Implementing Association Mapping and Genomic Selection to Advance Breeding for Complex Traits in Barley

A THESIS
SUBMITTED TO THE FACULTY OF
UNIVERSITY OF MINNESOTA
BY

Celeste Marie Falcon

IN PARTIAL FULFILLMENT OF THE REQUIREMENTS
FOR THE DEGREE OF
DOCTOR OF PHILOSOPHY

Dr. Kevin P. Smith, advisor

July 2016

Acknowledgements

First and foremost, I would like to thank my advisor, Dr. Kevin Smith for challenging and guiding me with both enthusiasm and patience. I truly could not have asked for more in a Ph.D. advisor. I would also like to thank the members of my committee, Drs. Rex Bernardo, Dan Kaiser, and Eric Watkins, for their useful input on my project.

I thank the members of the barley lab, past and present, for their assistance, mentoring, and enlightening conversations. Thank you to Ed Schiefelbein and Guillermo Velasquez for their help with designing, carrying out, and collecting data from field trials. Thank you to Karen Beaubien for assistance with tracking down genotype data and records of decisions made prior to my arrival. Thank you to the post-docs—Mohsen Mohammadi and Ana Poet—and graduate students—Ahmad Sallam, Vikas Vikram, Stephanie Navara, Leticia Kumar, Tyler Tiede, Alexandrea Ollhoff, Jeffrey Neyhart, Lu Yin, and John Hill Price—who have been part of the barley group in my time here. I am so grateful for the time and effort each of you has contributed to helping me over the years.

I thank my fellow applied plant sciences graduate students for their assistance and friendship. Extra gratitude goes to my officemates and to those who were members of the planning committees for the annual plant breeding symposium and the Borlaug memorial lecture.

I had the opportunity to mentor a number of undergraduate students: Tianqi (Gordon) Sun, Erin Pfarr, Elijah Rasmusson, Erik Vavra. I thank each of them not only for their assistance with my projects but also for all that I learned from mentoring them.

I was fortunate to have funding from a number of sources for my PhD studies. I'd like to acknowledge the Triticeae Coordinated Agriculture Project, which funded not only me as a graduate student but also my thesis projects and travel to multiple conferences. I also recognize the contributions two fellowships that I was awarded: the MnDrive Global Food Ventures fellowship and the University of Minnesota Doctoral Dissertation Fellowship. I also appreciate the support I received from the Rasmusson Fellowship, Rahr Fellowship, and The Microbial and Plant Genomics Institute travel grants.

Finally, I am extremely grateful for the love and support of my family and friends as I continue to work toward my dreams.

Dedication

I dedicate this thesis to my fiancé, Adam. He has celebrated with me on the best days and supported me on the difficult ones. I am so thankful to have his endless love, encouragement, and support.

Abstract

To efficiently respond to challenges presented by global climate change, plant breeders can implement methods that utilize genome-wide marker data to discover and deploy useful genes. We investigated the use of genome-wide association mapping and genomic selection to improve two traits related to protecting natural resources: nitrogen use efficiency (NUE) and winter hardiness. In our first study, we identified quantitative trait loci (QTL) for improved NUE using phenotypic data and calculated stress indices in conjunction with genome-wide marker data for 250 six-row and 250 two-row barley breeding lines. We identified a QTL for grain protein concentration (GPC) on chromosome 6H that has been mapped previously in barley and is collinear with the well-characterized *Gpc-B1* locus in wheat. Groups of lines defined by marker haplotypes at this locus exhibited significant differences in GPC but not in grain yield. Overall, our results indicated that potentially effective breeding strategies for NUE include selection based on stress indices, marker assisted selection for desirable alleles, and genomic selection to capture small effect loci. In a second study, we assessed the utility of genomic selection to initiate a breeding program for winter barley based on observed gains from selection, changes in phenotypic variation, and changes in marker allele frequencies. After conducting two cycles of genomic selection for a selection index that combined predictions for low temperature tolerance, malt extract, grain yield, heading date, and plant height, we assessed the selected sets of lines in field trials. Between cycles 0 and 2, genomic selection improved low temperature tolerance and malt extract while maintaining the other selection index traits. Phenotypic variance fluctuated but did not

change significantly. Three markers previously shown to be linked to winter hardiness traits shifted in genotypic frequency over the cycles of selection. Based on all marker data, the population shifted toward similarity with the winter growth-type parent lines after two cycles of genomic selection. Overall, this study demonstrated that genomic selection is an effective method for improving trait values in a population at the initiation of a breeding program. Together, these studies support the use of marker-based breeding strategies to improve genetically complex traits that contribute to sustainable agricultural systems that will address climate change.

