,18
SNP8.254	8		14,15,17,18
SNP8.259	8		14,15,17,18
SNP8.260	8		14,15,17,18
SNP8.272	8		14,15,17,18
SNP8.273	8		14,15,17,18
SNP8.279	8		14,15,17,18
SNP8.280	8		14,15,17,18
SNP8.281	8		14,15,17,18
SNP8.294	8		14,15,17,18
SNP8.325	8		14,15
SNP8.327	8		14,15
SNP8.333	8		14,15,17,18
SNP8.340	8		14,15
SNP8.349	8		14,15,17,18
SNP8.350	8		14,15

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP8.001	8		15,18
SNP8.002	8		15,18
SNP8.003	8		15,18
SNP8.005	8		15,18
SNP8.006	8		15,18
SNP8.007	8		15,18
SNP8.011	8		15,18
SNP8.013	8		15,18
SNP8.015	8		15,18
SNP8.018	8		18
SNP8.022	8		15,18
SNP8.023	8		15,18
SNP8.024	8		15,18
SNP8.025	8		15
SNP8.026	8		15,18
SNP8.028	8		15,18
SNP8.029	8		15,18
SNP8.030	8		15,18
SNP8.035	8		18
SNP8.040	8		15,18
SNP8.044	8		15,18
SNP8.046	8		15,18
SNP8.047	8		15,18
SNP8.048	8		15,18
SNP8.049	8		15,18
SNP8.050	8		15,18
SNP8.052	8		15,18
SNP8.056	8		15
SNP8.059	8		18
SNP8.060	8		15,18
SNP8.062	8		18
SNP8.063	8		15,18
SNP8.064	8		15,18
SNP8.065	8		15,18
SNP8.068	8		18
SNP8.069	8		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP8.071	8		18
SNP8.072	8		18
SNP8.073	8		18
SNP8.075	8		15,18
SNP8.078	8		15,18
SNP8.082	8		15,18
SNP8.083	8		15,18
SNP8.098	8		15,18
SNP8.099	8		15,18
SNP8.100	8		18
SNP8.102	8		15,18
SNP8.103	8		18
SNP8.104	8		15,18
SNP8.108	8		15,18
SNP8.109	8		15,18
SNP8.110	8		15,18
SNP8.111	8		15,18
SNP8.112	8		15
SNP8.113	8		15,18
SNP8.114	8		15,18
SNP8.115	8		15
SNP8.119	8		15
SNP8.120	8		15
SNP8.121	8		15
SNP8.122	8		15
SNP8.126	8		15
SNP8.129	8		15
SNP8.130	8		15,18
SNP8.131	8		15
SNP8.132	8		15
SNP8.133	8		15
SNP8.134	8		15
SNP8.138	8		15
SNP8.142	8		15,18
SNP8.143	8		15,18
SNP8.144	8		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP8.146	8		15,18
SNP8.148	8		15,18
SNP8.149	8		15,18
SNP8.152	8		15,18
SNP8.153	8		15,18
SNP8.158	8		15,18
SNP8.160	8		15,18
SNP8.161	8		15,18
SNP8.167	8		18
SNP8.168	8		15,18
SNP8.170	8		15,18
SNP8.171	8		15,18
SNP8.177	8		15,18
SNP8.178	8		15,18
SNP8.179	8		15,18
SNP8.181	8		15,18
SNP8.182	8		15,18
SNP8.183	8		15,18
SNP8.188	8		18
SNP8.193	8		15,18
SNP8.194	8		18
SNP8.199	8		15,18
SNP8.200	8		15,18
SNP8.201	8		15,18
SNP8.202	8		15,18
SNP8.203	8		15,18
SNP8.204	8		15,18
SNP8.205	8		15,18
SNP8.206	8		15,18
SNP8.207	8		15,18
SNP8.208	8		15,18
SNP8.209	8		15,18
SNP8.210	8		15,18
SNP8.212	8		15,18
SNP8.214	8		15,18
SNP8.215	8		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP8.218	8		15,18
SNP8.219	8		15,18
SNP8.222	8		15,18
SNP8.223	8		15,18
SNP8.225	8		15,18
SNP8.226	8		15,18
SNP8.228	8		15,18
SNP8.229	8		15,18
SNP8.230	8		15,18
SNP8.231	8		15,18
SNP8.233	8		15,18
SNP8.235	8		15,18
SNP8.236	8		15,18
SNP8.237	8		15,18
SNP8.238	8		15,18
SNP8.240	8		15,18
SNP8.241	8		15,18
SNP8.243	8		15,18
SNP8.244	8		15,18
SNP8.245	8		15,18
SNP8.246	8		15
SNP8.249	8		15,18
SNP8.250	8		15,18
SNP8.251	8		15
SNP8.255	8		15
SNP8.256	8		15,18
SNP8.257	8		15,18
SNP8.258	8		15,18
SNP8.261	8		15,18
SNP8.262	8		15,18
SNP8.263	8		15,18
SNP8.264	8		15
SNP8.265	8		15,18
SNP8.266	8		15,18
SNP8.267	8		15,18
SNP8.268	8		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP8.270	8		15,18
SNP8.271	8		15,18
SNP8.274	8		15,18
SNP8.275	8		15,18
SNP8.276	8		15,18
SNP8.277	8		15,18
SNP8.278	8		14,15,17,18
SNP8.282	8		15,18
SNP8.283	8		15,18
SNP8.284	8		15,18
SNP8.285	8		18
SNP8.287	8		18
SNP8.289	8		18
SNP8.290	8		18
SNP8.293	8		15,18
SNP8.295	8		15,18
SNP8.299	8		18
SNP8.300	8		18
SNP8.302	8		18
SNP8.305	8		18
SNP8.306	8		18
SNP8.307	8		18
SNP8.319	8		15,18
SNP8.320	8		15,18
SNP8.321	8		15,18
SNP8.322	8		15,18
SNP8.323	8		15,18
SNP8.324	8		15,18
SNP8.326	8		15
SNP8.328	8		15,18
SNP8.329	8		15,18
SNP8.330	8		15,18
SNP8.331	8		15,18
SNP8.332	8		15,18
SNP8.334	8		15,18
SNP8.335	8		15,18



Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP8.337	8		15
SNP8.339	8		15,18
SNP8.341	8		15,18
SNP8.342	8		15,18
SNP8.343	8		15,18
SNP8.345	8		15,18
SNP8.346	8		15,18
SNP8.347	8		15,18
SNP8.348	8		15,18
SNP8.352	8		15,18
SNP8.355	8		15,18
SNP8.356	8		15,18
SNP8.357	8		15,18
SNP8.358	8		15,18
SNP8.359	8		15,18
SNP8.360	8		15,18
SNP8.361	8		15,18
SNP8.362	8		15,18
SNP8.363	8		15,18
SNP8.365	8		15
SNP8.366	8		15
SNP8.367	8		15,18
SNP8.368	8		15
SNP8.370	8		15,18
SNP8.375	8		15,18
SNP8.376	8		15,18
SNP8.377	8		15,18
SNP8.378	8		15,18
SNP9.159	9	BARC_1.01_Gm09_18850556_T_G	14,15,17,18
SNP9.042	9	BARC_1.01_Gm09_2716792_A_G	14,15,17,18
SNP9.067	9	BARC_1.01_Gm09_4224050_G_A	14,15,17,18
SNP9.076	9	BARC_1.01_Gm09_4700107_A_C	18
SNP9.115	9	BARC_1.01_Gm09_7508484_T_C	14,15,17,18
SNP9.013	9	BARC_1.01_Gm09_850718_G_A	14
SNP9.003	9		14,15,17,18
SNP9.012	9		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP9.019	9		14,15,17,18
SNP9.024	9		14,15,17,18
SNP9.028	9		14,15,17,18
SNP9.032	9		14
SNP9.035	9		14,17
SNP9.037	9		14,15,17,18
SNP9.043	9		14,15
SNP9.045	9		15
SNP9.046	9		14,15,17,18
SNP9.050	9		14,15,17,18
SNP9.052	9		14,15,17,18
SNP9.054	9		14,15,17,18
SNP9.057	9		14,15
SNP9.058	9		14,15,17,18
SNP9.066	9		14,15,17,18
SNP9.071	9		14,15,17,18
SNP9.080	9		14,15,17,18
SNP9.081	9		14,15,17,18
SNP9.082	9		14,15,17,18
SNP9.083	9		14,15,17,18
SNP9.092	9		14,15,17,18
SNP9.095	9		14,15,17,18
SNP9.097	9		14,15,17,18
SNP9.104	9		14,15,17,18
SNP9.108	9		14,15,17,18
SNP9.109	9		14,15,17,18
SNP9.113	9		14,15,17,18
SNP9.116	9		14,15,17,18
SNP9.117	9		14,15,17,18
SNP9.118	9		14,15,17,18
SNP9.120	9		14,15,17,18
SNP9.121	9		14,15,17,18
SNP9.126	9		14,15,17,18
SNP9.130	9		14,15,17,18
SNP9.132	9		14,15,17,18
SNP9.135	9		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP9.140	9		14,15,17,18
SNP9.142	9		14,15,17,18
SNP9.143	9		14,15,17,18
SNP9.150	9		15,18
SNP9.151	9		14,15,17,18
SNP9.153	9		14,15,17,18
SNP9.157	9		14,15,17,18
SNP9.161	9		14,15,17,18
SNP9.164	9		14,15,17,18
SNP9.175	9		14,15,17,18
SNP9.182	9		14,15,17,18
SNP9.188	9		14,15
SNP9.193	9		14,15,17,18
SNP9.196	9		14,15,17,18
SNP9.198	9		14,15
SNP9.202	9		14,15,18
SNP9.205	9		14,15,17,18
SNP9.208	9		14,15
SNP9.216	9		14,15,17,18
SNP9.217	9		14,15,17,18
SNP9.221	9		14,15,17,18
SNP9.223	9		14,15
SNP9.248	9		14,15,17,18
SNP9.251	9		14,15,17,18
SNP9.255	9		14,15,17,18
SNP9.265	9		15,17,18
SNP9.268	9		14,15,17,18
SNP9.269	9		18
SNP9.270	9		14,15,17,18
SNP9.272	9		17,18
SNP9.276	9		15,17,18
SNP9.278	9		14,15
SNP9.280	9		14,15,17,18
SNP9.281	9		14,15,17,18
SNP9.282	9		14,15,17,18
SNP9.283	9		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP9.287	9		15,18
SNP9.292	9		14,15
SNP9.293	9		14,15,17,18
SNP9.294	9		14,15,17,18
SNP9.298	9		14,15
SNP9.300	9		14,15,17,18
SNP9.302	9		14,15
SNP9.303	9		15
SNP9.304	9		14,15,17
SNP9.305	9		14,15
SNP9.306	9		14,15,17
SNP9.307	9		14,15,17
SNP9.308	9		14,15,17
SNP9.309	9		14,15,17
SNP9.314	9		14,15,17
SNP9.315	9		14,15,17
SNP9.330	9		15
SNP9.332	9		15
SNP9.343	9		14,15,17
SNP9.346	9		14,15,17,18
SNP9.347	9		14,15,17
SNP9.349	9		14,15,17,18
SNP9.350	9		14,15,17,18
SNP9.001	9		15,18
SNP9.002	9		15,18
SNP9.005	9		15,18
SNP9.006	9		15,18
SNP9.007	9		15,18
SNP9.010	9		15,18
SNP9.011	9		15,18
SNP9.015	9		15,18
SNP9.016	9		15,18
SNP9.017	9		15,18
SNP9.018	9		15,18
SNP9.020	9		15,18
SNP9.021	9		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP9.023	9		15,18
SNP9.025	9		15,18
SNP9.026	9		15,18
SNP9.027	9		15,18
SNP9.029	9		15,18
SNP9.030	9		15,18
SNP9.031	9		15,18
SNP9.033	9		18
SNP9.034	9		18
SNP9.038	9		15,18
SNP9.039	9		15,18
SNP9.040	9		15,18
SNP9.041	9		15,18
SNP9.044	9		15,18
SNP9.047	9		15,18
SNP9.049	9		15,18
SNP9.051	9		15,18
SNP9.053	9		15,18
SNP9.055	9		15,18
SNP9.059	9		15,18
SNP9.060	9		15,18
SNP9.061	9		15,18
SNP9.063	9		15,18
SNP9.064	9		15,18
SNP9.065	9		15,18
SNP9.068	9		15,18
SNP9.069	9		15,18
SNP9.070	9		15,18
SNP9.072	9		15
SNP9.073	9		15
SNP9.074	9		15,18
SNP9.075	9		18
SNP9.077	9		15,18
SNP9.078	9		15,18
SNP9.084	9		15,18
SNP9.085	9		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP9.090	9		15,18
SNP9.091	9		15,18
SNP9.093	9		15,18
SNP9.094	9		15,18
SNP9.096	9		15,18
SNP9.102	9		15,18
SNP9.103	9		15,18
SNP9.105	9		15,18
SNP9.106	9		15,18
SNP9.107	9		15,18
SNP9.110	9		15,18
SNP9.111	9		15,18
SNP9.112	9		15,18
SNP9.114	9		15,18
SNP9.119	9		15,18
SNP9.122	9		15,18
SNP9.123	9		15,18
SNP9.124	9		15,18
SNP9.125	9		15,18
SNP9.127	9		15,18
SNP9.128	9		15,18
SNP9.129	9		15,18
SNP9.131	9		15,18
SNP9.133	9		15,18
SNP9.134	9		15,18
SNP9.138	9		15,18
SNP9.139	9		15,18
SNP9.141	9		15,18
SNP9.144	9		15,18
SNP9.145	9		15,18
SNP9.146	9		15,18
SNP9.147	9		15,18
SNP9.148	9		15,18
SNP9.149	9		15,18
SNP9.152	9		15,18
SNP9.154	9		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP9.158	9		15,18
SNP9.160	9		15,18
SNP9.162	9		15,18
SNP9.163	9		15,18
SNP9.165	9		15,18
SNP9.166	9		18
SNP9.169	9		15,18
SNP9.170	9		15,18
SNP9.171	9		15,18
SNP9.173	9		15,18
SNP9.176	9		18
SNP9.177	9		15,18
SNP9.178	9		15,18
SNP9.180	9		15,18
SNP9.181	9		15,18
SNP9.183	9		15,18
SNP9.184	9		15,18
SNP9.186	9		15,18
SNP9.187	9		15,18
SNP9.189	9		15,18
SNP9.190	9		15,18
SNP9.191	9		15,18
SNP9.192	9		15,18
SNP9.194	9		15,18
SNP9.195	9		15,18
SNP9.197	9		15,18
SNP9.199	9		15
SNP9.200	9		15
SNP9.201	9		15
SNP9.203	9		15,18
SNP9.204	9		15,18
SNP9.206	9		15,18
SNP9.207	9		15,18
SNP9.209	9		15,18
SNP9.211	9		18
SNP9.212	9		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP9.218	9		15,18
SNP9.219	9		18
SNP9.220	9		15,18
SNP9.224	9		15,18
SNP9.226	9		18
SNP9.229	9		18
SNP9.245	9		18
SNP9.249	9		15,18
SNP9.253	9		15,18
SNP9.254	9		15,18
SNP9.257	9		15,18
SNP9.260	9		15,18
SNP9.263	9		15,18
SNP9.266	9		18
SNP9.267	9		18
SNP9.271	9		15,18
SNP9.273	9		18
SNP9.275	9		15,18
SNP9.277	9		15,18
SNP9.279	9		15,18
SNP9.284	9		15,18
SNP9.286	9		15,18
SNP9.288	9		15
SNP9.289	9		15,18
SNP9.290	9		15,18
SNP9.295	9		15,18
SNP9.296	9		15,18
SNP9.297	9		15,18
SNP9.299	9		15,18
SNP9.301	9		15,18
SNP9.310	9		15
SNP9.311	9		15,18
SNP9.312	9		15
SNP9.313	9		15,18
SNP9.316	9		15
SNP9.317	9		15,18



Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP9.320	9		14,15,17,18
SNP9.321	9		15
SNP9.322	9		15
SNP9.323	9		15,18
SNP9.324	9		15,18
SNP9.328	9		15,18
SNP9.331	9		15,18
SNP9.333	9		15
SNP9.334	9		15,18
SNP9.337	9		18
SNP9.339	9		15,18
SNP9.340	9		15,18
SNP9.342	9		15
SNP9.344	9		15,18
SNP9.345	9		15,18
SNP9.348	9		15
SNP9.351	9		15
SNP9.352	9		15,18
SNP9.353	9		15
SNP9.354	9		15
SNP9.356	9		15
SNP9.357	9		15
SNP9.358	9		15
SNP9.362	9		15
SNP9.363	9		15
SNP9.364	9		15
SNP9.367	9		15
SNP9.369	9		15
SNP9.370	9		15
SNP9.371	9		15
SNP9.373	9		15
SNP9.374	9		15
SNP9.375	9		15
SNP9.376	9		15
SNP9.377	9		15,18
SNP9.378	9		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP9.380	9		15,18
SNP9.381	9		15,18
SNP9.383	9		15,18
SNP9.384	9		15,18
SNP10.400	10	BARC_1.01_Gm10_1280627_G_A	14,15,17,18
SNP10.407	10	BARC_1.01_Gm10_1577269_A_G	14,15,17,18
SNP10.412	10	BARC_1.01_Gm10_1693846_T_C	14,15,17,18
SNP10.413	10	BARC_1.01_Gm10_1694367_T_C	14,15,17,18
SNP10.541	10	BARC_1.01_Gm10_19797767_A_C	14,15
SNP10.570	10	BARC_1.01_Gm10_36934121_T_C	14,15,17,18
SNP10.592	10	BARC_1.01_Gm10_38678793_A_G	14,15,17,18
SNP10.601	10	BARC_1.01_Gm10_38920364_T_C	14,15,17,18
SNP10.607	10	BARC_1.01_Gm10_39415112_A_G	14,15,17,18
SNP10.629	10	BARC_1.01_Gm10_41032294_A_C	14,15,17,18
SNP10.453	10	BARC_1.01_Gm10_4145590_T_C	14,15,17,18
SNP10.454	10	BARC_1.01_Gm10_4175424_G_A	14,15
SNP10.659	10	BARC_1.01_Gm10_43812212_C_T	14,15,17,18
SNP10.460	10	BARC_1.01_Gm10_4419573_T_G	14,15,17,18
SNP10.666	10	BARC_1.01_Gm10_44227652_C_T	15,18
SNP10.464	10	BARC_1.01_Gm10_4609130_G_A	14,15,17,18
SNP10.729	10	BARC_1.01_Gm10_49055867_T_C	14,15,17,18
SNP10.500	10	BARC_1.01_Gm10_7507435_C_T	14,15,17,18
SNP10.390	10		14,15,17,18
SNP10.392	10		14,15,17,18
SNP10.393	10		14,15,17,18
SNP10.398	10		14,15,17,18
SNP10.401	10		14,15,17,18
SNP10.402	10		14,15,17,18
SNP10.403	10		14,15,17,18
SNP10.404	10		14,15,17,18
SNP10.405	10		14,15,17,18
SNP10.406	10		14,15,17,18
SNP10.409	10		14,15,18
SNP10.411	10		14,15,17,18
SNP10.414	10		14,15,17,18
SNP10.418	10		15

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP10.420	10		14,15
SNP10.421	10		14,15,17,18
SNP10.422	10		14,15
SNP10.424	10		14,15,17,18
SNP10.425	10		14,15,17,18
SNP10.429	10		14,15,17,18
SNP10.431	10		14,15,17,18
SNP10.435	10		14,15,17,18
SNP10.441	10		14,15,17,18
SNP10.446	10		14,15,17,18
SNP10.448	10		15,18
SNP10.449	10		14,15,17,18
SNP10.450	10		14,15,17,18
SNP10.451	10		14,15,17,18
SNP10.461	10		14,15,17,18
SNP10.462	10		14,15,17,18
SNP10.463	10		14,15,17,18
SNP10.465	10		14,15,17,18
SNP10.467	10		14,15,17,18
SNP10.468	10		14,15,17,18
SNP10.470	10		14,15
SNP10.471	10		14,15,17,18
SNP10.472	10		14,15,17,18
SNP10.473	10		14,15,17,18
SNP10.474	10		14,15,17,18
SNP10.475	10		14,15
SNP10.476	10		14,15,17,18
SNP10.477	10		14,15,17,18
SNP10.478	10		14,15,17,18
SNP10.479	10		14,15,17,18
SNP10.480	10		14,15,17,18
SNP10.481	10		14,15,17,18
SNP10.483	10		14,15,17,18
SNP10.484	10		14,15,17,18
SNP10.485	10		14,15,17,18
SNP10.486	10		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP10.489	10		14,15,17,18
SNP10.493	10		17,18
SNP10.507	10		14,15,17,18
SNP10.508	10		14,15,17,18
SNP10.513	10		14,15,17,18
SNP10.514	10		14,15,17,18
SNP10.516	10		14,15,17,18
SNP10.519	10		14,15,17,18
SNP10.523	10		14,15,17,18
SNP10.524	10		14,15,17,18
SNP10.526	10		14,15,17,18
SNP10.528	10		14,15,17,18
SNP10.529	10		14,15,17,18
SNP10.544	10		14,15,17,18
SNP10.551	10		14,15,17,18
SNP10.558	10		14,15,17,18
SNP10.560	10		14,15,17,18
SNP10.575	10		14
SNP10.583	10		14,15,17,18
SNP10.591	10		14,15,17,18
SNP10.593	10		14,15,17,18
SNP10.594	10		14,15
SNP10.596	10		14,15,17,18
SNP10.597	10		14,15,17,18
SNP10.598	10		14,15,17,18
SNP10.599	10		14,15,17,18
SNP10.600	10		14,15,17,18
SNP10.603	10		14,15,17,18
SNP10.605	10		14,15,17,18
SNP10.606	10		14,15,17,18
SNP10.608	10		14,15,17,18
SNP10.612	10		14,15,17,18
SNP10.613	10		14,15
SNP10.614	10		14,15,17,18
SNP10.615	10		14,15,17,18
SNP10.616	10		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP10.618	10		14,15,17,18
SNP10.622	10		14,15,17,18
SNP10.627	10		14,15,17,18
SNP10.630	10		14,15
SNP10.634	10		15
SNP10.635	10		14,15
SNP10.640	10		18
SNP10.641	10		18
SNP10.644	10		14,15,17,18
SNP10.656	10		14,15,17,18
SNP10.664	10		14,15,17,18
SNP10.665	10		14,15,17,18
SNP10.686	10		17,18
SNP10.691	10		14,15,17,18
SNP10.693	10		14,15,17,18
SNP10.694	10		14,15,17,18
SNP10.695	10		14,15,17,18
SNP10.697	10		14,15,17,18
SNP10.707	10		14,15,17,18
SNP10.709	10		14,15,17,18
SNP10.710	10		15,18
SNP10.714	10		14,17,18
SNP10.715	10		14
SNP10.719	10		14,15
SNP10.722	10		14,15,17,18
SNP10.723	10		14,15,17,18
SNP10.748	10		18
SNP10.385	10		15,18
SNP10.386	10		15,18
SNP10.387	10		15,18
SNP10.388	10		15,18
SNP10.389	10		15,18
SNP10.391	10		15,18
SNP10.394	10		15,18
SNP10.395	10		15,18
SNP10.396	10		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP10.399	10		15,18
SNP10.408	10		15,18
SNP10.410	10		15,18
SNP10.415	10		15,18
SNP10.417	10		15
SNP10.428	10		18
SNP10.432	10		15,18
SNP10.434	10		15,18
SNP10.436	10		18
SNP10.437	10		18
SNP10.438	10		15,18
SNP10.442	10		18
SNP10.459	10		15,18
SNP10.482	10		15,18
SNP10.487	10		15,18
SNP10.490	10		15,18
SNP10.491	10		15,18
SNP10.494	10		18
SNP10.495	10		18
SNP10.497	10		15,18
SNP10.501	10		15,18
SNP10.503	10		15,18
SNP10.504	10		15,18
SNP10.505	10		15,18
SNP10.506	10		15,18
SNP10.509	10		15,18
SNP10.510	10		15,18
SNP10.511	10		15,18
SNP10.512	10		15,18
SNP10.515	10		15,18
SNP10.517	10		15,18
SNP10.518	10		15,18
SNP10.520	10		15,18
SNP10.521	10		15,18
SNP10.522	10		15,18
SNP10.525	10		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP10.530	10		15,18
SNP10.531	10		15,18
SNP10.532	10		15,18
SNP10.533	10		15,18
SNP10.535	10		15,18
SNP10.536	10		15,18
SNP10.537	10		15,18
SNP10.538	10		15,18
SNP10.539	10		15,18
SNP10.540	10		15,18
SNP10.542	10		15,18
SNP10.543	10		15,18
SNP10.545	10		15,18
SNP10.546	10		15,18
SNP10.547	10		15,18
SNP10.548	10		15,18
SNP10.549	10		15,18
SNP10.550	10		15,18
SNP10.552	10		15,18
SNP10.553	10		15,18
SNP10.557	10		15,18
SNP10.559	10		15,18
SNP10.561	10		15,18
SNP10.562	10		15,18
SNP10.563	10		15,18
SNP10.564	10		15,18
SNP10.565	10		15,18
SNP10.566	10		15,18
SNP10.567	10		15,18
SNP10.568	10		15,18
SNP10.569	10		15,18
SNP10.571	10		15,18
SNP10.572	10		15,18
SNP10.573	10		15
SNP10.574	10		15
SNP10.576	10		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP10.609	10		15,18
SNP10.610	10		15,18
SNP10.611	10		15,18
SNP10.619	10		15,18
SNP10.620	10		15,18
SNP10.621	10		15,18
SNP10.623	10		15,18
SNP10.624	10		15,18
SNP10.626	10		15,18
SNP10.628	10		15,18
SNP10.631	10		15,18
SNP10.632	10		15,18
SNP10.636	10		15,18
SNP10.637	10		15,18
SNP10.638	10		15,18
SNP10.639	10		18
SNP10.642	10		18
SNP10.643	10		15,18
SNP10.653	10		15,18
SNP10.654	10		15,18
SNP10.657	10		15,18
SNP10.660	10		15,18
SNP10.661	10		15,18
SNP10.670	10		15
SNP10.678	10		15
SNP10.679	10		15
SNP10.682	10		15
SNP10.683	10		15,18
SNP10.688	10		15,18
SNP10.689	10		15,18
SNP10.690	10		15,18
SNP10.692	10		15,18
SNP10.701	10		15,18
SNP10.702	10		15,18
SNP10.703	10		15,18
SNP10.705	10		15,18



Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP10.708	10		15,18
SNP10.711	10		15,18
SNP10.713	10		18
SNP10.716	10		15,18
SNP10.717	10		15,18
SNP10.718	10		15,18
SNP10.720	10		15,18
SNP10.721	10		15,18
SNP10.724	10		15,18
SNP10.725	10		15,18
SNP10.726	10		15,18
SNP10.727	10		15,18
SNP10.728	10		15,18
SNP10.730	10		15,18
SNP10.731	10		15,18
SNP10.733	10		15,18
SNP10.734	10		15,18
SNP10.740	10		15
SNP10.741	10		15
SNP10.742	10		18
SNP10.743	10		18
SNP10.744	10		18
SNP10.745	10		18
SNP10.746	10		18
SNP10.747	10		18
SNP10.749	10		18
SNP10.750	10		18
SNP10.751	10		18
SNP11.149	11	BARC_1.01_Gm11_10319200_G_T	14,15,17,18
SNP11.161	11	BARC_1.01_Gm11_15147134_T_C	17,18
SNP11.179	11	BARC_1.01_Gm11_17415728_G_A	15
SNP11.037	11	BARC_1.01_Gm11_3277472_C_T	15,18
SNP11.220	11	BARC_1.01_Gm11_33148571_C_T	14,15,17,18
SNP11.043	11	BARC_1.01_Gm11_3641716_A_C	14,15,17,18
SNP11.236	11	BARC_1.01_Gm11_36522210_G_A	14,15,17,18
SNP11.250	11	BARC_1.01_Gm11_37283308_A_C	14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP11.076	11	BARC_1.01_Gm11_5231500_T_G	14,15,17,18
SNP11.105	11	BARC_1.01_Gm11_7133690_T_C	14,15,17,18
SNP11.118	11	BARC_1.01_Gm11_8139480_C_T	14,15,17,18
SNP11.131	11	BARC_1.01_Gm11_8942593_T_C	14,15,17,18
SNP11.133	11	BARC_1.01_Gm11_8951295_T_C	14,15,17,18
SNP11.145	11	BARC_1.01_Gm11_9963410_G_A	14,15,17,18
SNP11.028	11		14,15,17,18
SNP11.026	11		14,15,17,18
SNP11.022	11		14,15,17,18
SNP11.016	11		14,15,17,18
SNP11.008	11		14,15,18
SNP11.005	11		15
SNP11.004	11		18
SNP11.032	11		14,15,17,18
SNP11.033	11		14,15
SNP11.035	11		14,15
SNP11.042	11		15,18
SNP11.044	11		14,15
SNP11.045	11		14,15,17
SNP11.047	11		14,15
SNP11.049	11		14,15,17,18
SNP11.050	11		14,15,17,18
SNP11.052	11		14,15,17,18
SNP11.053	11		14,15,17,18
SNP11.054	11		14,15,17,18
SNP11.055	11		14,15,17,18
SNP11.056	11		14,15
SNP11.057	11		14,15,17,18
SNP11.058	11		15,18
SNP11.059	11		14,15,17,18
SNP11.060	11		14,15,17,18
SNP11.061	11		14,15
SNP11.062	11		14,15,17,18
SNP11.063	11		14,15,17,18
SNP11.064	11		14,15,17,18
SNP11.065	11		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP11.068	11		15,18
SNP11.069	11		14,15
SNP11.070	11		14,15,17
SNP11.073	11		14,15,17,18
SNP11.074	11		14,15,17,18
SNP11.077	11		14,15
SNP11.088	11		14,15,17,18
SNP11.089	11		14,15,17,18
SNP11.091	11		14,15,17,18
SNP11.100	11		14,15
SNP11.101	11		14,15,17,18
SNP11.102	11		14,15,17,18
SNP11.109	11		14,15,17,18
SNP11.111	11		14,15,17,18
SNP11.112	11		14,15,17,18
SNP11.115	11		14,15,17,18
SNP11.114	11		14,15,17,18
SNP11.121	11		14,15
SNP11.122	11		14,15
SNP11.125	11		15,18
SNP11.127	11		14,15,17,18
SNP11.128	11		14,15,17,18
SNP11.129	11		14,15,17,18
SNP11.130	11		14,15,17,18
SNP11.132	11		14,15,17,18
SNP11.134	11		14,15,17,18
SNP11.135	11		14,15,17,18
SNP11.136	11		14,15,17,18
SNP11.137	11		15,18
SNP11.138	11		14,15,17,18
SNP11.139	11		14,15,17,18
SNP11.140	11		14,15,17,18
SNP11.141	11		14,15,17,18
SNP11.147	11		14,15,17,18
SNP11.148	11		14,15,17,18
SNP11.150	11		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP11.178	11		14,15,17,18
SNP11.180	11		14,15,17,18
SNP11.182	11		14,15,17,18
SNP11.184	11		14,15,17,18
SNP11.187	11		15,18
SNP11.189	11		14,15,17,18
SNP11.190	11		14,15,17,18
SNP11.191	11		14,15,17,18
SNP11.192	11		14,15,17,18
SNP11.193	11		14,15,17,18
SNP11.194	11		14,15,17,18
SNP11.196	11		14,15,17,18
SNP11.209	11		15,18
SNP11.199	11		14,15
SNP11.215	11		14,15,17,18
SNP11.217	11		14,15,17,18
SNP11.218	11		14,15,17,18
SNP11.228	11		14,15
SNP11.232	11		14,15,17,18
SNP11.233	11		14,15,17,18
SNP11.241	11		14,15,17,18
SNP11.243	11		14,15,17,18
SNP11.244	11		14,15,17,18
SNP11.246	11		14,15,17,18
SNP11.247	11		14,15,17,18
SNP11.248	11		14,15,17,18
SNP11.251	11		14,15,17,18
SNP11.252	11		14,15,17,18
SNP11.253	11		14,15,17,18
SNP11.257	11		14,15,17,18
SNP11.282	11		14,15,17,18
SNP11.281	11		14,15,17,18
SNP11.279	11		14,15,17,18
SNP11.276	11		14,15,17,18
SNP11.275	11		14,15,17,18
SNP11.273	11		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP11.272	11		15,18
SNP11.271	11		14,15,17,18
SNP11.269	11		14,15,17,18
SNP11.001	11		15,18
SNP11.002	11		15,18
SNP11.003	11		15,18
SNP11.006	11		15,18
SNP11.007	11		15,18
SNP11.009	11		15,18
SNP11.010	11		15,18
SNP11.011	11		15,18
SNP11.012	11		15,18
SNP11.014	11		15,18
SNP11.015	11		15,18
SNP11.017	11		15,18
SNP11.018	11		15,18
SNP11.020	11		15,18
SNP11.021	11		15,18
SNP11.023	11		15,18
SNP11.024	11		15,18
SNP11.025	11		15,18
SNP11.027	11		15,18
SNP11.029	11		15,18
SNP11.031	11		15,18
SNP11.034	11		15
SNP11.036	11		15,18
SNP11.038	11		15,18
SNP11.039	11		15,18
SNP11.040	11		15,18
SNP11.046	11		15,18
SNP11.048	11		15,18
SNP11.051	11		15,18
SNP11.067	11		15,18
SNP11.071	11		15,18
SNP11.072	11		15,18
SNP11.078	11		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP11.081	11		15,18
SNP11.086	11		15,18
SNP11.087	11		15,18
SNP11.090	11		15,18
SNP11.092	11		15,18
SNP11.093	11		15,18
SNP11.094	11		15,18
SNP11.095	11		15,18
SNP11.096	11		15,18
SNP11.097	11		15,18
SNP11.098	11		15,18
SNP11.099	11		15,18
SNP11.103	11		15,18
SNP11.104	11		15,18
SNP11.106	11		15
SNP11.107	11		15
SNP11.110	11		15,18
SNP11.113	11		15,18
SNP11.116	11		15,18
SNP11.117	11		15,18
SNP11.119	11		15,18
SNP11.120	11		15,18
SNP11.123	11		15,18
SNP11.143	11		15,18
SNP11.144	11		15,18
SNP11.152	11		15,18
SNP11.153	11		15,18
SNP11.154	11		15,18
SNP11.155	11		15,18
SNP11.156	11		15,18
SNP11.157	11		15,18
SNP11.158	11		15,18
SNP11.159	11		15,18
SNP11.160	11		15,18
SNP11.162	11		18
SNP11.163	11		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP11.165	11		15,18
SNP11.166	11		15,18
SNP11.167	11		15,18
SNP11.168	11		15,18
SNP11.169	11		15,18
SNP11.170	11		15,18
SNP11.171	11		15,18
SNP11.172	11		15,18
SNP11.173	11		15,18
SNP11.174	11		15,18
SNP11.175	11		15,18
SNP11.176	11		15,18
SNP11.177	11		15,18
SNP11.181	11		15,18
SNP11.183	11		15,18
SNP11.185	11		15,18
SNP11.186	11		15,18
SNP11.188	11		15,18
SNP11.195	11		15,18
SNP11.197	11		15,18
SNP11.198	11		15
SNP11.201	11		15,18
SNP11.202	11		15,18
SNP11.206	11		15,18
SNP11.208	11		18
SNP11.210	11		15,18
SNP11.211	11		15,18
SNP11.212	11		15,18
SNP11.216	11		15,18
SNP11.219	11		15,18
SNP11.221	11		15,18
SNP11.224	11		18
SNP11.225	11		15,18
SNP11.226	11		15
SNP11.227	11		15
SNP11.229	11		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP11.231	11		15,18
SNP11.234	11		15,18
SNP11.235	11		15,18
SNP11.237	11		15,18
SNP11.238	11		15,18
SNP11.239	11		15,18
SNP11.240	11		15,18
SNP11.242	11		15,18
SNP11.245	11		15,18
SNP11.249	11		15,18
SNP11.258	11		15,18
SNP11.259	11		15,18
SNP11.260	11		15,18
SNP11.261	11		15,18
SNP11.263	11		15,18
SNP11.264	11		15,18
SNP11.265	11		15,18
SNP11.266	11		15,18
SNP11.267	11		15,18
SNP11.270	11		15,18
SNP11.277	11		15,18
SNP11.278	11		15,18
SNP11.280	11		15,18
SNP12.003	12	BARC_1.01_Gm12_114432_G_A	14,15,17,18
SNP12.044	12	BARC_1.01_Gm12_2827118_C_T	14,15,17,18
SNP12.006	12	BARC_1.01_Gm12_297432_G_A	14,15,17,18
SNP12.051	12	BARC_1.01_Gm12_3377791_C_A	14,15,17,18
SNP12.257	12	BARC_1.01_Gm12_37973529_T_C	14,15,17,18
SNP12.258	12	BARC_1.01_Gm12_37997350_T_C	14,15,17,18
SNP12.262	12	BARC_1.01_Gm12_38202617_T_C	14,15,17,18
SNP12.011	12	BARC_1.01_Gm12_553862_G_T	18
SNP12.098	12	BARC_1.01_Gm12_7039369_A_G	14,15,17,18
SNP12.104	12	BARC_1.01_Gm12_7454324_T_C	14,15,17,18
SNP12.111	12	BARC_1.01_Gm12_7942712_A_G	14,15,17,18
SNP12.001	12		14,15,17,18
SNP12.002	12		14,15,17,18



Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP12.005	12		14,15,17,18
SNP12.010	12		14,15,17,18
SNP12.017	12		14,15
SNP12.020	12		14,15,17,18
SNP12.021	12		14,15
SNP12.024	12		15,17,18
SNP12.026	12		14,15,17,18
SNP12.038	12		14,15,17,18
SNP12.042	12		14,15,17,18
SNP12.045	12		14,15,17,18
SNP12.046	12		14,15,17,18
SNP12.048	12		14,15,17,18
SNP12.049	12		14,15
SNP12.050	12		14,15,17,18
SNP12.056	12		14,15,17,18
SNP12.062	12		14,15,17,18
SNP12.063	12		14,15,17,18
SNP12.069	12		14,15,17,18
SNP12.077	12		14,15,17,18
SNP12.082	12		14,15,17,18
SNP12.085	12		14,15,17,18
SNP12.088	12		14,15
SNP12.099	12		14,15
SNP12.113	12		14,15,17,18
SNP12.118	12		15,17,18
SNP12.120	12		14,15,17,18
SNP12.145	12		14,15,17,18
SNP12.147	12		14,15,17,18
SNP12.152	12		14,15
SNP12.199	12		14,15,17,18
SNP12.203	12		14,15,17,18
SNP12.205	12		14,15,17,18
SNP12.208	12		14,15,17,18
SNP12.210	12		14,15,17,18
SNP12.211	12		17,18
SNP12.218	12		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP12.220	12		14,15,17,18
SNP12.224	12		14,15,17,18
SNP12.229	12		14,15,17,18
SNP12.235	12		14,15,17,18
SNP12.236	12		14,15,17,18
SNP12.238	12		14,15,17,18
SNP12.243	12		14,15,17,18
SNP12.244	12		14,15,17,18
SNP12.246	12		14,15,17,18
SNP12.248	12		14,15,17,18
SNP12.249	12		18
SNP12.254	12		14,15,17,18
SNP12.261	12		14,15,17,18
SNP12.007	12		15,18
SNP12.008	12		15,18
SNP12.009	12		18
SNP12.012	12		15,18
SNP12.013	12		15,18
SNP12.014	12		15,18
SNP12.015	12		15,18
SNP12.016	12		15,18
SNP12.018	12		15,18
SNP12.019	12		15,18
SNP12.023	12		15,18
SNP12.025	12		15,18
SNP12.027	12		15,18
SNP12.028	12		15,18
SNP12.029	12		15,18
SNP12.030	12		18
SNP12.031	12		15,18
SNP12.032	12		15,18
SNP12.033	12		15,18
SNP12.034	12		15,18
SNP12.035	12		15,18
SNP12.036	12		15,18
SNP12.037	12		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP12.040	12		15,18
SNP12.041	12		15,18
SNP12.043	12		15,18
SNP12.047	12		15,18
SNP12.052	12		15,18
SNP12.053	12		15,18
SNP12.054	12		15,18
SNP12.055	12		15,18
SNP12.057	12		15,18
SNP12.058	12		15,18
SNP12.059	12		15,18
SNP12.060	12		15,18
SNP12.061	12		15,18
SNP12.064	12		15,18
SNP12.065	12		15,18
SNP12.066	12		15,18
SNP12.067	12		15,18
SNP12.068	12		15,18
SNP12.070	12		15
SNP12.071	12		15,18
SNP12.072	12		15,18
SNP12.078	12		15,18
SNP12.081	12		15,18
SNP12.083	12		15,18
SNP12.084	12		15,18
SNP12.086	12		15,18
SNP12.087	12		15,18
SNP12.089	12		15,18
SNP12.090	12		15,18
SNP12.091	12		18
SNP12.092	12		15,18
SNP12.093	12		18
SNP12.094	12		15,18
SNP12.095	12		15,18
SNP12.096	12		15,18
SNP12.097	12		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP12.101	12		15,18
SNP12.102	12		15,18
SNP12.103	12		15,18
SNP12.105	12		15,18
SNP12.106	12		15,18
SNP12.108	12		18
SNP12.109	12		15,18
SNP12.110	12		15,18
SNP12.112	12		15,18
SNP12.114	12		15,18
SNP12.115	12		15,18
SNP12.116	12		15
SNP12.117	12		15,18
SNP12.119	12		15,18
SNP12.121	12		15
SNP12.143	12		15,18
SNP12.144	12		15,18
SNP12.146	12		15,18
SNP12.148	12		15,18
SNP12.149	12		15,18
SNP12.150	12		15,18
SNP12.151	12		15,18
SNP12.186	12		15,18
SNP12.187	12		15
SNP12.188	12		15,18
SNP12.190	12		15
SNP12.192	12		15
SNP12.193	12		18
SNP12.194	12		18
SNP12.195	12		18
SNP12.196	12		18
SNP12.197	12		15,18
SNP12.198	12		15,18
SNP12.200	12		15,18
SNP12.201	12		15,18
SNP12.202	12		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP12.206	12		15,18
SNP12.207	12		15,18
SNP12.209	12		15,18
SNP12.213	12		15,18
SNP12.214	12		15,18
SNP12.216	12		15,18
SNP12.217	12		15,18
SNP12.221	12		15,18
SNP12.222	12		15,18
SNP12.223	12		15,18
SNP12.227	12		15,18
SNP12.228	12		18
SNP12.230	12		15,18
SNP12.231	12		18
SNP12.233	12		15,18
SNP12.234	12		15,18
SNP12.237	12		15,18
SNP12.239	12		15,18
SNP12.240	12		15
SNP12.241	12		15,18
SNP12.242	12		14,15,17,18
SNP12.247	12		15,18
SNP12.250	12		15,18
SNP12.253	12		15,18
SNP12.255	12		15,18
SNP12.256	12		15,18
SNP12.260	12		15,18
SNP12.263	12		15,18
SNP12.264	12		18
SNP12.265	12		15,18
SNP12.267	12		15,18
SNP12.268	12		15,18
SNP12.269	12		15,18
SNP12.270	12		15,18
SNP12.273	12		15,18
SNP12.274	12		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP12.278	12		15,18
SNP12.279	12		15,18
SNP12.280	12		15,18
SNP12.283	12		15,18
SNP12.284	12		15,18
SNP12.287	12		18
SNP12.288	12		15,18
SNP12.289	12		15,18
SNP13.142	13	BARC_1.01_Gm13_1338620_T_G	17,18
SNP13.195	13	BARC_1.01_Gm13_24441863_C_T	14,15,17,18
SNP13.224	13	BARC_1.01_Gm13_27049303_T_G	14,15
SNP13.283	13	BARC_1.01_Gm13_30581811_C_T	14,15,17,18
SNP13.116	13	BARC_1.01_Gm13_3348282_A_G	14,15
SNP13.350	13	BARC_1.01_Gm13_34437456_A_G	14,15,17,18
SNP13.357	13	BARC_1.01_Gm13_34895902_A_G	14,15,17,18
SNP13.393	13	BARC_1.01_Gm13_38116142_G_T	15,18
SNP13.407	13	BARC_1.01_Gm13_39087013_G_A	14,15,17,18
SNP13.414	13	BARC_1.01_Gm13_39401900_T_C	14,15,17,18
SNP13.441	13	BARC_1.01_Gm13_40983805_C_T	17,18
SNP13.450	13	BARC_1.01_Gm13_41885784_A_G	14,15
SNP13.102	13	BARC_1.01_Gm13_4556157_A_G	14,15
SNP13.100	13	BARC_1.01_Gm13_4687210_A_G	14,15
SNP13.094	13	BARC_1.01_Gm13_5006288_C_T	14,15,17,18
SNP13.049	13	BARC_1.01_Gm13_8264628_A_C	14,15,17,18
SNP13.157	13		14,15,17,18
SNP13.151	13		14,15,18
SNP13.149	13		14,15,17,18
SNP13.148	13		14,15,17,18
SNP13.130	13		14,15,17,18
SNP13.126	13		14,15,18
SNP13.120	13		14,15
SNP13.114	13		14,15,17,18
SNP13.109	13		14,15,17,18
SNP13.106	13		14,15,17,18
SNP13.104	13		14,15,17,18
SNP13.103	13		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP13.095	13		14,15
SNP13.092	13		14,15
SNP13.082	13		14,15,17,18
SNP13.081	13		14,15,17,18
SNP13.077	13		14
SNP13.071	13		14,15,17,18
SNP13.047	13		14,15,17,18
SNP13.046	13		14,15,17,18
SNP13.045	13		14,15
SNP13.043	13		14,15,17,18
SNP13.042	13		14,15,17,18
SNP13.039	13		14,15,17,18
SNP13.030	13		15,17,18
SNP13.006	13		14,15,17,18
SNP13.007	13		14,15,17,18
SNP13.012	13		14,15,17,18
SNP13.015	13		14,15,17,18
SNP13.022	13		14,15,17,18
SNP13.027	13		14,15,17,18
SNP13.162	13		14,15,17,18
SNP13.164	13		14,15,17,18
SNP13.167	13		14,15,17,18
SNP13.168	13		14,15,17,18
SNP13.171	13		14,15,17,18
SNP13.174	13		14,15,17,18
SNP13.177	13		14,15,17,18
SNP13.182	13		14,15,17,18
SNP13.184	13		14,15,17,18
SNP13.187	13		14,15,18
SNP13.189	13		14,15,17,18
SNP13.191	13		14,15,17,18
SNP13.202	13		14,15,17,18
SNP13.213	13		14,15
SNP13.219	13		14,15,17,18
SNP13.222	13		14,15
SNP13.223	13		14,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP13.230	13		14,15,17,18
SNP13.234	13		14,15,17,18
SNP13.236	13		14,17,18
SNP13.238	13		14,15,17,18
SNP13.241	13		17,18
SNP13.244	13		14,15,17,18
SNP13.246	13		14,15,17,18
SNP13.247	13		14,15,17,18
SNP13.250	13		14,15,17,18
SNP13.255	13		14,15
SNP13.264	13		14,15,17,18
SNP13.267	13		14,15,17,18
SNP13.271	13		14,15,17,18
SNP13.276	13		14,15,17,18
SNP13.277	13		14,15,17,18
SNP13.285	13		14,15,17,18
SNP13.286	13		14,15,17,18
SNP13.287	13		14,15,17,18
SNP13.297	13		14,15,17,18
SNP13.299	13		14,15,17,18
SNP13.304	13		14,15,17,18
SNP13.307	13		17,18
SNP13.312	13		14,15,17,18
SNP13.313	13		14,15,17,18
SNP13.314	13		14,15,17,18
SNP13.315	13		14,15,17,18
SNP13.317	13		14,15
SNP13.325	13		14,15
SNP13.328	13		14,15,17,18
SNP13.332	13		14,15,17,18
SNP13.333	13		14,15,17,18
SNP13.334	13		14,15,17,18
SNP13.336	13		14,15
SNP13.338	13		14,15,17,18
SNP13.340	13		14,15,17,18
SNP13.341	13		14,15



Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP13.344	13		14,15,17,18
SNP13.345	13		14,15,17,18
SNP13.346	13		14,15,17,18
SNP13.351	13		14,15,17,18
SNP13.356	13		14,15,17,18
SNP13.358	13		14,15,17,18
SNP13.360	13		14,15,17,18
SNP13.361	13		14,15,17,18
SNP13.366	13		14,15,17,18
SNP13.372	13		14,15,17,18
SNP13.377	13		14,15,17,18
SNP13.379	13		14,15,17,18
SNP13.380	13		14,15,17,18
SNP13.381	13		14,15,17,18
SNP13.383	13		14,15,17,18
SNP13.386	13		14,15,17,18
SNP13.388	13		14,15,17,18
SNP13.389	13		14,15,17,18
SNP13.390	13		14,15,17,18
SNP13.394	13		14,15,17,18
SNP13.396	13		14,15
SNP13.398	13		14,15,17,18
SNP13.399	13		14,15,17,18
SNP13.404	13		14,15,17,18
SNP13.405	13		14,15,17,18
SNP13.406	13		14,15,17,18
SNP13.408	13		14,15,17,18
SNP13.409	13		14,15,17,18
SNP13.413	13		14,15,17,18
SNP13.415	13		14,15
SNP13.416	13		14,15,17,18
SNP13.419	13		14,15,17,18
SNP13.421	13		14,15,17,18
SNP13.422	13		14,15,17,18
SNP13.423	13		14,15,17,18
SNP13.424	13		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP13.427	13		14,15,17,18
SNP13.428	13		14,15,17,18
SNP13.431	13		14,15,17,18
SNP13.444	13		14,17,18
SNP13.445	13		14,15,17,18
SNP13.458	13		14,15
SNP13.459	13		14,15
SNP13.472	13		15,17
SNP13.001	13		15,18
SNP13.002	13		15,18
SNP13.003	13		15,18
SNP13.004	13		15,18
SNP13.005	13		15,18
SNP13.008	13		15,18
SNP13.009	13		15,18
SNP13.010	13		15,18
SNP13.011	13		15,18
SNP13.013	13		15,18
SNP13.014	13		14,15,17,18
SNP13.016	13		15,18
SNP13.017	13		15,18
SNP13.018	13		15,18
SNP13.019	13		15,18
SNP13.020	13		15,18
SNP13.021	13		15,18
SNP13.023	13		15,18
SNP13.024	13		15,18
SNP13.025	13		15,18
SNP13.026	13		15,18
SNP13.028	13		15,18
SNP13.029	13		15
SNP13.031	13		15,18
SNP13.032	13		15,18
SNP13.034	13		15,18
SNP13.035	13		15,18
SNP13.036	13		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP13.038	13		15,18
SNP13.040	13		15,18
SNP13.041	13		15,18
SNP13.044	13		15,18
SNP13.048	13		15,18
SNP13.050	13		15,18
SNP13.051	13		15,18
SNP13.053	13		15,18
SNP13.056	13		15
SNP13.057	13		15
SNP13.061	13		15,18
SNP13.062	13		15,18
SNP13.063	13		15,18
SNP13.064	13		15,18
SNP13.065	13		15,18
SNP13.066	13		15,18
SNP13.067	13		15,18
SNP13.070	13		15,18
SNP13.072	13		15,18
SNP13.073	13		15,18
SNP13.074	13		15,18
SNP13.075	13		18
SNP13.076	13		18
SNP13.078	13		15,18
SNP13.079	13		15,18
SNP13.080	13		15,18
SNP13.083	13		15,18
SNP13.084	13		15,18
SNP13.086	13		15
SNP13.087	13		18
SNP13.088	13		15,18
SNP13.090	13		15,18
SNP13.091	13		15,18
SNP13.093	13		15,18
SNP13.097	13		15,18
SNP13.098	13		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP13.101	13		14,15,17,18
SNP13.105	13		15,18
SNP13.107	13		15,18
SNP13.108	13		15,18
SNP13.110	13		15,18
SNP13.111	13		15,18
SNP13.112	13		15,18
SNP13.113	13		15,18
SNP13.115	13		15,18
SNP13.117	13		15,18
SNP13.118	13		15,18
SNP13.122	13		15,18
SNP13.123	13		15,18
SNP13.124	13		15,18
SNP13.125	13		15,18
SNP13.127	13		15,18
SNP13.128	13		18
SNP13.129	13		15,18
SNP13.131	13		15,18
SNP13.132	13		15,18
SNP13.133	13		18
SNP13.134	13		18
SNP13.135	13		15,18
SNP13.136	13		15,18
SNP13.137	13		15,18
SNP13.138	13		15,18
SNP13.139	13		15,18
SNP13.140	13		15,18
SNP13.141	13		15,18
SNP13.143	13		18
SNP13.144	13		18
SNP13.145	13		18
SNP13.146	13		18
SNP13.147	13		15,18
SNP13.150	13		15,18
SNP13.152	13		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP13.154	13		15,18
SNP13.155	13		15,18
SNP13.156	13		15,18
SNP13.158	13		15,18
SNP13.159	13		15,18
SNP13.160	13		15,18
SNP13.161	13		15,18
SNP13.163	13		15,18
SNP13.165	13		15,18
SNP13.166	13		15,18
SNP13.169	13		15,18
SNP13.170	13		15,18
SNP13.172	13		15,18
SNP13.173	13		15,18
SNP13.175	13		15,18
SNP13.178	13		15,18
SNP13.179	13		15,18
SNP13.180	13		15,18
SNP13.183	13		15,18
SNP13.185	13		15,18
SNP13.186	13		15,18
SNP13.188	13		15
SNP13.190	13		15,18
SNP13.192	13		15,18
SNP13.193	13		15,18
SNP13.194	13		15,18
SNP13.196	13		15,18
SNP13.199	13		15,18
SNP13.200	13		15,18
SNP13.207	13		15,18
SNP13.208	13		15,18
SNP13.210	13		15,18
SNP13.214	13		15,18
SNP13.215	13		15,18
SNP13.216	13		18
SNP13.217	13		18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP13.220	13		15,18
SNP13.221	13		15,18
SNP13.226	13		15,18
SNP13.227	13		15,18
SNP13.228	13		15,18
SNP13.231	13		15,18
SNP13.232	13		15,18
SNP13.233	13		15,18
SNP13.235	13		18
SNP13.237	13		15,18
SNP13.239	13		15,18
SNP13.240	13		18
SNP13.242	13		15,18
SNP13.245	13		15,18
SNP13.248	13		15,18
SNP13.253	13		18
SNP13.254	13		15,18
SNP13.260	13		14,15,17,18
SNP13.262	13		15,18
SNP13.265	13		15,18
SNP13.266	13		15,18
SNP13.268	13		15,18
SNP13.269	13		15,18
SNP13.272	13		18
SNP13.273	13		18
SNP13.274	13		15,18
SNP13.275	13		18
SNP13.278	13		15,18
SNP13.279	13		15,18
SNP13.280	13		15,18
SNP13.281	13		15,18
SNP13.282	13		15,18
SNP13.284	13		15,18
SNP13.288	13		15,18
SNP13.289	13		15,18
SNP13.290	13		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP13.292	13		15,18
SNP13.293	13		15,18
SNP13.294	13		15,18
SNP13.295	13		15,18
SNP13.296	13		15,18
SNP13.298	13		15,18
SNP13.300	13		15,18
SNP13.301	13		15,18
SNP13.302	13		15,18
SNP13.303	13		15
SNP13.306	13		15,18
SNP13.308	13		15,18
SNP13.309	13		15,18
SNP13.310	13		15,18
SNP13.311	13		15,18
SNP13.316	13		15,18
SNP13.319	13		15
SNP13.322	13		15
SNP13.323	13		15
SNP13.324	13		15
SNP13.326	13		15,18
SNP13.327	13		15,18
SNP13.329	13		15,18
SNP13.330	13		15,18
SNP13.335	13		15,18
SNP13.337	13		15,18
SNP13.339	13		15,18
SNP13.343	13		15,18
SNP13.347	13		15,18
SNP13.348	13		15,18
SNP13.349	13		15,18
SNP13.352	13		15,18
SNP13.353	13		15,18
SNP13.354	13		15,18
SNP13.355	13		15,18
SNP13.359	13		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP13.363	13		15,18
SNP13.365	13		15,18
SNP13.367	13		15,18
SNP13.368	13		15,18
SNP13.369	13		15,18
SNP13.370	13		15
SNP13.371	13		15,18
SNP13.373	13		15,18
SNP13.374	13		15,18
SNP13.375	13		15,18
SNP13.376	13		15,18
SNP13.378	13		15,17,18
SNP13.382	13		15,18
SNP13.387	13		15,18
SNP13.391	13		15,18
SNP13.392	13		15,18
SNP13.395	13		15,18
SNP13.397	13		15,18
SNP13.400	13		18
SNP13.402	13		15,18
SNP13.403	13		15,18
SNP13.410	13		15,18
SNP13.411	13		15,18
SNP13.412	13		15,18
SNP13.420	13		15,18
SNP13.426	13		15,18
SNP13.439	13		15,18
SNP13.440	13		18
SNP13.442	13		15,18
SNP13.443	13		15,18
SNP13.447	13		15,18
SNP13.451	13		15,18
SNP13.452	13		15,18
SNP13.453	13		15
SNP13.454	13		15
SNP13.455	13		15



Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP13.457	13		15
SNP13.460	13		15
SNP13.461	13		15,18
SNP13.474	13		15
SNP14.181	14	BARC_1.01_Gm14_10641197_A_G	14,15,17,18
SNP14.024	14	BARC_1.01_Gm14_1442735_A_G	14,15,17,18
SNP14.032	14	BARC_1.01_Gm14_1748042_C_A	15
SNP14.045	14	BARC_1.01_Gm14_2250656_A_C	14,15,17,18
SNP14.082	14	BARC_1.01_Gm14_3841343_G_T	14,15,17,18
SNP14.090	14	BARC_1.01_Gm14_4199432_A_G	14,15,17,18
SNP14.330	14	BARC_1.01_Gm14_47884956_G_A	14,15,17,18
SNP14.337	14	BARC_1.01_Gm14_48449269_G_A	14,15,17,18
SNP14.105	14	BARC_1.01_Gm14_5028737_T_C	14,15,17,18
SNP14.145	14	BARC_1.01_Gm14_7482987_T_C	17,18
SNP14.171	14	BARC_1.01_Gm14_9966572_T_C	14,15,17,18
SNP14.002	14		17,18
SNP14.010	14		14,15,17,18
SNP14.015	14		15,17,18
SNP14.016	14		14,15,17,18
SNP14.021	14		14,15,17,18
SNP14.023	14		14,15,17,18
SNP14.025	14		14,15,17,18
SNP14.026	14		14,15,17,18
SNP14.027	14		14,15,17,18
SNP14.028	14		14,15,17,18
SNP14.030	14		14,15,17,18
SNP14.035	14		14,15
SNP14.036	14		15
SNP14.038	14		14,15,17,18
SNP14.040	14		14,15,17,18
SNP14.042	14		14,15,17,18
SNP14.043	14		14,15,17,18
SNP14.044	14		14,15,17,18
SNP14.046	14		14,15,17,18
SNP14.048	14		14,15,17,18
SNP14.049	14		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP14.054	14		14,15,17,18
SNP14.055	14		14,15,17,18
SNP14.056	14		14,15,17,18
SNP14.057	14		14,15
SNP14.058	14		14,15,17,18
SNP14.059	14		14,15,17,18
SNP14.060	14		14,15,17,18
SNP14.061	14		14,15,17,18
SNP14.062	14		14,15,17,18
SNP14.063	14		14,15,17,18
SNP14.064	14		14,15,17,18
SNP14.065	14		14,15,17,18
SNP14.066	14		14,15,17,18
SNP14.067	14		14,15,17,18
SNP14.068	14		14,15
SNP14.069	14		14,15,17,18
SNP14.070	14		14,15,17,18
SNP14.071	14		14,15,18
SNP14.072	14		14,15,17,18
SNP14.073	14		14,15,17,18
SNP14.075	14		14,15,17,18
SNP14.076	14		14,15,17,18
SNP14.077	14		14,15
SNP14.078	14		14,15,17,18
SNP14.080	14		14,15,17,18
SNP14.084	14		14,15,17,18
SNP14.085	14		14,15,17,18
SNP14.086	14		14,15,17,18
SNP14.088	14		14,15,17,18
SNP14.089	14		14,15,17,18
SNP14.094	14		14,15,17,18
SNP14.096	14		14,15,17,18
SNP14.099	14		14,15,17,18
SNP14.102	14		14,15,17,18
SNP14.106	14		14,15,17,18
SNP14.110	14		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP14.112	14		14,15,17,18
SNP14.123	14		14,15,17,18
SNP14.124	14		14,15,17,18
SNP14.125	14		15,17,18
SNP14.127	14		14,15,17,18
SNP14.128	14		14,15,17,18
SNP14.129	14		14,15,17,18
SNP14.130	14		14,15,17,18
SNP14.132	14		14,15
SNP14.134	14		14,15,17,18
SNP14.135	14		14,15,17,18
SNP14.137	14		14,15,17,18
SNP14.143	14		14,15
SNP14.148	14		15,18
SNP14.149	14		14,15,17,18
SNP14.152	14		14,15,17,18
SNP14.154	14		14,15,17,18
SNP14.161	14		14,15,17
SNP14.163	14		14,15,17
SNP14.165	14		14,15,17
SNP14.166	14		14,15,17
SNP14.170	14		14,15,17,18
SNP14.172	14		14,15
SNP14.173	14		14,15,17,18
SNP14.174	14		14,15
SNP14.175	14		14,15,17,18
SNP14.176	14		14,15,17,18
SNP14.177	14		14,15,17
SNP14.182	14		14,15,17,18
SNP14.183	14		14,15,17,18
SNP14.184	14		14,15,17,18
SNP14.185	14		14,15,17,18
SNP14.195	14		14,15,17,18
SNP14.199	14		14,15,17,18
SNP14.206	14		14,15
SNP14.208	14		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP14.223	14		18
SNP14.226	14		14,15,17,18
SNP14.227	14		14,15,17,18
SNP14.231	14		14,15,17,18
SNP14.236	14		14,15,17,18
SNP14.241	14		14,15,17,18
SNP14.249	14		14,15,17,18
SNP14.264	14		14,15,17,18
SNP14.265	14		14,15,17,18
SNP14.266	14		14,15,17,18
SNP14.269	14		14,15,17,18
SNP14.274	14		14,15,17,18
SNP14.276	14		14,15,17,18
SNP14.284	14		14,15,17,18
SNP14.286	14		14,15,17,18
SNP14.298	14		14,15,17,18
SNP14.301	14		14,15,17,18
SNP14.302	14		14,15,17,18
SNP14.306	14		14,15,17,18
SNP14.307	14		14,15,17,18
SNP14.308	14		14,15,17,18
SNP14.324	14		14,15,17,18
SNP14.336	14		14,15,17,18
SNP14.338	14		14,15
SNP14.355	14		14,15
SNP14.353	14		14,15
SNP14.001	14		15,18
SNP14.003	14		15,18
SNP14.004	14		15,18
SNP14.005	14		15,18
SNP14.006	14		15,18
SNP14.007	14		15,18
SNP14.008	14		15,18
SNP14.009	14		15,18
SNP14.011	14		15,18
SNP14.012	14		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP14.014	14		15,18
SNP14.017	14		15,18
SNP14.018	14		15,18
SNP14.019	14		15,18
SNP14.020	14		15,18
SNP14.022	14		15,18
SNP14.029	14		15,18
SNP14.031	14		15
SNP14.037	14		15,18
SNP14.039	14		15,18
SNP14.041	14		15,18
SNP14.047	14		15,18
SNP14.050	14		15,18
SNP14.074	14		15,18
SNP14.079	14		15,18
SNP14.081	14		15,18
SNP14.083	14		15,18
SNP14.087	14		15,18
SNP14.092	14		15,18
SNP14.093	14		15,18
SNP14.095	14		15,18
SNP14.097	14		15,18
SNP14.098	14		15,18
SNP14.100	14		15,18
SNP14.101	14		15,18
SNP14.103	14		15,18
SNP14.104	14		18
SNP14.108	14		18
SNP14.109	14		15,18
SNP14.113	14		18
SNP14.114	14		18
SNP14.115	14		18
SNP14.116	14		18
SNP14.117	14		15,18
SNP14.118	14		15,18
SNP14.119	14		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP14.126	14		15,18
SNP14.131	14		15,18
SNP14.133	14		15,18
SNP14.136	14		15,18
SNP14.138	14		15,18
SNP14.139	14		15,18
SNP14.140	14		15,18
SNP14.141	14		15,18
SNP14.142	14		15,18
SNP14.146	14		15,18
SNP14.147	14		15,18
SNP14.150	14		15,18
SNP14.153	14		15,18
SNP14.157	14		15,18
SNP14.158	14		15,18
SNP14.159	14		15,18
SNP14.160	14		15
SNP14.162	14		15
SNP14.164	14		15
SNP14.167	14		15
SNP14.168	14		15,18
SNP14.169	14		15
SNP14.178	14		15,18
SNP14.179	14		15,18
SNP14.180	14		15,18
SNP14.186	14		15,18
SNP14.187	14		15,18
SNP14.188	14		15,18
SNP14.189	14		15,18
SNP14.190	14		15,18
SNP14.191	14		15,18
SNP14.192	14		15
SNP14.193	14		15,18
SNP14.194	14		15,18
SNP14.196	14		15,18
SNP14.197	14		15

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP14.200	14		15,18
SNP14.201	14		15,18
SNP14.202	14		15,18
SNP14.203	14		15,18
SNP14.204	14		15,18
SNP14.205	14		15,18
SNP14.207	14		15
SNP14.209	14		15,18
SNP14.211	14		15,18
SNP14.212	14		15
SNP14.213	14		15,18
SNP14.214	14		15,18
SNP14.215	14		15,18
SNP14.216	14		15,18
SNP14.217	14		15,18
SNP14.218	14		15,18
SNP14.219	14		15,18
SNP14.220	14		15,18
SNP14.222	14		15
SNP14.224	14		15,18
SNP14.225	14		15,18
SNP14.228	14		15,18
SNP14.229	14		15,18
SNP14.230	14		15,18
SNP14.232	14		15,18
SNP14.233	14		15,18
SNP14.234	14		15,18
SNP14.235	14		15,18
SNP14.237	14		15,18
SNP14.238	14		15,18
SNP14.239	14		15,18
SNP14.240	14		15,18
SNP14.242	14		15,18
SNP14.243	14		15,18
SNP14.244	14		15,18
SNP14.245	14		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP14.247	14		15,18
SNP14.248	14		15,18
SNP14.250	14		15,18
SNP14.251	14		15,18
SNP14.252	14		15,18
SNP14.253	14		15,18
SNP14.254	14		15,18
SNP14.255	14		15,18
SNP14.256	14		15,18
SNP14.257	14		15,18
SNP14.258	14		15,18
SNP14.259	14		15,18
SNP14.260	14		15,18
SNP14.261	14		15,18
SNP14.262	14		15,18
SNP14.263	14		15,18
SNP14.267	14		15,18
SNP14.268	14		15,18
SNP14.270	14		15,18
SNP14.271	14		15,18
SNP14.272	14		15,18
SNP14.273	14		15,18
SNP14.275	14		15,18
SNP14.277	14		15,18
SNP14.278	14		15,18
SNP14.279	14		15,18
SNP14.281	14		15,18
SNP14.282	14		15,18
SNP14.283	14		15,18
SNP14.287	14		15,18
SNP14.288	14		15,18
SNP14.290	14		18
SNP14.291	14		15,18
SNP14.292	14		15,18
SNP14.293	14		15,18
SNP14.294	14		15,18



Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP14.299	14		15,18
SNP14.300	14		15,18
SNP14.303	14		15,18
SNP14.304	14		15,18
SNP14.305	14		15,18
SNP14.309	14		15,18
SNP14.320	14		15,18
SNP14.321	14		15,18
SNP14.322	14		15,18
SNP14.325	14		15,18
SNP14.327	14		15,18
SNP14.328	14		15
SNP14.329	14		15
SNP14.331	14		15,18
SNP14.332	14		15
SNP14.333	14		15,18
SNP14.334	14		15,18
SNP14.335	14		15,18
SNP14.339	14		15,18
SNP14.340	14		15,18
SNP14.341	14		15,18
SNP14.342	14		15,18
SNP14.343	14		15,18
SNP14.344	14		15,18
SNP14.349	14		18
SNP14.350	14		18
SNP14.351	14		15,18
SNP14.352	14		15,18
SNP15.151	15	BARC_1.01_Gm15_10832601_C_A	14,15,17,18
SNP15.158	15	BARC_1.01_Gm15_11287058_T_G	14,15,17,18
SNP15.177	15	BARC_1.01_Gm15_12376572_A_G	14,15,17,18
SNP15.190	15	BARC_1.01_Gm15_13180039_C_T	15,18
SNP15.016	15	BARC_1.01_Gm15_1541381_T_C	14,15,17,18
SNP15.026	15	BARC_1.01_Gm15_2127691_A_G	14,15,17,18
SNP15.043	15	BARC_1.01_Gm15_3298898_T_C	14,15,17,18
SNP15.366	15	BARC_1.01_Gm15_45395118_A_G	14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP15.466	15	BARC_1.01_Gm15_50837234_G_A	14,15,17,18
SNP15.103	15	BARC_1.01_Gm15_7660710_A_G	14,15,17,18
SNP15.111	15	BARC_1.01_Gm15_8134735_A_G	14,15,17,18
SNP15.126	15	BARC_1.01_Gm15_9035408_T_C	14,15,17,18
SNP15.003	15		14,15
SNP15.010	15		14,15,17,18
SNP15.017	15		14,15,17,18
SNP15.022	15		14,15,17,18
SNP15.025	15		14,15,17,18
SNP15.037	15		14,15,17,18
SNP15.039	15		14,15,17,18
SNP15.054	15		14,15,17,18
SNP15.058	15		14,15,17,18
SNP15.064	15		14,15,17,18
SNP15.066	15		14,15,17,18
SNP15.067	15		14,15,17,18
SNP15.068	15		14,15,17,18
SNP15.070	15		17,18
SNP15.081	15		14,15,17,18
SNP15.087	15		14,15,17,18
SNP15.092	15		14,15,17,18
SNP15.101	15		14,15,17,18
SNP15.105	15		14,15,17,18
SNP15.107	15		18
SNP15.114	15		14,15,17,18
SNP15.115	15		14,15,17,18
SNP15.120	15		14,15,17,18
SNP15.124	15		14,15,17,18
SNP15.127	15		14,15,17,18
SNP15.134	15		14,15,17,18
SNP15.137	15		14,15,17,18
SNP15.138	15		14,15,17,18
SNP15.143	15		14,15
SNP15.144	15		14,15,17,18
SNP15.149	15		14,15,17,18
SNP15.153	15		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP15.156	15		14,15,17,18
SNP15.157	15		14,15,17,18
SNP15.161	15		14,15,17,18
SNP15.173	15		14,15,17,18
SNP15.174	15		14,15,17,18
SNP15.175	15		14,15,17,18
SNP15.176	15		14,15,17,18
SNP15.179	15		14,15,17,18
SNP15.180	15		14,15,17,18
SNP15.185	15		15,18
SNP15.186	15		14,15,17,18
SNP15.188	15		15,18
SNP15.189	15		14,15,17,18
SNP15.192	15		14,15
SNP15.195	15		14,15,17,18
SNP15.197	15		14,15,17,18
SNP15.200	15		17,18
SNP15.212	15		14,15,17,18
SNP15.213	15		14,15,17,18
SNP15.214	15		14,15,17,18
SNP15.216	15		14,15,17,18
SNP15.218	15		14,15,17,18
SNP15.220	15		14,15,17,18
SNP15.221	15		14,15,17,18
SNP15.222	15		14,15,17,18
SNP15.223	15		14,15,17,18
SNP15.224	15		14,15,17,18
SNP15.225	15		15,18
SNP15.226	15		14,15,17,18
SNP15.230	15		14,15,18
SNP15.232	15		14,15,17,18
SNP15.233	15		14,15,17,18
SNP15.234	15		14,15,17,18
SNP15.239	15		14,15,17,18
SNP15.240	15		14,15,17,18
SNP15.243	15		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP15.257	15		17,18
SNP15.259	15		14,15,17,18
SNP15.261	15		14,15,17,18
SNP15.263	15		14,15,17,18
SNP15.267	15		17,18
SNP15.269	15		14,15,17,18
SNP15.274	15		14,15,17,18
SNP15.275	15		14,15,17,18
SNP15.276	15		14,15,17,18
SNP15.277	15		14,15,17,18
SNP15.279	15		17,18
SNP15.280	15		14,15,17,18
SNP15.284	15		14,15,17,18
SNP15.287	15		18
SNP15.291	15		18
SNP15.293	15		14,15,17,18
SNP15.301	15		17,18
SNP15.307	15		18
SNP15.312	15		14,15,17,18
SNP15.318	15		18
SNP15.322	15		14,15,17,18
SNP15.321	15		14,15
SNP15.326	15		17,18
SNP15.325	15		18
SNP15.324	15		14,15,17,18
SNP15.334	15		18
SNP15.337	15		18
SNP15.340	15		18
SNP15.344	15		18
SNP15.347	15		18
SNP15.348	15		14,15,17,18
SNP15.352	15		14,15,17,18
SNP15.357	15		14,15,17,18
SNP15.360	15		14,15,17,18
SNP15.363	15		14,15,17,18
SNP15.364	15		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP15.368	15		14,15,17,18
SNP15.369	15		14,15
SNP15.370	15		14,15,17,18
SNP15.371	15		14,15,17,18
SNP15.372	15		14,15,17,18
SNP15.373	15		14,15,17,18
SNP15.374	15		14,15,17,18
SNP15.375	15		14,15,17,18
SNP15.376	15		14,15
SNP15.379	15		14,15,17,18
SNP15.380	15		14,15,17,18
SNP15.381	15		14,15,17,18
SNP15.382	15		14,15,17,18
SNP15.383	15		14,15,17,18
SNP15.384	15		14,15,17,18
SNP15.385	15		14,15
SNP15.386	15		14,15,17,18
SNP15.388	15		14,15,17,18
SNP15.389	15		14,15,17,18
SNP15.390	15		14,15,17,18
SNP15.392	15		14,15,17,18
SNP15.405	15		14,15,18
SNP15.406	15		14,15
SNP15.407	15		14,15,17,18
SNP15.409	15		14,15,17,18
SNP15.411	15		14,15,17
SNP15.414	15		14,15,17,18
SNP15.415	15		14,15
SNP15.416	15		14,15,17,18
SNP15.418	15		14,15,17,18
SNP15.419	15		14,15,17,18
SNP15.420	15		14,15,17,18
SNP15.421	15		14,15,17,18
SNP15.423	15		14,15,17,18
SNP15.425	15		14,15,17,18
SNP15.426	15		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP15.430	15		14,15
SNP15.432	15		14,15,17,18
SNP15.434	15		14,15,17,18
SNP15.435	15		14,15,17,18
SNP15.436	15		14,15,17,18
SNP15.437	15		14,15,17,18
SNP15.440	15		14,15,17
SNP15.441	15		14,15,17
SNP15.442	15		14,15
SNP15.444	15		17
SNP15.461	15		14,15,17,18
SNP15.463	15		14,15,17,18
SNP15.467	15		14,15,17,18
SNP15.001	15		15,18
SNP15.002	15		15,18
SNP15.004	15		15,18
SNP15.005	15		15,18
SNP15.006	15		15,18
SNP15.007	15		15,18
SNP15.008	15		15,18
SNP15.009	15		15,18
SNP15.011	15		15,18
SNP15.012	15		15,18
SNP15.013	15		17,18
SNP15.014	15		15
SNP15.018	15		15,18
SNP15.019	15		15,18
SNP15.020	15		15,18
SNP15.021	15		15,18
SNP15.023	15		15,18
SNP15.032	15		15,18
SNP15.036	15		14,15,17,18
SNP15.038	15		15,18
SNP15.040	15		15,18
SNP15.041	15		15,17,18
SNP15.042	15		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP15.045	15		15,18
SNP15.046	15		15,18
SNP15.052	15		15,18
SNP15.056	15		15,18
SNP15.057	15		15
SNP15.059	15		15,18
SNP15.060	15		15,18
SNP15.061	15		15,18
SNP15.062	15		15,18
SNP15.063	15		15,18
SNP15.065	15		15,18
SNP15.069	15		15,18
SNP15.071	15		18
SNP15.072	15		15,18
SNP15.073	15		15,18
SNP15.074	15		15,18
SNP15.075	15		15,18
SNP15.076	15		15,18
SNP15.077	15		15,18
SNP15.078	15		15,18
SNP15.079	15		15,18
SNP15.080	15		15,18
SNP15.082	15		15,18
SNP15.083	15		15,18
SNP15.085	15		15,18
SNP15.086	15		15,18
SNP15.089	15		15,18
SNP15.090	15		15,18
SNP15.091	15		15,18
SNP15.093	15		15,18
SNP15.094	15		15,18
SNP15.095	15		15,18
SNP15.096	15		15,18
SNP15.097	15		18
SNP15.098	15		15,18
SNP15.099	15		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP15.102	15		15,18
SNP15.104	15		15,18
SNP15.106	15		15,18
SNP15.108	15		15,18
SNP15.113	15		15,18
SNP15.116	15		15,18
SNP15.117	15		15,18
SNP15.118	15		15,18
SNP15.119	15		15,18
SNP15.121	15		15,18
SNP15.122	15		15,18
SNP15.123	15		15,18
SNP15.125	15		15,18
SNP15.129	15		15,18
SNP15.130	15		15,18
SNP15.131	15		15,18
SNP15.132	15		15,18
SNP15.133	15		15,18
SNP15.135	15		15,18
SNP15.136	15		15,18
SNP15.139	15		15,18
SNP15.141	15		15,18
SNP15.142	15		15,18
SNP15.145	15		15,18
SNP15.146	15		15,18
SNP15.147	15		15,18
SNP15.148	15		15,18
SNP15.150	15		15,18
SNP15.152	15		15,18
SNP15.154	15		15
SNP15.159	15		15,18
SNP15.160	15		15,18
SNP15.162	15		15,18
SNP15.164	15		18
SNP15.165	15		18
SNP15.166	15		18



Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP15.172	15		15
SNP15.178	15		15,18
SNP15.181	15		15,18
SNP15.183	15		15,18
SNP15.184	15		18
SNP15.187	15		15,18
SNP15.193	15		15,18
SNP15.194	15		15,18
SNP15.196	15		15,18
SNP15.198	15		15
SNP15.199	15		15,18
SNP15.201	15		18
SNP15.202	15		15,18
SNP15.203	15		15,18
SNP15.204	15		18
SNP15.211	15		15,18
SNP15.215	15		15,18
SNP15.217	15		15,18
SNP15.219	15		15,18
SNP15.228	15		18
SNP15.229	15		15,18
SNP15.231	15		15,18
SNP15.235	15		18
SNP15.236	15		18
SNP15.238	15		15,18
SNP15.241	15		15,18
SNP15.242	15		15,18
SNP15.244	15		15,18
SNP15.246	15		15,18
SNP15.248	15		18
SNP15.258	15		15,18
SNP15.260	15		15,18
SNP15.262	15		15,18
SNP15.264	15		15,18
SNP15.265	15		15,18
SNP15.266	15		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP15.270	15		15,18
SNP15.271	15		15,18
SNP15.272	15		15,18
SNP15.273	15		15,18
SNP15.278	15		15,18
SNP15.281	15		15,18
SNP15.282	15		15,18
SNP15.283	15		15,18
SNP15.286	15		15,18
SNP15.288	15		15,18
SNP15.289	15		18
SNP15.290	15		15,18
SNP15.292	15		15,18
SNP15.294	15		15,18
SNP15.295	15		18
SNP15.298	15		18
SNP15.300	15		18
SNP15.302	15		18
SNP15.305	15		18
SNP15.308	15		18
SNP15.309	15		18
SNP15.311	15		18
SNP15.314	15		18
SNP15.315	15		18
SNP15.316	15		18
SNP15.317	15		18
SNP15.319	15		18
SNP15.320	15		18
SNP15.323	15		15,18
SNP15.327	15		15,18
SNP15.328	15		15,18
SNP15.329	15		15,18
SNP15.330	15		15,18
SNP15.331	15		15,18
SNP15.332	15		15,18
SNP15.333	15		18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP15.338	15		18
SNP15.341	15		18
SNP15.343	15		18
SNP15.346	15		18
SNP15.349	15		15,18
SNP15.353	15		15,18
SNP15.355	15		15,18
SNP15.359	15		15,18
SNP15.361	15		15
SNP15.362	15		15,18
SNP15.365	15		15,18
SNP15.377	15		15,18
SNP15.396	15		18
SNP15.404	15		18
SNP15.410	15		15,18
SNP15.412	15		15,18
SNP15.413	15		15,18
SNP15.422	15		15,18
SNP15.429	15		15,18
SNP15.431	15		15,18
SNP15.433	15		15,18
SNP15.438	15		15,18
SNP15.439	15		15,18
SNP15.443	15		15,18
SNP15.462	15		15,18
SNP15.464	15		15,18
SNP16.027	16	BARC_1.01_Gm16_1794642_A_C	14,15,17,18
SNP16.032	16	BARC_1.01_Gm16_2314458_C_T	14,15,17,18
SNP16.038	16	BARC_1.01_Gm16_2713797_A_G	14,15
SNP16.039	16	BARC_1.01_Gm16_2746738_C_A	15
SNP16.229	16	BARC_1.01_Gm16_30022654_C_T	14,15,17,18
SNP16.232	16	BARC_1.01_Gm16_30151465_A_G	14,15,17,18
SNP16.256	16	BARC_1.01_Gm16_31461554_C_T	14,15,17,18
SNP16.264	16	BARC_1.01_Gm16_31938726_G_A	14,15,17,18
SNP16.051	16	BARC_1.01_Gm16_3534754_A_C	14,15,17,18
SNP16.337	16	BARC_1.01_Gm16_37026443_G_T	14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP16.061	16	BARC_1.01_Gm16_3962328_C_A	14,15,17,18
SNP16.077	16	BARC_1.01_Gm16_5531307_C_T	14,15,17,18
SNP16.091	16	BARC_1.01_Gm16_6510537_A_G	14,15,17,18
SNP16.098	16	BARC_1.01_Gm16_7070805_G_A	14,15,17,18
SNP16.001	16		14,15,17,18
SNP16.002	16		14,15,18
SNP16.003	16		14,15,17,18
SNP16.006	16		14,15,17,18
SNP16.010	16		14,15,17,18
SNP16.014	16		14,15,17,18
SNP16.015	16		14,15,17,18
SNP16.017	16		14,15,17,18
SNP16.018	16		14,15,17,18
SNP16.025	16		14,15
SNP16.033	16		14,15,17,18
SNP16.047	16		14,15,17,18
SNP16.048	16		14,15,17,18
SNP16.052	16		14,15,17,18
SNP16.053	16		14,15,17,18
SNP16.054	16		14,15
SNP16.055	16		14,15,17,18
SNP16.056	16		14,15,17,18
SNP16.057	16		14,15,17,18
SNP16.058	16		14,15,17,18
SNP16.059	16		14,15,17,18
SNP16.060	16		14,15,17,18
SNP16.062	16		14,15,17,18
SNP16.063	16		14,15,17,18
SNP16.065	16		14,15,17,18
SNP16.066	16		14,15,17,18
SNP16.074	16		15,17,18
SNP16.083	16		14,15,17,18
SNP16.086	16		14,15,17,18
SNP16.090	16		14,15,17,18
SNP16.100	16		14,15
SNP16.101	16		14,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP16.104	16		14,15,17,18
SNP16.105	16		15,18
SNP16.108	16		14,15,17,18
SNP16.113	16		14,15,17
SNP16.120	16		14,15,17
SNP16.122	16		14,15,17
SNP16.124	16		14,15,17,18
SNP16.138	16		14,15,17,18
SNP16.167	16		14,15,17
SNP16.168	16		14,15
SNP16.172	16		14,15,17
SNP16.179	16		14,15,17
SNP16.185	16		14,15,17
SNP16.188	16		14,15,17
SNP16.189	16		14,15
SNP16.190	16		14,15,17
SNP16.191	16		14,15,17
SNP16.193	16		14,15,17
SNP16.194	16		14,15,17
SNP16.202	16		14,15,17,18
SNP16.214	16		14,15,17,18
SNP16.221	16		14,15,17,18
SNP16.227	16		14,15,17,18
SNP16.231	16		14,15,17,18
SNP16.236	16		14,15
SNP16.250	16		14,15,17,18
SNP16.254	16		14,15,17,18
SNP16.255	16		14,15,17,18
SNP16.257	16		14,15,17,18
SNP16.259	16		14,15,17,18
SNP16.265	16		14,15,17,18
SNP16.266	16		14,15,17,18
SNP16.268	16		14,15,17,18
SNP16.270	16		14,15,17,18
SNP16.274	16		14,15,17,18
SNP16.275	16		14,15

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP16.284	16		14,15
SNP16.288	16		14,15,17,18
SNP16.289	16		14,15,17,18
SNP16.294	16		14,15,17,18
SNP16.297	16		14,15,17,18
SNP16.301	16		14,15
SNP16.308	16		14,15,17,18
SNP16.309	16		14,15,17,18
SNP16.314	16		14,15,17,18
SNP16.317	16		14,15,17,18
SNP16.321	16		14,15,17,18
SNP16.324	16		14,15,17,18
SNP16.326	16		14,15
SNP16.338	16		14,15,17,18
SNP16.340	16		14,15,17,18
SNP16.341	16		14,15
SNP16.004	16		15,18
SNP16.005	16		15,18
SNP16.007	16		15,18
SNP16.008	16		15,18
SNP16.009	16		15,18
SNP16.011	16		15,18
SNP16.012	16		15,18
SNP16.013	16		15,18
SNP16.016	16		15,18
SNP16.019	16		15,18
SNP16.020	16		18
SNP16.021	16		15,18
SNP16.022	16		15,18
SNP16.023	16		15,18
SNP16.024	16		15,18
SNP16.026	16		15,18
SNP16.028	16		15,18
SNP16.029	16		15,18
SNP16.030	16		15,18
SNP16.034	16		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP16.036	16		15,18
SNP16.037	16		15,18
SNP16.041	16		18
SNP16.042	16		18
SNP16.043	16		18
SNP16.044	16		15,18
SNP16.045	16		15,18
SNP16.046	16		15,18
SNP16.049	16		15,18
SNP16.050	16		15,18
SNP16.064	16		15,18
SNP16.067	16		15,18
SNP16.068	16		15,18
SNP16.072	16		15,18
SNP16.073	16		15,18
SNP16.075	16		14,15,17,18
SNP16.076	16		15,18
SNP16.078	16		15,18
SNP16.079	16		15,18
SNP16.080	16		15,18
SNP16.081	16		15,18
SNP16.082	16		15,18
SNP16.084	16		15,18
SNP16.085	16		14,15,17,18
SNP16.087	16		15,18
SNP16.089	16		15,18
SNP16.093	16		14,15,17,18
SNP16.094	16		15,18
SNP16.097	16		15,18
SNP16.102	16		15,18
SNP16.106	16		15,18
SNP16.107	16		15,18
SNP16.109	16		15,18
SNP16.110	16		15,18
SNP16.115	16		15
SNP16.116	16		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP16.118	16		15,18
SNP16.119	16		15
SNP16.123	16		15
SNP16.125	16		15,18
SNP16.126	16		15,18
SNP16.127	16		15,18
SNP16.128	16		15,18
SNP16.129	16		15,18
SNP16.130	16		15,18
SNP16.131	16		15,18
SNP16.132	16		15,18
SNP16.133	16		15,18
SNP16.134	16		15,18
SNP16.136	16		15,18
SNP16.140	16		15,18
SNP16.155	16		15,18
SNP16.157	16		15,18
SNP16.165	16		15,18
SNP16.166	16		15,18
SNP16.169	16		15,18
SNP16.170	16		15,18
SNP16.171	16		15,18
SNP16.173	16		15
SNP16.175	16		15,18
SNP16.176	16		15,18
SNP16.177	16		15,18
SNP16.180	16		15,18
SNP16.181	16		15,18
SNP16.183	16		15,18
SNP16.184	16		15,18
SNP16.186	16		15,18
SNP16.187	16		15,18
SNP16.192	16		15,18
SNP16.195	16		15,18
SNP16.204	16		15,18
SNP16.209	16		15,18



Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP16.216	16		15,18
SNP16.217	16		15,18
SNP16.218	16		15,18
SNP16.219	16		15,18
SNP16.222	16		15,18
SNP16.223	16		15,18
SNP16.224	16		15,18
SNP16.226	16		15,18
SNP16.228	16		15,18
SNP16.234	16		15,18
SNP16.235	16		15,18
SNP16.237	16		15
SNP16.238	16		15
SNP16.239	16		15
SNP16.241	16		15
SNP16.242	16		15
SNP16.244	16		15
SNP16.245	16		15,18
SNP16.246	16		15,18
SNP16.247	16		15,18
SNP16.251	16		15,18
SNP16.253	16		15,18
SNP16.258	16		15,18
SNP16.260	16		15,18
SNP16.261	16		15,18
SNP16.262	16		15,18
SNP16.263	16		15,18
SNP16.267	16		15,18
SNP16.269	16		15,18
SNP16.271	16		15,18
SNP16.272	16		15,17,18
SNP16.273	16		15,17,18
SNP16.278	16		15,18
SNP16.279	16		15,18
SNP16.280	16		15,18
SNP16.281	16		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP16.283	16		15,18
SNP16.285	16		15
SNP16.286	16		15,18
SNP16.287	16		15,18
SNP16.290	16		15,18
SNP16.291	16		14,15,17,18
SNP16.292	16		15,18
SNP16.295	16		15,18
SNP16.298	16		14,15,17,18
SNP16.299	16		15,18
SNP16.300	16		15,18
SNP16.302	16		15,18
SNP16.303	16		15,18
SNP16.304	16		15,18
SNP16.305	16		15,18
SNP16.306	16		15,18
SNP16.307	16		15,18
SNP16.312	16		15,18
SNP16.313	16		15,18
SNP16.315	16		15,18
SNP16.316	16		15,18
SNP16.318	16		15,18
SNP16.320	16		15,18
SNP16.325	16		15,17,18
SNP16.328	16		15,18
SNP16.329	16		15
SNP16.333	16		15,18
SNP16.335	16		15,18
SNP16.336	16		15,18
SNP16.339	16		15,18
SNP16.343	16		15,18
SNP17.124	17	BARC_1.01_Gm17_11683326_G_A	14,15,17,18
SNP17.126	17	BARC_1.01_Gm17_11742611_G_T	14,15,17,18
SNP17.205	17	BARC_1.01_Gm17_32099963_G_A	14,15,17,18
SNP17.218	17	BARC_1.01_Gm17_35393607_A_G	14,15,17,18
SNP17.273	17	BARC_1.01_Gm17_39532657_C_A	18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP17.283	17	BARC_1.01_Gm17_40102736_A_C	14,15,17,18
SNP17.306	17	BARC_1.01_Gm17_41674343_A_C	14,15,17,18
SNP17.080	17	BARC_1.01_Gm17_8231124_A_G	14,15,17,18
SNP17.086	17	BARC_1.01_Gm17_8449684_G_A	14,15,17,18
SNP17.107	17	BARC_1.01_Gm17_9505624_A_G	14,15,18
SNP17.109	17	BARC_1.01_Gm17_9541344_T_C	15,18
SNP17.006	17		14,15,17,18
SNP17.010	17		14,15,17,18
SNP17.012	17		14,15,17,18
SNP17.035	17		14,15,17,18
SNP17.041	17		14,15
SNP17.049	17		14,15,17,18
SNP17.054	17		14,15,17,18
SNP17.060	17		14,15,17
SNP17.061	17		14,15
SNP17.066	17		14,15,17,18
SNP17.068	17		14,15,17,18
SNP17.073	17		14,15,17,18
SNP17.082	17		14,15,17,18
SNP17.083	17		14,15,17,18
SNP17.084	17		14,15,17,18
SNP17.085	17		14,15,17,18
SNP17.087	17		14,15,17,18
SNP17.088	17		14,15,17,18
SNP17.089	17		14,15,17,18
SNP17.091	17		14,15,18
SNP17.092	17		14,18
SNP17.095	17		14,15,17,18
SNP17.098	17		14,15,18
SNP17.099	17		14,15,18
SNP17.100	17		14,15,18
SNP17.101	17		14,15,17,18
SNP17.102	17		14,15,18
SNP17.108	17		14,15,18
SNP17.110	17		14,15,18
SNP17.114	17		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP17.120	17		14,15,17,18
SNP17.121	17		14,15,17,18
SNP17.142	17		14,15,17,18
SNP17.149	17		15,18
SNP17.163	17		14,15,17,18
SNP17.166	17		14,15,17,18
SNP17.167	17		14,15,17,18
SNP17.169	17		14,15
SNP17.170	17		14,15,17,18
SNP17.171	17		14,15
SNP17.172	17		14,15,17,18
SNP17.174	17		14,15,17,18
SNP17.175	17		14,15,17,18
SNP17.180	17		14,15,17,18
SNP17.179	17		14,15,17,18
SNP17.181	17		14,15,17,18
SNP17.182	17		14,15,17,18
SNP17.184	17		14,15,17,18
SNP17.186	17		14,15,17,18
SNP17.187	17		14,15,17,18
SNP17.196	17		14,15,17,18
SNP17.197	17		14,15,17,18
SNP17.198	17		14,15,17,18
SNP17.200	17		14,15,17,18
SNP17.203	17		14,15,17,18
SNP17.204	17		14,15,17,18
SNP17.209	17		14,15,17,18
SNP17.210	17		14,15,17,18
SNP17.212	17		18
SNP17.219	17		14,15,17,18
SNP17.223	17		14,15,17,18
SNP17.234	17		14,15,17,18
SNP17.237	17		14,15,17,18
SNP17.241	17		14,15,17,18
SNP17.251	17		15,17,18
SNP17.255	17		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP17.272	17		14,15,17,18
SNP17.279	17		14,15,17,18
SNP17.291	17		14,15,17,18
SNP17.293	17		14,15,17,18
SNP17.297	17		17,18
SNP17.301	17		14,15,17,18
SNP17.308	17		14,15,17,18
SNP17.307	17		14,15,17,18
SNP17.001	17		15,18
SNP17.002	17		15,18
SNP17.003	17		18
SNP17.004	17		15,18
SNP17.005	17		15,18
SNP17.007	17		15,18
SNP17.008	17		15,18
SNP17.009	17		15,18
SNP17.011	17		15,18
SNP17.023	17		15,18
SNP17.024	17		15,18
SNP17.025	17		15,18
SNP17.026	17		15,18
SNP17.030	17		15,18
SNP17.031	17		15,18
SNP17.032	17		15,18
SNP17.033	17		15,18
SNP17.034	17		15,18
SNP17.036	17		15,18
SNP17.037	17		15,18
SNP17.038	17		15,18
SNP17.039	17		15,18
SNP17.040	17		15,18
SNP17.043	17		15,18
SNP17.044	17		15,18
SNP17.046	17		15,18
SNP17.047	17		15,18
SNP17.048	17		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP17.051	17		15,18
SNP17.052	17		15,18
SNP17.053	17		15,18
SNP17.055	17		15,18
SNP17.057	17		18
SNP17.058	17		15
SNP17.063	17		18
SNP17.067	17		15,18
SNP17.070	17		15,18
SNP17.071	17		15,18
SNP17.072	17		15,18
SNP17.074	17		15,18
SNP17.075	17		15,18
SNP17.076	17		15,18
SNP17.077	17		15,18
SNP17.078	17		15,18
SNP17.079	17		15,18
SNP17.081	17		15,18
SNP17.090	17		15,18
SNP17.093	17		15,18
SNP17.094	17		15,18
SNP17.096	17		15,18
SNP17.097	17		15,18
SNP17.103	17		15,18
SNP17.111	17		15,18
SNP17.117	17		15,18
SNP17.119	17		15,18
SNP17.125	17		15,18
SNP17.127	17		15
SNP17.131	17		15,18
SNP17.137	17		18
SNP17.138	17		18
SNP17.139	17		18
SNP17.140	17		18
SNP17.141	17		15,18
SNP17.143	17		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP17.145	17		15,18
SNP17.147	17		15,18
SNP17.150	17		15,18
SNP17.151	17		15,18
SNP17.152	17		15,18
SNP17.153	17		15,18
SNP17.154	17		15,18
SNP17.164	17		15,18
SNP17.165	17		15,18
SNP17.168	17		15,18
SNP17.173	17		15,18
SNP17.176	17		15,18
SNP17.177	17		15,18
SNP17.178	17		15,18
SNP17.183	17		15,18
SNP17.188	17		15,18
SNP17.189	17		15,18
SNP17.190	17		15,18
SNP17.191	17		15,18
SNP17.192	17		15,18
SNP17.193	17		15,18
SNP17.194	17		15,18
SNP17.195	17		15,18
SNP17.199	17		15,18
SNP17.201	17		15,18
SNP17.202	17		15,18
SNP17.206	17		15,18
SNP17.207	17		15,18
SNP17.208	17		15,18
SNP17.211	17		15,18
SNP17.213	17		18
SNP17.214	17		18
SNP17.215	17		18
SNP17.217	17		18
SNP17.220	17		15,18
SNP17.221	17		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP17.224	17		15,18
SNP17.225	17		15,18
SNP17.226	17		15,18
SNP17.227	17		15,18
SNP17.228	17		15,18
SNP17.229	17		15,18
SNP17.230	17		15,18
SNP17.231	17		15,18
SNP17.232	17		15,18
SNP17.233	17		15,18
SNP17.235	17		15,18
SNP17.236	17		15,18
SNP17.238	17		15,18
SNP17.240	17		15,18
SNP17.242	17		15,18
SNP17.243	17		15,18
SNP17.244	17		15,18
SNP17.245	17		15,18
SNP17.246	17		15,18
SNP17.247	17		15,18
SNP17.248	17		15,18
SNP17.249	17		15,18
SNP17.250	17		15,18
SNP17.252	17		15,18
SNP17.253	17		15,18
SNP17.254	17		15,18
SNP17.256	17		15,18
SNP17.257	17		15,18
SNP17.260	17		18
SNP17.261	17		18
SNP17.264	17		18
SNP17.265	17		18
SNP17.266	17		15,18
SNP17.267	17		15,18
SNP17.268	17		15,18
SNP17.269	17		15,18



Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP17.275	17		15,18
SNP17.276	17		15,18
SNP17.277	17		15,18
SNP17.280	17		15,18
SNP17.282	17		15,18
SNP17.284	17		15,18
SNP17.285	17		15,18
SNP17.286	17		15,18
SNP17.287	17		15,18
SNP17.288	17		15,18
SNP17.289	17		15
SNP17.290	17		15,18
SNP17.292	17		15,18
SNP17.294	17		15,18
SNP17.295	17		15,18
SNP17.296	17		18
SNP17.298	17		15,18
SNP17.300	17		15,18
SNP17.302	17		15,18
SNP17.303	17		15,18
SNP17.304	17		15,18
SNP17.305	17		15,18
SNP17.309	17		15,18
SNP18.164	18	BARC_1.01_Gm18_10714843_A_G	14,15,17,18
SNP18.031	18	BARC_1.01_Gm18_1295849_G_A	14,15,17,18
SNP18.223	18	BARC_1.01_Gm18_19415953_T_C	15
SNP18.249	18	BARC_1.01_Gm18_24296638_T_C	14,15,17,18
SNP18.008	18	BARC_1.01_Gm18_335349_A_G	14,15,17,18
SNP18.010	18	BARC_1.01_Gm18_441081_G_A	14,15,17,18
SNP18.002	18	BARC_1.01_Gm18_54979_G_A	14,15,17,18
SNP18.380	18	BARC_1.01_Gm18_55000978_G_A	14,15
SNP18.400	18	BARC_1.01_Gm18_56429507_G_A	14,15,17,18
SNP18.403	18	BARC_1.01_Gm18_56713153_C_T	14,15
SNP18.413	18	BARC_1.01_Gm18_57353881_T_C	14,15,17,18
SNP18.479	18	BARC_1.01_Gm18_60840873_C_A	14
SNP18.131	18	BARC_1.01_Gm18_7454790_G_A	14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP18.144	18	BARC_1.01_Gm18_8828934_C_T	14,15,17,18
SNP18.150	18	BARC_1.01_Gm18_9325429_C_T	14,15,17,18
SNP18.004	18		14,15,17,18
SNP18.007	18		14,15,17,18
SNP18.009	18		14,15,17,18
SNP18.011	18		14,15,17,18
SNP18.012	18		14,15,17,18
SNP18.013	18		14,15,17,18
SNP18.016	18		14,15,17,18
SNP18.017	18		14,15,17,18
SNP18.018	18		14,15,17,18
SNP18.019	18		14,15,17,18
SNP18.020	18		14,15,17,18
SNP18.021	18		14,15,17,18
SNP18.023	18		14,15,17,18
SNP18.024	18		14,15,17,18
SNP18.025	18		14,15,17,18
SNP18.027	18		14,15,17,18
SNP18.028	18		14,15,17,18
SNP18.029	18		14,15,17,18
SNP18.030	18		14,15,17,18
SNP18.032	18		14,15,17,18
SNP18.033	18		15,18
SNP18.034	18		14,15,17,18
SNP18.035	18		14,15,17,18
SNP18.036	18		14,15,18
SNP18.037	18		14,15
SNP18.038	18		14,15
SNP18.039	18		18
SNP18.040	18		15
SNP18.041	18		15,18
SNP18.042	18		14,15
SNP18.044	18		18
SNP18.045	18		15,18
SNP18.046	18		15,18
SNP18.047	18		18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP18.060	18		14,15,17,18
SNP18.063	18		14,15,17,18
SNP18.064	18		14,15,17,18
SNP18.072	18		18
SNP18.073	18		14
SNP18.083	18		14,15,17,18
SNP18.090	18		14,15,17,18
SNP18.093	18		14,15,17,18
SNP18.094	18		14,15,17,18
SNP18.098	18		14,15,17,18
SNP18.102	18		14,15,17,18
SNP18.116	18		14,15,17,18
SNP18.118	18		14,15,17,18
SNP18.121	18		14,15,17,18
SNP18.125	18		17,18
SNP18.127	18		14,15,17,18
SNP18.126	18		14,15,17,18
SNP18.133	18		14,15,17,18
SNP18.134	18		14,15,17,18
SNP18.141	18		14,15,17,18
SNP18.145	18		14,15,17,18
SNP18.155	18		14,15
SNP18.159	18		14,15,17,18
SNP18.163	18		14,15,17,18
SNP18.167	18		14,15,17,18
SNP18.168	18		14,15,17,18
SNP18.173	18		14,15,17
SNP18.177	18		14,15,17,18
SNP18.184	18		14,15,17,18
SNP18.185	18		14,15,17,18
SNP18.186	18		14,15,17,18
SNP18.191	18		14,15,17,18
SNP18.192	18		14,15,17,18
SNP18.195	18		14,15,17,18
SNP18.200	18		14,15,17,18
SNP18.202	18		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP18.212	18		14,15,17,18
SNP18.215	18		14,15,17,18
SNP18.221	18		14,15,17,18
SNP18.225	18		15
SNP18.230	18		15
SNP18.232	18		14,15,17,18
SNP18.234	18		15
SNP18.241	18		14,15,17,18
SNP18.242	18		14,15,17,18
SNP18.244	18		15,17
SNP18.245	18		14,15
SNP18.246	18		14,15,17,18
SNP18.247	18		14,15,17,18
SNP18.251	18		14,15,17,18
SNP18.254	18		14,15,17,18
SNP18.275	18		14,15,17,18
SNP18.287	18		14,15,17,18
SNP18.290	18		14,15,17,18
SNP18.293	18		14,15,17
SNP18.295	18		14,15,17
SNP18.307	18		14,15,17,18
SNP18.318	18		14
SNP18.329	18		14,15,17,18
SNP18.331	18		14,15,17,18
SNP18.333	18		14,15,17,18
SNP18.338	18		14,15,17,18
SNP18.343	18		14
SNP18.352	18		14,15,17,18
SNP18.355	18		14,15,17,18
SNP18.358	18		14,15,17,18
SNP18.359	18		14,15,17,18
SNP18.361	18		14,15,17,18
SNP18.364	18		14,15,17,18
SNP18.365	18		14,15,17,18
SNP18.367	18		14,15,17,18
SNP18.368	18		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP18.370	18		14,15,17,18
SNP18.371	18		14,15,17,18
SNP18.377	18		14,15,17,18
SNP18.384	18		14,15,17,18
SNP18.386	18		14,15,17,18
SNP18.388	18		14,15,17,18
SNP18.391	18		14,15,17,18
SNP18.393	18		14,15
SNP18.394	18		14,15,17,18
SNP18.395	18		14,15,17,18
SNP18.397	18		14,15,17,18
SNP18.411	18		14,15,17,18
SNP18.412	18		14,15,17,18
SNP18.415	18		14,15,17,18
SNP18.419	18		14,15,17,18
SNP18.425	18		14,15,17,18
SNP18.427	18		14,15,17
SNP18.432	18		14,15,17
SNP18.440	18		14,15,17,18
SNP18.441	18		14,15
SNP18.442	18		14,15,17,18
SNP18.443	18		14,15,17,18
SNP18.446	18		14,15,17,18
SNP18.448	18		14,15,17,18
SNP18.450	18		14,15,17,18
SNP18.452	18		14,15,17,18
SNP18.459	18		14,15,17,18
SNP18.461	18		14,15,17,18
SNP18.464	18		14,15,17,18
SNP18.469	18		14,15,17,18
SNP18.468	18		14,15,17,18
SNP18.470	18		14,15,17,18
SNP18.473	18		14,15
SNP18.484	18		14,15,17,18
SNP18.491	18		14,15
SNP18.495	18		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP18.501	18		14,15,17,18
SNP18.502	18		14,15,17,18
SNP18.001	18		15,18
SNP18.003	18		15,18
SNP18.005	18		15,18
SNP18.006	18		15,18
SNP18.014	18		15,18
SNP18.015	18		15,18
SNP18.026	18		18
SNP18.043	18		14,15,17,18
SNP18.050	18		15,18
SNP18.051	18		15
SNP18.054	18		18
SNP18.058	18		15,18
SNP18.059	18		15,18
SNP18.061	18		15,18
SNP18.062	18		18
SNP18.065	18		15,18
SNP18.066	18		15,18
SNP18.067	18		15,18
SNP18.068	18		15,18
SNP18.069	18		15,18
SNP18.070	18		18
SNP18.071	18		18
SNP18.075	18		15,18
SNP18.076	18		15,18
SNP18.077	18		15,18
SNP18.078	18		15,18
SNP18.079	18		15,18
SNP18.080	18		15,18
SNP18.081	18		15,18
SNP18.082	18		15,18
SNP18.084	18		15,18
SNP18.085	18		15,18
SNP18.086	18		15,18
SNP18.087	18		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP18.089	18		15,18
SNP18.091	18		18
SNP18.092	18		15,18
SNP18.095	18		15,18
SNP18.096	18		15,18
SNP18.099	18		15,18
SNP18.100	18		15,18
SNP18.101	18		15,18
SNP18.104	18		15,18
SNP18.105	18		15,18
SNP18.106	18		15,18
SNP18.107	18		15,18
SNP18.108	18		15,18
SNP18.110	18		15,18
SNP18.111	18		15,18
SNP18.112	18		15,18
SNP18.114	18		15,18
SNP18.115	18		15,18
SNP18.117	18		15,18
SNP18.119	18		15,18
SNP18.120	18		15,18
SNP18.122	18		15,18
SNP18.123	18		15,18
SNP18.124	18		15,18
SNP18.128	18		15,18
SNP18.129	18		15,18
SNP18.130	18		15,18
SNP18.132	18		15,18
SNP18.135	18		15,18
SNP18.136	18		18
SNP18.137	18		15,18
SNP18.140	18		14,15,17,18
SNP18.142	18		15,18
SNP18.143	18		15,18
SNP18.146	18		15,18
SNP18.147	18		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP18.149	18		15,18
SNP18.151	18		15,18
SNP18.152	18		15,18
SNP18.153	18		15,18
SNP18.154	18		15,18
SNP18.156	18		15,18
SNP18.157	18		15,18
SNP18.158	18		15,18
SNP18.160	18		15,18
SNP18.161	18		15,18
SNP18.162	18		15,18
SNP18.165	18		15,18
SNP18.166	18		15,18
SNP18.169	18		15,18
SNP18.170	18		15,18
SNP18.171	18		15,18
SNP18.172	18		15,18
SNP18.174	18		15,18
SNP18.175	18		15,18
SNP18.176	18		15,18
SNP18.178	18		15,18
SNP18.180	18		15,18
SNP18.181	18		15,18
SNP18.182	18		15,18
SNP18.183	18		15,18
SNP18.187	18		15,18
SNP18.188	18		15,18
SNP18.189	18		15,18
SNP18.190	18		15,18
SNP18.193	18		15,18
SNP18.194	18		15
SNP18.196	18		15,18
SNP18.197	18		15,18
SNP18.198	18		15,18
SNP18.199	18		15,18
SNP18.201	18		15,18



Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP18.204	18		15,18
SNP18.205	18		15,18
SNP18.207	18		15,18
SNP18.208	18		15,18
SNP18.209	18		15,18
SNP18.210	18		15
SNP18.211	18		15
SNP18.213	18		15,18
SNP18.214	18		15,18
SNP18.216	18		15,18
SNP18.217	18		15,18
SNP18.218	18		15,18
SNP18.219	18		15,18
SNP18.220	18		15,18
SNP18.222	18		15,18
SNP18.224	18		15
SNP18.226	18		15,18
SNP18.227	18		15,18
SNP18.229	18		15,18
SNP18.231	18		15
SNP18.233	18		15,18
SNP18.235	18		15
SNP18.236	18		15
SNP18.237	18		15,18
SNP18.238	18		15
SNP18.240	18		15,18
SNP18.243	18		15,18
SNP18.250	18		15,18
SNP18.252	18		15,18
SNP18.253	18		15,18
SNP18.255	18		15,18
SNP18.256	18		15,18
SNP18.257	18		15
SNP18.258	18		15,18
SNP18.259	18		15,18
SNP18.260	18		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP18.262	18		15,18
SNP18.263	18		15,18
SNP18.264	18		15,18
SNP18.265	18		15,18
SNP18.266	18		15,18
SNP18.267	18		15,18
SNP18.268	18		15,18
SNP18.269	18		15,18
SNP18.270	18		15,18
SNP18.271	18		15,18
SNP18.272	18		15,18
SNP18.273	18		15,18
SNP18.274	18		15,18
SNP18.276	18		15,18
SNP18.277	18		15,18
SNP18.278	18		15,18
SNP18.279	18		15,18
SNP18.280	18		15,18
SNP18.281	18		15,18
SNP18.282	18		15,18
SNP18.283	18		15,18
SNP18.285	18		15,18
SNP18.288	18		15,18
SNP18.294	18		15
SNP18.296	18		15
SNP18.297	18		15
SNP18.298	18		15
SNP18.299	18		15
SNP18.300	18		15,18
SNP18.301	18		15
SNP18.302	18		15
SNP18.303	18		15
SNP18.304	18		15,18
SNP18.305	18		15,18
SNP18.306	18		15,18
SNP18.308	18		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP18.310	18		15
SNP18.311	18		15
SNP18.312	18		15
SNP18.313	18		15
SNP18.323	18		15,18
SNP18.324	18		15,18
SNP18.325	18		15,18
SNP18.334	18		15,18
SNP18.335	18		15,18
SNP18.336	18		15,18
SNP18.337	18		15,18
SNP18.339	18		15,18
SNP18.340	18		15,18
SNP18.341	18		15,18
SNP18.345	18		15,18
SNP18.354	18		15,18
SNP18.356	18		15,18
SNP18.357	18		15,18
SNP18.360	18		15,18
SNP18.362	18		15,18
SNP18.363	18		15,18
SNP18.366	18		15,18
SNP18.372	18		18
SNP18.376	18		15,18
SNP18.378	18		15,18
SNP18.379	18		15,18
SNP18.382	18		15,18
SNP18.387	18		15,18
SNP18.389	18		15,18
SNP18.396	18		15,18
SNP18.398	18		15,18
SNP18.399	18		15,18
SNP18.401	18		15,18
SNP18.402	18		15,18
SNP18.404	18		15,18
SNP18.405	18		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP18.407	18		15,18
SNP18.408	18		18
SNP18.409	18		15,18
SNP18.410	18		15,18
SNP18.414	18		15,18
SNP18.416	18		15,18
SNP18.418	18		15,18
SNP18.420	18		15,18
SNP18.421	18		15,18
SNP18.422	18		15,18
SNP18.423	18		15,18
SNP18.424	18		15,18
SNP18.426	18		15
SNP18.428	18		15
SNP18.429	18		15
SNP18.430	18		15
SNP18.433	18		15
SNP18.434	18		15,18
SNP18.435	18		15
SNP18.436	18		15
SNP18.437	18		15,18
SNP18.438	18		15,18
SNP18.439	18		15,18
SNP18.444	18		15,18
SNP18.445	18		15,18
SNP18.447	18		15,18
SNP18.449	18		15,18
SNP18.453	18		15,18
SNP18.454	18		15,18
SNP18.455	18		15,18
SNP18.456	18		15,18
SNP18.457	18		15,18
SNP18.458	18		14,15,17,18
SNP18.460	18		14,15,17,18
SNP18.463	18		15,18
SNP18.465	18		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP18.467	18		15,18
SNP18.475	18		15,18
SNP18.476	18		15,18
SNP18.480	18		15
SNP18.481	18		14,15,17,18
SNP18.482	18		15,18
SNP18.483	18		15,18
SNP18.485	18		15,18
SNP18.486	18		15,18
SNP18.487	18		15
SNP18.488	18		15,18
SNP18.489	18		15,18
SNP18.490	18		15,18
SNP18.494	18		15,18
SNP18.497	18		15,18
SNP18.498	18		14,15,17,18
SNP18.499	18		15,18
SNP18.500	18		15,18
SNP18.503	18		15,18
SNP18.505	18		15,18
SNP19.023	19	BARC_1.01_Gm19_1306591_T_C	14,15,17,18
SNP19.122	19	BARC_1.01_Gm19_15231327_A_G	14,15
SNP19.118	19	BARC_1.01_Gm19_24435936_A_G	14,15,17,18
SNP19.283	19	BARC_1.01_Gm19_42655124_T_C	14,15,17,18
SNP19.306	19	BARC_1.01_Gm19_44686482_T_C	14,15,17,18
SNP19.338	19	BARC_1.01_Gm19_47114567_T_G	15,18
SNP19.353	19	BARC_1.01_Gm19_48091800_G_A	14,15,17,18
SNP19.060	19	BARC_1.01_Gm19_5225109_T_G	18
SNP19.001	19	BARC_1.01_Gm19_549103_T_G	15
SNP19.066	19	BARC_1.01_Gm19_7147219_T_C	14,15,17,18
SNP19.069	19	BARC_1.01_Gm19_7484988_G_A	14,15,17,18
SNP19.006	19		14,15,17
SNP19.010	19		14,15,17,18
SNP19.013	19		14,15,17,18
SNP19.021	19		14,17,18
SNP19.027	19		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP19.031	19		14,15,17,18
SNP19.032	19		14,15,17,18
SNP19.033	19		14,15
SNP19.035	19		14,15,17,18
SNP19.036	19		14,15,17,18
SNP19.037	19		14,15,17,18
SNP19.038	19		14,15,17,18
SNP19.039	19		14,15,17,18
SNP19.041	19		18
SNP19.047	19		14,15,17,18
SNP19.053	19		15,18
SNP19.054	19		15,18
SNP19.056	19		14,15
SNP19.062	19		14,15,17,18
SNP19.063	19		18
SNP19.065	19		14,15,17,18
SNP19.070	19		14,15
SNP19.075	19		14,15,17,18
SNP19.083	19		14,15,17,18
SNP19.086	19		14,15
SNP19.087	19		14,15,17,18
SNP19.090	19		14,15
SNP19.097	19		14,15,17,18
SNP19.095	19		14,15
SNP19.094	19		14,15,17,18
SNP19.096	19		14,15,17,18
SNP19.108	19		14,15,17,18
SNP19.124	19		14,15,17,18
SNP19.121	19		14,15,17,18
SNP19.120	19		14,15,17,18
SNP19.102	19		14,15,17,18
SNP19.103	19		14,15,17,18
SNP19.104	19		14,15,17,18
SNP19.109	19		14,15,17,18
SNP19.111	19		14,15,17,18
SNP19.112	19		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP19.115	19		14,15,17,18
SNP19.116	19		14,15
SNP19.119	19		14,15,17,18
SNP19.127	19		14,15
SNP19.131	19		14,15
SNP19.135	19		14,15,17,18
SNP19.138	19		14,15,17,18
SNP19.139	19		14,15,17,18
SNP19.141	19		14,15,17,18
SNP19.146	19		14,17,18
SNP19.158	19		14,15,17,18
SNP19.182	19		14,15
SNP19.184	19		14,15
SNP19.189	19		14,15,17,18
SNP19.190	19		14,15
SNP19.193	19		14,15,17,18
SNP19.197	19		14,15,17,18
SNP19.198	19		14,15,17,18
SNP19.203	19		14,15,17,18
SNP19.208	19		14,15
SNP19.210	19		14,15,17,18
SNP19.232	19		14,15,17,18
SNP19.236	19		14,15,17,18
SNP19.237	19		14,15,17,18
SNP19.238	19		14,15,17,18
SNP19.239	19		14,15,17,18
SNP19.240	19		14,15,17,18
SNP19.248	19		14,15,17,18
SNP19.249	19		14,15,17,18
SNP19.254	19		14,15,17,18
SNP19.262	19		14,15,18
SNP19.286	19		14,15,17,18
SNP19.294	19		14,15,17,18
SNP19.305	19		14,15,17,18
SNP19.307	19		14,15,17,18
SNP19.309	19		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP19.311	19		14,15,17,18
SNP19.314	19		14,15,17,18
SNP19.349	19		14,15,17,18
SNP19.351	19		14,15,17,18
SNP19.354	19		14,15,17,18
SNP19.355	19		14,15,17,18
SNP19.356	19		14,15,17,18
SNP19.357	19		14,15,17,18
SNP19.359	19		14,15,17,18
SNP19.360	19		14,15
SNP19.361	19		14,15,17,18
SNP19.362	19		14,15,17,18
SNP19.363	19		14,15,17,18
SNP19.365	19		14,15,17,18
SNP19.366	19		14,15
SNP19.367	19		14,15,17,18
SNP19.368	19		14,15,17,18
SNP19.371	19		14,15,17,18
SNP19.372	19		14,15,17,18
SNP19.373	19		14,15,17,18
SNP19.377	19		14,15
SNP19.379	19		14,15,17
SNP19.385	19		14,15,17
SNP19.388	19		14,15,17
SNP19.391	19		14,15,17,18
SNP19.394	19		14,15,17,18
SNP19.395	19		14,15,17
SNP19.002	19		14,15,17
SNP19.003	19		14,15,17
SNP19.005	19		15
SNP19.007	19		15
SNP19.008	19		15
SNP19.009	19		15,18
SNP19.012	19		15
SNP19.014	19		15,18
SNP19.018	19		15,18



Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP19.020	19		15,18
SNP19.022	19		15,18
SNP19.024	19		15,18
SNP19.025	19		15,18
SNP19.026	19		15,18
SNP19.029	19		15,18
SNP19.030	19		15,18
SNP19.034	19		15,18
SNP19.040	19		15,18
SNP19.042	19		15,18
SNP19.043	19		15,18
SNP19.044	19		15,18
SNP19.045	19		15,18
SNP19.046	19		15,18
SNP19.048	19		15,18
SNP19.049	19		15,18
SNP19.050	19		15,18
SNP19.051	19		15,18
SNP19.052	19		15,18
SNP19.055	19		15,18
SNP19.057	19		15,18
SNP19.058	19		18
SNP19.059	19		18
SNP19.061	19		18
SNP19.064	19		15,18
SNP19.067	19		15,18
SNP19.068	19		15,18
SNP19.071	19		15,18
SNP19.072	19		15,18
SNP19.073	19		15,18
SNP19.074	19		15,18
SNP19.077	19		15,18
SNP19.079	19		15,18
SNP19.080	19		15,18
SNP19.081	19		15,18
SNP19.082	19		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP19.085	19		18
SNP19.088	19		15,18
SNP19.089	19		18
SNP19.091	19		15,18
SNP19.092	19		15,18
SNP19.093	19		15,18
SNP19.098	19		15,18
SNP19.099	19		15,18
SNP19.100	19		15,18
SNP19.101	19		15,18
SNP19.105	19		15,18
SNP19.106	19		15,18
SNP19.107	19		15,18
SNP19.110	19		15,18
SNP19.114	19		15,18
SNP19.117	19		15,18
SNP19.125	19		15,18
SNP19.126	19		15,18
SNP19.128	19		15,18
SNP19.129	19		15
SNP19.130	19		15,18
SNP19.132	19		15,18
SNP19.133	19		15,18
SNP19.134	19		15,18
SNP19.136	19		15,18
SNP19.137	19		15,18
SNP19.140	19		15,18
SNP19.142	19		15,18
SNP19.144	19		15,18
SNP19.145	19		15,18
SNP19.147	19		15,18
SNP19.148	19		15,18
SNP19.149	19		15,18
SNP19.150	19		15,18
SNP19.151	19		15,18
SNP19.152	19		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP19.154	19		15,18
SNP19.155	19		15,18
SNP19.156	19		15,18
SNP19.157	19		15,18
SNP19.159	19		15,18
SNP19.160	19		15,18
SNP19.161	19		15,18
SNP19.162	19		15,18
SNP19.163	19		15,18
SNP19.164	19		15,18
SNP19.165	19		15,18
SNP19.166	19		15,18
SNP19.167	19		15,18
SNP19.169	19		15,18
SNP19.170	19		15,18
SNP19.171	19		15,18
SNP19.172	19		15,18
SNP19.173	19		15,18
SNP19.174	19		15,18
SNP19.175	19		15,18
SNP19.176	19		15,18
SNP19.177	19		15,18
SNP19.178	19		15,18
SNP19.180	19		15,18
SNP19.181	19		15,18
SNP19.183	19		15,18
SNP19.185	19		15,18
SNP19.186	19		14,15,17,18
SNP19.187	19		15,18
SNP19.188	19		15,18
SNP19.192	19		15,18
SNP19.194	19		15,18
SNP19.195	19		15,18
SNP19.196	19		15,18
SNP19.202	19		15
SNP19.204	19		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP19.206	19		15,18
SNP19.207	19		15,18
SNP19.209	19		15,18
SNP19.211	19		15,18
SNP19.213	19		15,18
SNP19.214	19		15,18
SNP19.215	19		15
SNP19.217	19		15,18
SNP19.218	19		15,18
SNP19.223	19		15,18
SNP19.225	19		15,18
SNP19.226	19		15,18
SNP19.227	19		15,18
SNP19.228	19		15,18
SNP19.229	19		15,18
SNP19.230	19		15,18
SNP19.231	19		15,18
SNP19.233	19		15,18
SNP19.234	19		15,18
SNP19.235	19		14,15,17,18
SNP19.241	19		15,18
SNP19.242	19		15,18
SNP19.243	19		15,18
SNP19.244	19		15,18
SNP19.250	19		15,18
SNP19.252	19		15,18
SNP19.253	19		15,18
SNP19.260	19		15,18
SNP19.261	19		15,18
SNP19.263	19		15,18
SNP19.264	19		15
SNP19.265	19		15
SNP19.266	19		15
SNP19.272	19		15
SNP19.273	19		15
SNP19.278	19		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP19.280	19		15,18
SNP19.281	19		15,18
SNP19.282	19		15
SNP19.284	19		15,18
SNP19.285	19		15,18
SNP19.288	19		15,18
SNP19.289	19		15,18
SNP19.290	19		15,18
SNP19.291	19		15,18
SNP19.292	19		15,18
SNP19.293	19		15,18
SNP19.295	19		15,18
SNP19.296	19		15,18
SNP19.297	19		15,18
SNP19.298	19		15,18
SNP19.299	19		15,18
SNP19.300	19		15,18
SNP19.301	19		15,18
SNP19.302	19		15,18
SNP19.303	19		15,18
SNP19.304	19		15,18
SNP19.308	19		15,18
SNP19.312	19		15,18
SNP19.313	19		15,18
SNP19.315	19		15,18
SNP19.316	19		15,18
SNP19.317	19		15,18
SNP19.318	19		15,18
SNP19.319	19		15,18
SNP19.320	19		15,18
SNP19.321	19		15,18
SNP19.330	19		18
SNP19.334	19		15,18
SNP19.335	19		15,18
SNP19.336	19		15,18
SNP19.337	19		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP19.340	19		15,18
SNP19.341	19		15
SNP19.342	19		15
SNP19.343	19		15
SNP19.344	19		15
SNP19.346	19		15
SNP19.347	19		15,18
SNP19.348	19		15,18
SNP19.350	19		15,18
SNP19.352	19		15,18
SNP19.369	19		15,18
SNP19.370	19		15,18
SNP19.374	19		15,18
SNP19.375	19		15,18
SNP19.376	19		15,18
SNP19.378	19		15,18
SNP19.380	19		15,18
SNP19.381	19		15,18
SNP19.382	19		15,18
SNP19.383	19		15,18
SNP19.384	19		15
SNP19.386	19		15,18
SNP19.387	19		15,18
SNP19.389	19		15,18
SNP19.390	19		15
SNP19.392	19		15
SNP19.393	19		15,18
SNP20.043	20	BARC_1.01_Gm20_2005776_G_A	14,15,18
SNP20.044	20	BARC_1.01_Gm20_2053709_G_T	14,15,18
SNP20.132	20	BARC_1.01_Gm20_33501066_T_G	18
SNP20.142	20	BARC_1.01_Gm20_34101170_A_G	18
SNP20.158	20	BARC_1.01_Gm20_35628338_T_C	14,15,17,18
SNP20.273	20	BARC_1.01_Gm20_43583973_T_C	14,15,17,18
SNP20.297	20	BARC_1.01_Gm20_44848412_C_A	18
SNP20.302	20	BARC_1.01_Gm20_45308766_G_A	17,18
SNP20.313	20	BARC_1.01_Gm20_46031758_G_T	17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP20.006	20		14,15,17,18
SNP20.012	20		14,15,17,18
SNP20.015	20		14,15,17,18
SNP20.016	20		14,15,17,18
SNP20.017	20		14,15
SNP20.018	20		14,15,17,18
SNP20.019	20		14,15
SNP20.020	20		14,15,17,18
SNP20.022	20		14,15,17,18
SNP20.023	20		14,15,17,18
SNP20.024	20		14,15,17,18
SNP20.025	20		14,15,17,18
SNP20.026	20		14,15,17,18
SNP20.027	20		14,15,17,18
SNP20.028	20		14,15,17,18
SNP20.034	20		15,17,18
SNP20.036	20		14,15,17,18
SNP20.045	20		14,15,17,18
SNP20.046	20		14,15,17,18
SNP20.050	20		14,15,17,18
SNP20.051	20		14,15,17
SNP20.052	20		14,15,17,18
SNP20.056	20		14,15,17,18
SNP20.079	20		14,15,17,18
SNP20.088	20		14,15,17,18
SNP20.103	20		14,15,17,18
SNP20.104	20		14,15
SNP20.106	20		14,15,17,18
SNP20.112	20		14,15,17,18
SNP20.114	20		14,15,17,18
SNP20.116	20		15
SNP20.118	20		14,15,17,18
SNP20.121	20		14,15,17,18
SNP20.140	20		18
SNP20.143	20		14,15,17,18
SNP20.148	20		14,15,17,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP20.167	20		14
SNP20.176	20		14
SNP20.177	20		14,15
SNP20.178	20		14
SNP20.180	20		14
SNP20.181	20		14
SNP20.183	20		14
SNP20.191	20		15
SNP20.197	20		14,15,18
SNP20.199	20		18
SNP20.201	20		14
SNP20.211	20		15,18
SNP20.212	20		14,15,17,18
SNP20.214	20		14,15,17,18
SNP20.213	20		14,15,17,18
SNP20.220	20		14,15,17,18
SNP20.226	20		14,15,17,18
SNP20.227	20		14,15,17,18
SNP20.229	20		15,18
SNP20.230	20		14,15,17,18
SNP20.233	20		14,17,18
SNP20.234	20		14,15,17,18
SNP20.236	20		14,17,18
SNP20.238	20		14,15,17,18
SNP20.239	20		17,18
SNP20.249	20		14,15,17,18
SNP20.263	20		14,15,17,18
SNP20.276	20		14,15,17,18
SNP20.278	20		14,15,17,18
SNP20.280	20		14,15,17,18
SNP20.281	20		14,15,17,18
SNP20.282	20		14,15,17,18
SNP20.283	20		15,18
SNP20.284	20		14,15,17,18
SNP20.287	20		14,15,17,18
SNP20.291	20		14,15,17,18



Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP20.304	20		14,15,17,18
SNP20.305	20		14,15,17,18
SNP20.306	20		14,15,17,18
SNP20.316	20		17,18
SNP20.317	20		17,18
SNP20.318	20		14,15,17,18
SNP20.319	20		14,15,17,18
SNP20.001	20		15,18
SNP20.002	20		15,18
SNP20.003	20		15,18
SNP20.004	20		15,18
SNP20.005	20		15
SNP20.007	20		15,18
SNP20.008	20		15,18
SNP20.009	20		15,18
SNP20.010	20		15,18
SNP20.011	20		15,18
SNP20.014	20		15,18
SNP20.021	20		15,18
SNP20.030	20		15,18
SNP20.031	20		15,18
SNP20.032	20		15,18
SNP20.038	20		15,18
SNP20.048	20		15,18
SNP20.049	20		15,18
SNP20.053	20		15,18
SNP20.054	20		15,18
SNP20.055	20		15,18
SNP20.057	20		15,18
SNP20.058	20		15,18
SNP20.066	20		15,18
SNP20.067	20		15,18
SNP20.069	20		15,18
SNP20.071	20		15,18
SNP20.073	20		15,18
SNP20.084	20		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP20.091	20		15,18
SNP20.093	20		15,18
SNP20.097	20		15,18
SNP20.098	20		15,18
SNP20.099	20		15,18
SNP20.100	20		15,18
SNP20.101	20		15,18
SNP20.102	20		15,18
SNP20.105	20		15,18
SNP20.107	20		15,18
SNP20.108	20		15,18
SNP20.109	20		15,18
SNP20.110	20		15,18
SNP20.113	20		15,18
SNP20.115	20		15
SNP20.117	20		15
SNP20.127	20		15,18
SNP20.128	20		15,18
SNP20.129	20		18
SNP20.130	20		18
SNP20.135	20		18
SNP20.136	20		15,18
SNP20.137	20		15,18
SNP20.138	20		15
SNP20.141	20		18
SNP20.144	20		15,18
SNP20.147	20		15,18
SNP20.149	20		15,18
SNP20.151	20		15,18
SNP20.152	20		15,18
SNP20.153	20		15,18
SNP20.154	20		15,18
SNP20.155	20		15,18
SNP20.156	20		15,18
SNP20.159	20		15,18
SNP20.163	20		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP20.169	20		15,18
SNP20.170	20		15,18
SNP20.171	20		15,18
SNP20.172	20		15,18
SNP20.173	20		18
SNP20.174	20		18
SNP20.195	20		15,18
SNP20.196	20		18
SNP20.198	20		18
SNP20.200	20		18
SNP20.204	20		18
SNP20.206	20		18
SNP20.208	20		18
SNP20.209	20		18
SNP20.215	20		15,18
SNP20.219	20		15,18
SNP20.221	20		15,18
SNP20.222	20		15,18
SNP20.223	20		15,18
SNP20.224	20		15,18
SNP20.228	20		15,18
SNP20.231	20		15,18
SNP20.232	20		15,18
SNP20.235	20		15,18
SNP20.237	20		15,18
SNP20.240	20		15,18
SNP20.242	20		15,18
SNP20.243	20		15,18
SNP20.244	20		15,18
SNP20.245	20		15,18
SNP20.246	20		15,18
SNP20.247	20		15,18
SNP20.248	20		15,18
SNP20.252	20		15,18
SNP20.258	20		15,18
SNP20.259	20		15,18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP20.261	20		15,18
SNP20.262	20		15
SNP20.264	20		15,18
SNP20.265	20		15,18
SNP20.266	20		15,18
SNP20.267	20		15,18
SNP20.268	20		15,18
SNP20.270	20		15,18
SNP20.271	20		15,18
SNP20.272	20		15,18
SNP20.274	20		15,18
SNP20.275	20		15,18
SNP20.277	20		15,18
SNP20.279	20		15,18
SNP20.285	20		15,18
SNP20.286	20		15,18
SNP20.288	20		15,18
SNP20.289	20		15,18
SNP20.290	20		15,18
SNP20.292	20		15,18
SNP20.294	20		15,18
SNP20.295	20		15,18
SNP20.296	20		18
SNP20.298	20		18
SNP20.299	20		18
SNP20.300	20		15,18
SNP20.301	20		15,18
SNP20.303	20		18
SNP20.307	20		15,18
SNP20.309	20		15,18
SNP20.310	20		18
SNP20.311	20		18
SNP20.312	20		18
SNP20.314	20		15,18
SNP20.315	20		18
SNP20.321	20		18

Table A. Continued

Marker Name	Chromosome	Public Marker	Years
SNP20.322	20		18
SNP20.323	20		18

TABLE B

## ENTRY LSMEANS FOR WATERLOGGED TOLERANCE TRAITS

Table B1. 2014 LSMeans by growth habit (GH) of VS\_FLTFLD (score).

Genotypes	GH	2014 VS_FLTFLD (score)
COR-B-012	IND	7.01
COR-B-013	IND	8.00
COR-B-014	IND	5.50
COR-B-015	IND	5.37
COR-B-016	IND	7.01
COR-B-017	IND	5.25
COR-B-018	IND	6.25
COR-B-019	IND	4.01
COR-B-020	IND	8.01
COR-B-021	IND	6.01
COR-B-022	IND	9.01
COR-B-024	IND	2.60
COR-B-025	IND	6.40
COR-B-053	IND	5.68
COR-B-056	IND	6.34
COR-B-057	IND	3.68
COR-B-058	IND	4.50
COR-B-060	IND	3.40
COR-B-063	IND	6.25
COR-B-067	IND	4.50
COR-B-068	IND	5.00
COR-B-071	IND	6.34
COR-B-076	IND	2.34
COR-B-083	IND	7.25
COR-B-084	IND	4.34
COR-B-089	IND	6.00
COR-B-091	IND	7.68
COR-B-097	IND	7.00
COR-B-098	IND	6.34
COR-B-099	IND	4.20
COR-B-100	IND	3.01
COR-B-104	IND	5.47

Table B1. Continued

Genotypes	GH	2014 VS_FLTFLD (score)
COR-B-105	IND	5.00
COR-B-106	IND	6.09
COR-B-112	IND	5.75
COR-B-115	IND	7.01
COR-B-116	IND	2.34
COR-B-118	IND	5.17
COR-B-119	IND	7.01
COR-B-122	IND	8.20
COR-B-123	IND	6.20
COR-B-125	IND	3.00
COR-B-180	IND	4.34
COR-B-185	IND	5.68
COR-B-201	IND	7.01
COR-B-209	IND	5.01
COR-B-212	IND	4.34
COR-B-217	IND	7.01
COR-B-235	IND	5.00
COR-B-241	IND	7.01
COR-B-274	IND	3.01
COR-B-275	IND	4.34
COR-B-276	IND	5.68
COR-B-278	IND	6.34
COR-B-281	IND	5.01
COR-B-282	IND	4.34
COR-B-284	IND	7.01
COR-B-288	IND	3.01
COR-B-292	IND	6.34
COR-B-293	IND	6.34
COR-B-294	IND	4.34
COR-B-296	IND	5.68
COR-B-297	IND	7.34
COR-B-299	IND	7.01
COR-B-303	IND	5.68
COR-B-304	IND	3.00
COR-B-306	IND	7.80
COR-B-326	IND	5.01

Table B1. Continued

Genotypes	GH	2014 VS_FLTFLD (score)
COR-B-335	IND	9.00
COR-B-340	IND	5.68
COR-B-357	IND	2.60
COR-B-358	IND	3.80
COR-B-361	IND	4.20
COR-B-363	IND	4.20
COR-B-366	IND	3.00
COR-B-372	IND	4.34
COR-B-373	IND	4.34
COR-B-374	IND	4.34
COR-B-375	IND	4.34
COR-B-378	IND	5.01
COR-B-379	IND	4.34
COR-B-382	IND	5.01
COR-B-385	IND	6.34
COR-B-389	IND	5.68
COR-B-390	IND	6.34
COR-B-392	IND	4.34
COR-B-396	IND	5.68
COR-B-399	IND	7.01
COR-B-408	IND	4.34
COR-B-409	IND	4.01
COR-B-415	IND	5.01
COR-B-416	IND	4.01
COR-B-418	IND	4.00
COR-B-432	IND	3.00
COR-B-023	DET	4.20
COR-B-026	DET	3.00
COR-B-027	DET	5.80
COR-B-028	DET	6.77
COR-B-029	DET	6.40
COR-B-030	DET	7.80
COR-B-131	DET	4.64
COR-B-132	DET	5.00
COR-B-134	DET	7.00
COR-B-136	DET	6.42



Table B1. Continued

Genotypes	GH	2014 VS_FLTFLD (score)
COR-B-139	DET	4.42
COR-B-141	DET	3.80
COR-B-142	DET	5.00
COR-B-143	DET	3.40
COR-B-144	DET	5.40
COR-B-145	DET	4.20
COR-B-149	DET	5.00
COR-B-151	DET	6.60
COR-B-244	DET	7.80
COR-B-250	DET	5.40
COR-B-254	DET	5.00
COR-B-255	DET	5.80
COR-B-259	DET	3.80
COR-B-260	DET	5.00
COR-B-264	DET	6.20
COR-B-265	DET	5.00
COR-B-307	DET	4.20
COR-B-309	DET	4.20
COR-B-310	DET	4.60
COR-B-314	DET	5.00
COR-B-315	DET	3.40
COR-B-352	DET	5.80
COR-B-368	DET	5.80
COR-B-435	DET	5.80
COR-B-441	DET	4.60
COR-B-445	DET	7.40
COR-B-452	DET	6.60
COR-B-453	DET	6.20
	Mean of IND	5.34
	Mean of DET	5.33

Table B2. 2015 LSMMeans by growth habit (GH) of VS\_FLTFLD (score).

Genotypes	GH	2015 VS_FLTFLD (score)
COR-B-018	IND	4.61
COR-B-020	IND	5.41
COR-B-022	IND	7.41
COR-B-024	IND	7.01
COR-B-031	IND	3.81
COR-B-032	IND	3.81
COR-B-033	IND	4.61
COR-B-034	IND	1.81
COR-B-035	IND	3.81
COR-B-036	IND	5.01
COR-B-037	IND	3.81
COR-B-038	IND	4.61
COR-B-039	IND	3.81
COR-B-040	IND	5.41
COR-B-041	IND	3.41
COR-B-042	IND	5.01
COR-B-043	IND	4.61
COR-B-044	IND	3.01
COR-B-045	IND	2.21
COR-B-046	IND	5.01
COR-B-047	IND	2.61
COR-B-048	IND	5.01
COR-B-049	IND	7.01
COR-B-050	IND	4.25
COR-B-051	IND	4.25
COR-B-052	IND	4.65
COR-B-055	IND	3.05
COR-B-056	IND	4.25
COR-B-057	IND	6.25
COR-B-058	IND	3.81
COR-B-060	IND	3.01
COR-B-061	IND	4.29
COR-B-062	IND	6.65
COR-B-063	IND	5.41
COR-B-064	IND	5.45
COR-B-066	IND	4.61

Table B2. Continued

Genotypes	GH	2015 VS_FLTFLD (score)
COR-B-067	IND	4.21
COR-B-068	IND	5.81
COR-B-069	IND	3.81
COR-B-070	IND	5.85
COR-B-071	IND	6.41
COR-B-072	IND	4.61
COR-B-073	IND	4.21
COR-B-075	IND	5.81
COR-B-076	IND	2.21
COR-B-083	IND	4.81
COR-B-084	IND	5.01
COR-B-089	IND	5.21
COR-B-090	IND	5.41
COR-B-091	IND	6.21
COR-B-092	IND	4.21
COR-B-093	IND	5.41
COR-B-097	IND	6.21
COR-B-098	IND	6.21
COR-B-099	IND	5.81
COR-B-100	IND	5.01
COR-B-103	IND	3.81
COR-B-104	IND	4.21
COR-B-105	IND	6.21
COR-B-106	IND	7.01
COR-B-111	IND	5.81
COR-B-112	IND	4.01
COR-B-115	IND	5.21
COR-B-116	IND	3.81
COR-B-117	IND	5.41
COR-B-118	IND	5.81
COR-B-119	IND	6.61
COR-B-122	IND	7.81
COR-B-124	IND	3.01
COR-B-125	IND	7.81
COR-B-126	IND	2.55
COR-B-129	IND	4.95

Table B2. Continued

Genotypes	GH	2015 VS_FLTFLD (score)
COR-B-154	IND	3.45
COR-B-155	IND	3.01
COR-B-156	IND	5.05
COR-B-158	IND	5.05
COR-B-159	IND	4.25
COR-B-160	IND	7.05
COR-B-161	IND	5.45
COR-B-162	IND	4.65
COR-B-163	IND	6.25
COR-B-164	IND	5.05
COR-B-165	IND	4.25
COR-B-166	IND	3.65
COR-B-167	IND	5.05
COR-B-168	IND	5.05
COR-B-169	IND	5.45
COR-B-172	IND	6.65
COR-B-173	IND	5.45
COR-B-174	IND	3.45
COR-B-176	IND	4.21
COR-B-178	IND	3.41
COR-B-179	IND	4.21
COR-B-180	IND	5.63
COR-B-182	IND	3.81
COR-B-183	IND	3.41
COR-B-184	IND	4.21
COR-B-185	IND	6.21
COR-B-186	IND	5.01
COR-B-189	IND	5.01
COR-B-190	IND	6.21
COR-B-191	IND	3.01
COR-B-192	IND	3.81
COR-B-193	IND	3.81
COR-B-197	IND	4.61
COR-B-198	IND	5.49
COR-B-199	IND	6.21
COR-B-201	IND	3.81

Table B2. Continued

Genotypes	GH	2015 VS_FLTFLD (score)
COR-B-205	IND	4.61
COR-B-207	IND	5.41
COR-B-208	IND	3.01
COR-B-209	IND	4.21
COR-B-211	IND	5.01
COR-B-213	IND	5.81
COR-B-214	IND	4.61
COR-B-215	IND	7.01
COR-B-216	IND	5.81
COR-B-217	IND	3.84
COR-B-219	IND	3.39
COR-B-220	IND	4.99
COR-B-221	IND	4.19
COR-B-222	IND	6.59
COR-B-223	IND	5.19
COR-B-224	IND	5.01
COR-B-225	IND	4.21
COR-B-228	IND	5.01
COR-B-229	IND	6.21
COR-B-230	IND	3.37
COR-B-231	IND	3.77
COR-B-232	IND	3.79
COR-B-233	IND	3.97
COR-B-234	IND	4.17
COR-B-235	IND	4.19
COR-B-236	IND	5.41
COR-B-237	IND	3.35
COR-B-240	IND	2.95
COR-B-241	IND	4.55
COR-B-245	IND	2.15
COR-B-267	IND	4.65
COR-B-268	IND	3.45
COR-B-269	IND	5.85
COR-B-271	IND	3.45
COR-B-272	IND	3.85
COR-B-273	IND	2.25

Table B2. Continued

Genotypes	GH	2015 VS_FLTFLD (score)
COR-B-274	IND	3.05
COR-B-276	IND	3.05
COR-B-277	IND	4.83
COR-B-279	IND	6.25
COR-B-280	IND	4.21
COR-B-282	IND	3.01
COR-B-283	IND	6.61
COR-B-284	IND	2.21
COR-B-285	IND	3.01
COR-B-286	IND	5.81
COR-B-289	IND	5.81
COR-B-291	IND	5.01
COR-B-293	IND	6.24
COR-B-301	IND	3.81
COR-B-326	IND	2.65
COR-B-335	IND	5.81
COR-B-340	IND	4.59
COR-B-356	IND	7.05
COR-B-359	IND	5.45
COR-B-360	IND	5.45
COR-B-362	IND	4.61
COR-B-364	IND	5.41
COR-B-365	IND	6.61
COR-B-376	IND	4.25
COR-B-377	IND	5.05
COR-B-380	IND	5.05
COR-B-383	IND	3.81
COR-B-384	IND	3.81
COR-B-391	IND	3.01
COR-B-393	IND	5.01
COR-B-394	IND	5.41
COR-B-403	IND	5.81
COR-B-404	IND	5.01
COR-B-406	IND	3.01
COR-B-410	IND	5.41
COR-B-419	IND	5.01

Table B2. Continued

Genotypes	GH	2015 VS_FLTFLD (score)
COR-B-420	IND	3.81
COR-B-422	IND	3.35
COR-B-423	IND	3.35
COR-B-438	IND	4.95
COR-B-442	IND	2.55
COR-B-467	IND	4.65
COR-B-468	IND	6.65
COR-B-023	DET	4.20
COR-B-027	DET	6.60
COR-B-030	DET	4.60
COR-B-131	DET	5.80
COR-B-132	DET	5.00
COR-B-134	DET	4.20
COR-B-136	DET	4.20
COR-B-139	DET	4.60
COR-B-142	DET	4.20
COR-B-143	DET	3.80
COR-B-144	DET	5.00
COR-B-145	DET	3.80
COR-B-146	DET	4.20
COR-B-149	DET	5.80
COR-B-150	DET	7.00
COR-B-151	DET	5.00
COR-B-152	DET	7.80
COR-B-244	DET	4.40
COR-B-246	DET	8.20
COR-B-247	DET	3.40
COR-B-249	DET	4.60
COR-B-250	DET	2.60
COR-B-251	DET	3.80
COR-B-253	DET	4.00
COR-B-254	DET	5.00
COR-B-255	DET	5.00
COR-B-256	DET	3.40
COR-B-257	DET	5.40
COR-B-258	DET	3.40

Table B2. Continued

Genotypes	GH	2015 VS_FLTFLD (score)
COR-B-259	DET	1.40
COR-B-260	DET	4.20
COR-B-261	DET	6.20
COR-B-262	DET	7.00
COR-B-264	DET	4.60
COR-B-315	DET	4.60
COR-B-318	DET	5.00
COR-B-322	DET	3.80
COR-B-352	DET	5.80
COR-B-367	DET	4.20
COR-B-369	DET	4.20
COR-B-370	DET	6.20
COR-B-445	DET	4.80
COR-B-447	DET	8.20
COR-B-448	DET	5.00
COR-B-449	DET	4.60
COR-B-450	DET	4.20
COR-B-454	DET	3.80
COR-B-455	DET	3.00
COR-B-458	DET	2.60
COR-B-461	DET	3.00
COR-B-463	DET	3.40
COR-B-465	DET	3.00
	Mean of IND	4.70
	Mean of DET	4.65



Table B3. 2017 LSMeans by growth habit for traits VS\_FLTFLD (score), RS\_FLTFLD (score), RS\_FLTRCV (score), RS\_CANCVR (pct), RS\_CANHLTH (pct), and RS\_GRNHUE (pct). (Table B3 Continued)

Genotype	GH	2017	2017	2017	2017	2017	2017
		VS_FLT FLD (score)	RS_FLT FLD (score)	RS_FLT RCV (score)	RS_CAN CVR (pct)	RS_CAN HLTH (pct)	RS_GRN HUE (pct)
COR-B-001	IND	4.50	5.50	5.50	38.31	59.09	72.45
COR-B-003	IND	7.21	6.32	3.30	40.24	57.21	69.98
COR-B-005	IND	5.71	5.57	5.55	40.69	59.17	71.41
COR-B-006	IND	6.00	6.00	6.75	45.50	59.94	73.48
COR-B-007	IND	4.14	4.72	4.60	34.73	59.03	71.65
COR-B-008	IND	5.14	5.72	7.10	42.59	59.92	72.79
COR-B-022	IND	4.00	4.25	2.00	32.27	57.26	69.86
COR-B-024	IND	4.00	4.50	3.00	30.62	57.17	71.03
COR-B-054	IND	6.71	4.82	2.55	32.83	56.78	69.33
COR-B-055	IND	5.71	4.32	1.80	32.80	56.88	69.35
COR-B-065	IND	7.21	6.32	4.80	44.45	57.92	70.88
COR-B-066	IND	6.21	5.07	3.55	39.00	57.27	69.77
COR-B-073	IND	7.21	6.57	3.30	38.79	57.24	70.28
COR-B-074	IND	7.21	6.57	5.80	44.70	58.77	70.88
COR-B-077	IND	7.71	6.57	5.55	44.43	58.91	72.15
COR-B-078	IND	7.21	7.82	6.80	47.47	59.63	73.68
COR-B-079	IND	5.61	6.66	7.10	44.25	59.97	74.18
COR-B-080	IND	6.21	6.82	5.80	43.96	58.86	70.96
COR-B-081	IND	6.71	6.32	4.55	42.43	58.47	71.23
COR-B-082	IND	7.50	7.25	7.75	49.42	60.55	73.07
COR-B-086	IND	6.71	6.32	5.80	45.57	58.78	71.49
COR-B-088	IND	6.21	6.82	4.05	37.69	57.92	71.98
COR-B-089	IND	5.00	5.25	5.00	37.97	58.99	71.75
COR-B-090	IND	7.21	7.57	6.05	44.28	58.70	71.19
COR-B-093	IND	4.00	4.75	3.00	35.22	58.17	70.10
COR-B-094	IND	5.00	6.50	7.00	44.56	59.57	74.21
COR-B-096	IND	5.86	6.03	6.15	43.27	58.58	72.94
COR-B-101	IND	5.00	5.50	4.75	38.96	58.56	70.80
COR-B-102	IND	6.50	7.00	7.00	45.31	60.16	75.94
COR-B-103	IND	4.61	4.66	6.10	42.55	59.22	72.23
COR-B-104	IND	4.69	5.34	4.40	37.53	58.62	71.40
COR-B-105	IND	5.61	5.91	6.85	42.32	59.54	73.71
COR-B-106	IND	4.20	5.22	4.37	35.74	58.66	71.88
COR-B-107	IND	5.61	6.66	7.60	47.58	59.77	74.87
COR-B-108	IND	4.34	3.93	3.90	35.16	58.37	71.85
COR-B-110	IND	4.50	5.50	5.00	35.40	59.13	72.51
COR-B-111	IND	5.61	6.66	6.60	45.39	59.56	74.75

Table B3 Continued

Genotype	GH	2017 VS_FLT FLD (score)	2017 RS_FLT FLD (score)	2017 RS_FLT RCV (score)	2017 RS_CAN CVR (pct)	2017 RS_CAN HLTH (pct)	2017 RS_GRN HUE (pct)
COR-B-112	IND	5.61	5.66	7.10	42.92	59.44	72.77
COR-B-113	IND	5.25	5.50	4.13	38.89	58.84	71.23
COR-B-114	IND	5.50	5.75	6.50	43.83	60.02	73.27
COR-B-115	IND	5.61	4.66	3.10	32.91	58.59	71.64
COR-B-117	IND	5.50	6.50	5.00	44.59	58.36	69.67
COR-B-118	IND	4.61	5.66	4.10	39.13	58.93	71.37
COR-B-119	IND	4.61	5.66	5.10	39.41	59.17	72.36
COR-B-120	IND	3.64	3.47	2.60	27.90	58.21	70.07
COR-B-121	IND	6.61	6.66	8.10	50.61	60.52	74.47
COR-B-122	IND	4.61	5.16	3.60	34.49	58.36	72.17
COR-B-124	IND	4.61	5.66	6.60	39.71	58.72	74.67
COR-B-125	IND	5.19	4.50	4.68	36.24	58.81	72.43
COR-B-126	IND	4.61	5.16	6.10	37.24	58.51	74.01
COR-B-129	IND	4.61	3.66	2.10	29.36	57.81	70.31
COR-B-153	IND	5.83	4.73	3.97	34.85	57.09	70.39
COR-B-156	IND	5.83	5.06	4.64	39.97	57.66	69.66
COR-B-157	IND	3.83	3.39	1.31	28.33	56.44	68.61
COR-B-164	IND	7.21	4.82	2.80	32.38	56.96	69.53
COR-B-165	IND	3.83	2.73	1.97	23.51	56.71	68.35
COR-B-166	IND	5.83	5.06	3.64	38.40	58.18	69.63
COR-B-170	IND	4.50	3.06	2.31	29.19	57.10	70.50
COR-B-173	IND	7.21	5.57	3.55	37.53	57.26	70.13
COR-B-174	IND	4.50	5.39	2.64	34.33	57.14	70.07
COR-B-175	IND	6.71	5.82	4.30	38.67	57.55	71.01
COR-B-176	IND	7.83	6.39	6.97	52.60	59.54	71.40
COR-B-177	IND	5.50	5.73	4.81	40.25	58.41	71.29
COR-B-178	IND	5.83	5.73	4.97	40.03	58.01	70.95
COR-B-181	IND	6.21	4.32	2.05	32.59	57.43	70.00
COR-B-183	IND	5.71	4.82	1.80	31.74	56.63	69.48
COR-B-186	IND	5.17	4.39	2.64	35.23	56.94	70.08
COR-B-187	IND	6.50	5.39	4.31	38.30	57.74	71.24
COR-B-188	IND	5.17	5.39	4.64	39.20	57.69	71.95
COR-B-189	IND	5.17	6.73	3.97	42.30	57.58	70.22
COR-B-192	IND	4.50	5.06	2.64	33.98	56.83	69.76
COR-B-193	IND	6.71	7.32	5.05	43.89	58.18	70.93
COR-B-194	IND	8.21	7.57	5.80	53.07	58.07	70.51
COR-B-195	IND	8.71	7.82	6.80	46.68	59.52	72.27
COR-B-196	IND	5.21	4.57	4.05	37.56	57.93	70.03
COR-B-197	IND	4.50	5.06	1.97	31.28	56.85	69.56

Table B3 Continued

Genotype	GH	2017 VS_FLT FLD (score)	2017 RS_FLT FLD (score)	2017 RS_FLT RCV (score)	2017 RS_CAN CVR (pct)	2017 RS_CAN HLTH (pct)	2017 RS_GRN HUE (pct)
COR-B-200	IND	8.71	7.57	6.30	49.45	59.52	71.15
COR-B-201	IND	5.17	4.73	1.97	34.64	57.24	69.97
COR-B-202	IND	7.17	5.39	4.64	41.71	57.97	71.68
COR-B-203	IND	5.71	7.57	4.55	44.19	57.87	69.26
COR-B-204	IND	7.83	7.39	5.31	45.24	57.72	72.01
COR-B-205	IND	5.17	5.39	4.97	39.68	57.88	71.53
COR-B-206	IND	8.71	7.82	6.55	48.78	58.94	71.38
COR-B-208	IND	7.17	6.39	3.97	41.95	57.77	71.29
COR-B-209	IND	4.50	4.39	3.31	35.33	57.16	70.31
COR-B-210	IND	3.50	3.50	3.25	33.48	57.71	68.26
COR-B-213	IND	4.69	4.35	3.77	33.93	58.10	71.66
COR-B-214	IND	4.03	5.68	4.44	35.96	58.65	71.68
COR-B-215	IND	5.83	5.73	4.97	42.53	57.89	71.97
COR-B-217	IND	4.03	3.02	3.10	31.68	58.17	72.38
COR-B-218	IND	5.36	5.68	4.10	38.78	58.12	70.95
COR-B-223	IND	4.69	5.02	5.44	38.74	58.68	72.43
COR-B-224	IND	6.89	5.97	7.23	42.79	59.86	73.56
COR-B-225	IND	4.03	5.02	3.10	33.84	57.89	70.52
COR-B-226	IND	5.00	6.00	4.50	38.31	58.85	71.91
COR-B-227	IND	4.93	4.87	4.04	36.40	57.96	71.13
COR-B-229	IND	4.00	4.75	3.00	32.20	58.63	70.98
COR-B-231	IND	4.89	5.97	5.90	38.56	59.47	72.94
COR-B-232	IND	6.69	6.35	6.44	45.06	59.12	72.57
COR-B-234	IND	3.55	3.31	2.90	26.12	58.13	72.03
COR-B-236	IND	7.00	7.00	6.50	44.89	59.44	73.44
COR-B-237	IND	4.22	4.31	4.23	34.26	58.19	71.89
COR-B-238	IND	4.98	5.22	5.59	39.65	59.03	72.91
COR-B-239	IND	4.69	5.02	4.10	38.53	58.31	70.85
COR-B-241	IND	3.55	4.64	4.23	36.00	58.37	71.94
COR-B-270	IND	5.21	4.57	2.55	32.48	57.13	69.84
COR-B-287	IND	6.71	6.32	5.80	41.71	58.54	72.34
COR-B-290	IND	5.75	6.37	5.88	40.43	58.92	72.95
COR-B-295	IND	6.00	6.00	6.25	42.47	59.54	74.58
COR-B-302	IND	4.00	3.00	2.00	27.39	57.79	70.11
COR-B-305	IND	4.64	3.97	5.10	36.06	59.36	73.24
COR-B-328	IND	5.17	3.73	2.64	30.84	57.19	70.08
COR-B-329	IND	4.50	3.73	2.81	32.85	57.50	69.02
COR-B-330	IND	6.71	5.57	5.55	42.71	58.14	72.09
COR-B-331	IND	7.17	6.39	4.64	41.96	58.11	70.27

Table B3 Continued

Genotype	GH	2017 VS_FLT FLD (score)	2017 RS_FLT FLD (score)	2017 RS_FLT RCV (score)	2017 RS_CAN CVR (pct)	2017 RS_CAN HLTH (pct)	2017 RS_GRN HUE (pct)
COR-B-332	IND	5.50	4.89	3.97	37.96	57.57	71.20
COR-B-333	IND	6.00	6.50	6.25	43.87	59.56	72.63
COR-B-335	IND	4.50	5.50	3.75	35.84	57.61	71.80
COR-B-336	IND	6.50	5.73	3.97	40.76	57.64	71.02
COR-B-338	IND	6.60	6.21	5.37	42.10	58.33	72.02
COR-B-339	IND	4.50	5.25	6.00	42.47	58.85	72.40
COR-B-340	IND	5.00	5.25	5.25	39.15	58.25	72.29
COR-B-341	IND	5.36	5.35	5.77	42.59	58.97	72.26
COR-B-342	IND	4.03	4.68	4.10	33.86	58.71	71.76
COR-B-344	IND	4.09	3.85	4.39	32.86	57.80	72.53
COR-B-345	IND	5.64	6.22	6.60	44.51	59.89	71.96
COR-B-348	IND	2.89	2.64	2.90	27.11	57.73	70.10
COR-B-371	IND	6.21	4.32	2.55	31.97	56.74	71.59
COR-B-381	IND	6.21	5.57	5.05	40.46	58.93	71.67
COR-B-386	IND	5.71	4.32	5.30	37.05	58.46	72.43
COR-B-387	IND	8.71	7.57	6.55	52.13	59.27	72.27
COR-B-395	IND	8.21	7.82	6.30	45.31	59.77	71.93
COR-B-397	IND	7.21	6.82	6.05	47.36	58.62	71.68
COR-B-402	IND	4.00	4.75	3.50	34.80	58.25	70.76
COR-B-405	IND	4.50	4.75	3.50	34.32	58.66	71.69
COR-B-407	IND	6.00	6.50	6.75	43.27	59.54	72.78
COR-B-411	IND	2.50	2.50	1.75	25.23	57.83	69.94
COR-B-412	IND	4.50	5.00	4.75	38.60	58.84	72.22
COR-B-413	IND	5.00	5.50	6.00	43.54	59.28	72.36
COR-B-417	IND	4.50	5.00	5.25	36.77	59.05	72.46
COR-B-424	IND	4.14	4.47	4.35	33.49	59.08	72.62
COR-B-425	IND	5.64	6.72	7.85	47.27	60.58	73.39
COR-B-426	IND	5.64	5.22	5.85	41.36	59.27	73.23
COR-B-427	IND	5.14	5.22	5.10	39.48	59.25	72.17
COR-B-009	DET	5.63	5.64	6.46	41.10	58.60	73.06
COR-B-010	DET	5.13	7.14	7.21	46.10	58.18	74.70
COR-B-011	DET	3.63	4.14	3.71	33.74	57.20	71.25
COR-B-030	DET	4.50	4.75	4.00	34.48	57.48	70.96
COR-B-127	DET	5.63	6.64	6.71	42.95	58.79	72.15
COR-B-128	DET	4.63	5.64	5.46	38.35	58.73	73.48
COR-B-130	DET	4.63	4.14	3.96	31.81	58.25	71.49
COR-B-131	DET	4.66	4.86	4.27	38.44	58.17	69.73
COR-B-132	DET	4.66	4.61	3.27	31.89	57.98	72.31
COR-B-133	DET	3.63	4.14	4.46	35.19	57.86	70.22

Table B3 Continued

Genotype	GH	2017 VS_FLT FLD (score)	2017 RS_FLT FLD (score)	2017 RS_FLT RCV (score)	2017 RS_CAN CVR (pct)	2017 RS_CAN HLTH (pct)	2017 RS_GRN HUE (pct)
COR-B-134	DET	4.66	4.61	5.27	37.23	58.11	72.26
COR-B-135	DET	3.82	4.82	4.73	33.01	58.22	71.02
COR-B-136	DET	4.66	5.61	4.52	36.96	58.37	71.96
COR-B-137	DET	4.79	5.57	6.12	38.14	58.33	73.79
COR-B-138	DET	5.64	4.96	5.23	37.92	58.20	73.20
COR-B-139	DET	2.66	3.61	1.77	24.58	56.89	70.27
COR-B-140	DET	5.16	4.11	3.52	31.32	57.62	71.86
COR-B-142	DET	4.66	4.61	4.27	32.79	57.76	72.45
COR-B-144	DET	5.16	5.86	6.52	41.53	58.54	72.95
COR-B-147	DET	4.13	6.14	4.96	37.76	57.77	73.61
COR-B-148	DET	5.13	6.14	5.71	39.56	58.01	73.29
COR-B-242	DET	5.63	6.64	7.21	43.72	59.39	73.85
COR-B-243	DET	5.13	5.14	4.21	37.03	58.11	69.21
COR-B-244	DET	4.93	4.56	3.81	34.21	58.40	71.98
COR-B-248	DET	4.13	4.64	4.46	36.09	57.98	69.11
COR-B-252	DET	3.60	4.56	4.14	33.91	58.19	70.74
COR-B-254	DET	3.62	3.78	3.79	31.94	57.63	71.07
COR-B-255	DET	4.02	3.78	2.39	29.82	57.07	69.90
COR-B-256	DET	4.01	5.10	4.44	38.16	57.69	70.57
COR-B-258	DET	3.66	4.61	2.27	33.44	56.69	70.48
COR-B-260	DET	4.42	4.38	3.99	35.84	57.70	70.51
COR-B-263	DET	4.63	5.39	5.46	35.30	57.82	73.69
COR-B-264	DET	4.13	4.39	3.71	34.82	57.32	71.01
COR-B-266	DET	5.13	6.14	6.21	43.42	58.16	72.47
COR-B-308	DET	5.63	4.64	5.46	34.90	58.83	73.09
COR-B-311	DET	4.98	5.30	5.40	36.67	58.24	73.43
COR-B-312	DET	5.31	5.96	6.90	40.56	58.73	73.56
COR-B-315	DET	4.50	4.50	4.00	35.32	57.37	70.13
COR-B-319	DET	5.13	6.64	7.46	43.44	58.51	74.02
COR-B-320	DET	4.63	4.39	3.96	34.49	57.58	72.31
COR-B-346	DET	4.13	4.64	4.71	33.94	58.06	71.74
COR-B-350	DET	3.60	4.56	4.14	32.83	57.83	70.65
COR-B-428	DET	3.63	4.64	3.96	34.67	57.71	71.21
COR-B-429	DET	3.63	4.64	5.21	37.37	58.03	70.20
COR-B-430	DET	5.13	5.14	5.21	37.40	58.25	71.90
COR-B-431	DET	5.13	4.89	5.96	37.97	58.79	73.10
COR-B-433	DET	5.63	5.64	7.21	40.07	58.81	73.57
COR-B-434	DET	4.63	6.14	5.96	39.88	58.62	72.41
COR-B-436	DET	4.63	5.14	5.96	37.77	58.27	73.41

Table B3 Continued

Genotype	GH	2017	2017	2017	2017	2017	2017
		VS_FLT FLD (score)	RS_FLT FLD (score)	RS_FLT RCV (score)	RS_CAN CVR (pct)	RS_CAN HLTH (pct)	RS_GRN HUE (pct)
COR-B-439	DET	4.13	4.14	4.21	32.87	57.82	71.58
COR-B-446	DET	3.13	3.14	3.21	30.09	57.49	70.60
COR-B-451	DET	2.63	3.14	2.46	25.15	57.59	70.00
COR-B-457	DET	4.13	4.64	4.46	35.50	57.49	72.24
COR-B-462	DET	5.63	4.89	3.96	36.86	57.68	72.24
COR-B-469	DET	4.50	4.50	6.25	36.80	58.47	72.41
Mean of IND		5.53	5.45	4.68	38.92	58.42	71.57
Mean of DET		4.52	4.95	4.80	36.13	58.03	71.90

Table B4. 2018 LSMeans by growth habit for traits VS\_FLTFLD (score), RS\_FLTFLD (score), RS\_FLTRCV (score), RS\_CANCVR (pct), RS\_CANHLTH (pct), and RS\_GRNHUE (pct).

Genotype	GH	2018 VS_FLT FLD (score)	2018 RS_FLT FLD (score)	2018 RS_FLT RCV (score)	2018 RS_CAN CVR (pct)	2018 RS_CAN HLTH (pct)	2018 RS_GRN HUE (pct)
COR-B-002	IND	1.50	1.50	5.00	47.77	59.77	67.30
COR-B-004	IND	3.25	3.75	6.35	47.26	60.77	64.89
COR-B-005	IND	4.00	5.25	7.00	48.86	61.91	65.88
COR-B-006	IND	1.16	2.05	4.34	42.36	59.54	64.93
COR-B-007	IND	3.16	4.05	6.34	45.38	62.17	63.53
COR-B-008	IND	3.25	3.50	4.25	42.52	59.17	65.65
COR-B-022	IND	2.75	3.25	2.00	28.50	58.14	63.06
COR-B-024	IND	4.16	4.38	4.34	34.37	59.76	64.82
COR-B-059	IND	3.00	4.75	4.50	40.49	60.35	65.28
COR-B-070	IND	2.50	3.00	5.00	41.73	59.54	66.17
COR-B-082	IND	3.89	4.29	4.84	43.52	60.70	64.70
COR-B-085	IND	3.25	4.25	7.75	48.99	61.87	65.89
COR-B-086	IND	2.00	3.75	3.03	44.10	59.66	67.43
COR-B-087	IND	1.33	1.50	3.14	35.90	57.66	64.65
COR-B-091	IND	4.00	4.50	2.34	31.34	57.82	63.39
COR-B-092	IND	1.00	1.00	3.00	40.43	57.45	64.22
COR-B-094	IND	2.07	2.74	4.72	44.40	59.55	64.70
COR-B-095	IND	2.16	2.72	1.67	30.87	56.92	64.68
COR-B-096	IND	3.48	3.80	5.02	43.91	60.28	65.01
COR-B-099	IND	1.75	2.75	3.25	40.49	58.47	64.44
COR-B-102	IND	4.25	5.00	7.50	49.24	62.39	69.04
COR-B-103	IND	4.50	4.50	4.75	49.47	60.96	64.75
COR-B-105	IND	2.00	2.75	5.25	45.62	61.10	64.21
COR-B-107	IND	1.89	2.59	6.55	47.02	61.71	66.78
COR-B-108	IND	2.67	2.87	4.35	41.48	59.83	65.87
COR-B-109	IND	3.75	4.50	4.25	36.79	59.33	63.29
COR-B-111	IND	5.00	4.75	7.34	52.28	62.23	67.60
COR-B-114	IND	6.25	6.75	7.50	48.54	62.67	67.77
COR-B-121	IND	1.34	1.93	5.65	50.92	61.09	64.71
COR-B-124	IND	3.75	3.75	6.00	43.24	61.02	65.82
COR-B-126	IND	2.75	3.00	4.00	40.65	60.10	64.13
COR-B-166	IND	3.25	3.75	3.02	38.20	59.00	65.47

Table B4. Continued

Genotype	GH	2018 VS_FLT FLD (score)	2018 RS_FLT FLD (score)	2018 RS_FLT RCV (score)	2018 RS_CAN CVR (pct)	2018 RS_CAN HLTH (pct)	2018 RS_GRN HUE (pct)
COR-B-170	IND	1.75	1.75	4.00	44.66	60.03	66.33
COR-B-171	IND	4.00	4.00	4.34	44.13	61.35	66.70
COR-B-174	IND	3.75	4.00	4.50	40.01	59.28	64.76
COR-B-176	IND	1.00	1.25	3.67	47.13	59.86	68.32
COR-B-177	IND	2.00	2.50	4.69	45.13	59.99	64.81
COR-B-186	IND	3.50	3.50	4.75	44.60	60.18	64.70
COR-B-195	IND	2.50	3.25	4.34	47.55	61.00	66.62
COR-B-201	IND	3.49	4.05	2.34	32.64	59.18	63.98
COR-B-202	IND	3.16	3.38	7.00	48.32	60.95	66.79
COR-B-204	IND	3.16	4.05	4.03	41.23	60.63	65.47
COR-B-205	IND	3.50	4.00	6.34	50.07	60.69	64.00
COR-B-206	IND	2.49	3.05	6.53	46.92	60.89	66.55
COR-B-208	IND	2.75	3.50	7.75	53.00	62.90	64.50
COR-B-213	IND	3.82	4.38	3.67	36.59	59.50	64.40
COR-B-217	IND	4.00	4.00	3.25	33.86	59.35	64.83
COR-B-218	IND	2.82	3.05	5.00	39.80	60.18	64.32
COR-B-223	IND	3.82	4.05	5.00	41.51	60.00	64.03
COR-B-224	IND	2.25	2.50	4.67	48.10	59.94	66.76
COR-B-225	IND	2.16	2.72	4.34	40.63	59.51	63.26
COR-B-226	IND	3.82	3.72	4.34	37.61	59.57	64.84
COR-B-227	IND	6.16	5.72	3.67	39.27	60.01	64.79
COR-B-231	IND	5.00	5.00	6.50	44.20	61.98	66.17
COR-B-234	IND	2.00	2.00	3.97	40.90	61.01	65.70
COR-B-237	IND	4.82	5.38	4.73	42.14	60.77	65.02
COR-B-238	IND	2.25	3.00	5.03	44.43	61.15	66.95
COR-B-239	IND	2.50	3.25	4.25	40.58	60.20	64.29
COR-B-282	IND	2.00	2.75	2.34	33.85	57.99	63.94
COR-B-295	IND	3.75	4.50	6.34	52.96	61.73	64.87
COR-B-298	IND	2.00	2.50	2.00	33.16	57.98	63.11
COR-B-300	IND	2.50	3.50	6.34	46.97	60.49	65.53
COR-B-325	IND	1.75	2.50	3.50	36.83	59.69	64.45
COR-B-327	IND	1.50	1.75	4.00	38.79	59.14	64.33
COR-B-330	IND	1.25	1.50	4.00	38.80	59.29	63.25
COR-B-333	IND	2.49	3.05	4.00	40.25	59.29	62.39



Table B4. Continued

Genotype	GH	2018 VS_FLT FLD (score)	2018 RS_FLT FLD (score)	2018 RS_FLT RCV (score)	2018 RS_CAN CVR (pct)	2018 RS_CAN HLTH (pct)	2018 RS_GRN HUE (pct)
COR-B-334	IND	2.75	3.25	6.75	49.18	61.68	66.54
COR-B-335	IND	4.50	4.75	4.25	40.47	60.26	63.89
COR-B-337	IND	4.25	4.75	7.50	48.38	63.00	64.82
COR-B-339	IND	2.00	2.75	4.00	43.67	59.81	63.95
COR-B-340	IND	3.00	3.50	4.67	43.85	60.76	61.61
COR-B-343	IND	3.00	3.25	2.83	28.65	57.98	64.43
COR-B-344	IND	3.50	4.75	3.75	34.68	59.03	64.70
COR-B-388	IND	3.00	4.00	4.00	40.46	59.54	65.88
COR-B-398	IND	6.50	7.00	7.75	55.19	63.04	64.91
COR-B-400	IND	5.00	6.00	6.25	49.13	62.63	65.80
COR-B-401	IND	4.25	4.50	5.25	40.40	60.31	64.91
COR-B-414	IND	3.75	4.25	4.00	37.44	59.37	65.24
COR-B-421	IND	2.55	2.59	3.03	33.88	58.15	64.33
COR-B-009	DET	3.00	3.75	5.25	46.37	60.71	64.29
COR-B-010	DET	4.50	4.50	5.75	47.60	60.21	66.51
COR-B-011	DET	4.00	5.00	3.89	44.07	60.57	64.71
COR-B-030	DET	4.25	4.25	4.93	40.00	60.06	63.97
COR-B-127	DET	4.80	5.29	5.26	46.71	60.11	64.86
COR-B-128	DET	4.50	4.25	7.49	49.31	62.14	65.12
COR-B-133	DET	2.50	2.75	4.91	42.23	59.83	64.47
COR-B-134	DET	3.50	3.75	4.50	40.85	60.47	63.88
COR-B-137	DET	3.65	4.50	5.87	49.30	60.21	66.21
COR-B-138	DET	2.48	2.81	4.94	41.67	59.93	64.78
COR-B-140	DET	3.69	4.25	5.13	44.31	60.55	64.55
COR-B-148	DET	5.50	5.75	4.83	43.64	60.11	65.83
COR-B-242	DET	1.50	2.00	6.00	44.10	60.34	65.86
COR-B-244	DET	2.25	2.25	4.75	39.05	60.67	65.12
COR-B-248	DET	4.25	5.25	5.60	45.79	61.18	64.79
COR-B-252	DET	5.00	4.50	5.75	45.58	61.57	66.28
COR-B-256	DET	2.75	3.25	4.75	44.16	60.10	61.27
COR-B-263	DET	5.50	5.75	5.49	47.25	60.69	67.35
COR-B-266	DET	4.25	4.25	4.60	45.49	60.28	65.23
COR-B-313	DET	3.25	3.50	4.27	40.42	61.20	65.83
COR-B-315	DET	3.25	3.75	3.75	38.66	58.46	63.38

Table B4. Continued

Genotype	GH	2018	2018	2018	2018	2018	2018
		VS_FLT FLD (score)	RS_FLT FLD (score)	RS_FLT RCV (score)	RS_CAN CVR (pct)	RS_CAN HLTH (pct)	RS_GRN HUE (pct)
COR-B-316	DET	3.75	4.25	5.25	46.36	61.02	64.70
COR-B-317	DET	4.75	5.00	5.75	45.07	60.57	65.05
COR-B-321	DET	3.50	3.25	6.93	51.69	62.23	64.73
COR-B-323	DET	5.25	5.25	5.50	46.45	60.60	67.44
COR-B-324	DET	3.75	4.00	3.39	35.75	59.83	66.31
COR-B-346	DET	3.00	3.75	2.93	39.46	58.85	63.19
COR-B-347	DET	2.75	3.25	5.25	49.11	60.43	65.57
COR-B-349	DET	2.50	2.75	4.50	43.46	60.12	63.89
COR-B-351	DET	1.25	2.50	3.91	38.45	58.52	63.80
COR-B-353	DET	5.50	6.00	5.91	48.10	61.01	67.37
COR-B-354	DET	3.00	3.25	3.39	39.60	59.95	66.29
COR-B-355	DET	4.75	5.00	7.25	46.68	62.22	66.52
COR-B-437	DET	2.50	3.75	6.25	50.41	61.01	65.35
COR-B-440	DET	1.75	2.75	2.75	33.75	58.11	62.68
COR-B-443	DET	1.00	1.50	4.75	37.42	59.87	64.76
COR-B-444	DET	1.00	1.25	2.66	37.22	57.85	64.19
COR-B-456	DET	2.50	2.75	5.75	47.58	60.52	64.64
COR-B-459	DET	5.25	5.25	6.75	51.37	61.99	66.69
COR-B-460	DET	4.25	4.25	5.75	46.76	60.37	65.35
COR-B-464	DET	5.75	6.00	6.00	47.82	61.96	66.31
COR-B-466	DET	4.75	4.75	6.50	47.58	60.60	66.61
COR-B-469	DET	1.25	1.50	4.60	42.91	60.27	62.47
Mean of IND		3.07	3.56	4.72	42.39	60.18	65.09
Mean of DET		3.54	3.89	5.10	44.18	60.40	65.07