Table of Contents

List of Tables

Chapter 1

Chapter 2

Appendix

List of Figures

Chapter 1

Chapter 2

Appendix

Chapter 1: Genome-wide association mapping for nitrogen use efficiency in elite two- and six-row spring barley germplasm

Growing crops with greater nitrogen use efficiency (NUE) could decrease fertilizer inputs and the negative environmental effects of nitrogen over-use. We aimed to identify quantitative trait loci (QTL) for improved NUE in barley (*Hordeum vulgare* L.) by evaluating 250 two-row and 250 six-row breeding lines for nine agronomic and yield-component traits under nitrogen-limiting and non-limiting treatments and for 3,072 single nucleotide polymorphism (SNP) markers. Four stress indices were calculated to quantify NUE. Association mapping was conducted separately for the two- and six-row lines. All traits and two stress indices—the geometric mean and the stress tolerance index—exhibited significant genetic variation. We considered a QTL region to be associated with NUE (versus the trait *per se*) if the locus was identified under the nitrogen-limiting treatment, for a stress index, or for both, but not under the non-limiting treatment. Of 25 QTL detected in the two-row panel and 36 detected in the six-row panel, only four were common to both panels. Four of the QTL detected in the two-row panel and 12 detected in the six-row panel affected NUE. We identified a QTL for grain protein concentration (GPC) on chromosome 6H that has been mapped previously in barley and is collinear with the well-characterized *Gpc-B1* locus in wheat. Groups of lines defined by marker haplotypes at this locus exhibited significant differences in GPC but not in grain yield. Breeding strategies for NUE include selection based on stress indices, marker assisted selection (MAS) for desirable alleles, and genomic selection to capture small effect loci.

Introduction

To increase agricultural production to feed the world's growing population while also mitigating the harmful effects of nitrogen overuse, plant breeders need to develop cultivars that use nitrogen more efficiently. Nitrogen fertilizer use contributes to air pollution and emissions of the greenhouse gas nitrous oxide. Plants only take up 30-50% of applied nitrogen fertilizer. The remaining fertilizer runs off into the surface and ground water, harming water quality, aquatic ecosystems, and fisheries (reviewed in Tilman et al., 2002). Nitrogen use efficiency (NUE) describes a plant's effectiveness in obtaining nitrogen (nitrogen uptake efficiency) and using nitrogen (nitrogen utilization efficiency) (Moll et al., 1982). Nitrogen uptake efficiency is more relevant under nitrogen-limiting conditions while nitrogen utilization efficiency is more relevant under non-limiting conditions (Gastal et al., 2015). Defined quantitatively, NUE is the change in grain yield per each additional unit of nitrogen fertilizer available (Moll et al., 1982).

Nitrogen use efficiency may be determined by various experimental designs and trait measurements. Plant performance may be tested at two nitrogen levels—a stressed treatment (no applied nitrogen) and non-stressed treatment (enough applied nitrogen to achieve yield potential)— (e.g. Wei et al., 2011, 2012) or at multiple levels of nitrogen application—representing different levels of stress (e.g. Delogu et al., 1997) or representing stressed, non-stressed, and over-fertilized treatments (e.g. Tong et al., 2011). Under extremely stressed conditions, trait heritability is reduced due to increased non-genetic effects. At the same time, some genes for adaptation to stress are only revealed in stressed environments. Evaluating germplasm under moderate stress treatments that realize 60-65% of the potential yield balances these conflicting issues (Gallais and

Coque, 2005). Traits measured to determine NUE include grain yield and components of grain yield—spikes per meter, kernels per spike, and 1,000 kernel weight—as well as aspects of nitrogen content such as grain nitrogen yield, grain nitrogen concentration, and nitrogen content of the straw and chaff (e.g. Le Gouis et al., 1999). So far, NUE studies in grain crops have been limited in terms of diversity assessed, involving fewer than 20 genotypes or fewer than 215 recombinant inbred lines (Delogu et al., 1997; Le Gouis et al., 1999, 2000; Hirel et al., 2001; Gallais and Hirel, 2003; Mickelson et al., 2003; Sinebo et al., 2003; Cho et al., 2007; Liu et al., 2007; Wei et al., 2011, 2012).

Improvements in NUE have been limited by the labor and expense involved in measuring biomass and grain nitrogen concentrations to evaluate this trait. An alternate method is to calculate stress indices, which quantify efficiency based on performance under stressed and non-stressed conditions. The stress index geometric mean (GM; Table 1; Fernandez, 1992) is less sensitive to extreme values than mean productivity (Table 1; Rosielle and Hamblin, 1981), making it more useful for identifying lines that are superior under both stressed and non-stressed conditions. The stress tolerance index (STI; Table 1; Fernandez, 1992) is similar to GM in that it identifies lines that exhibit superior performance in stressed and non-stressed conditions, but it also standardizes each line's performance by the mean performance of all lines in the experiment. The stress susceptibility index (SSI; Table 1; Fischer and Maurer, 1978) favors genotypes with relatively higher yield under stress conditions. However, it does not select for genotypes with higher yield in non-stressed conditions, which makes it less useful in breeding for NUE. These three stress indices have mostly been used for evaluating efficiency under water stress and have less frequently been used to evaluate NUE. A series of papers on

rapeseed (*Brassica napus* L.) have used GM, SSI, and STI and two other indices to evaluate NUE based on a number of traits. Studies in barley (Górny, 2001), wheat (*Triticum aestivum* L.; Górny and Garczyński, 2008; Górny et al., 2011), potato (*Solanum tuberosum* L.; Schum and Jansen, 2014), and rice (*Oryza sativa* L.; Kimani et al., 2011) used the SSI or a modified version of this index to characterize lines for NUE. Identifying QTL associated with these indices has not yet been attempted.

In addition to grain yield, the concentration of protein that accumulates in the grain is a useful trait to measure to assess NUE. Previously, researchers have identified QTL for NUE and related traits like grain protein concentration (GPC) in barley (Mickelson et al., 2003; Berger et al., 2013; Cai et al., 2013; Pauli et al., 2014; Mohammadi et al., 2015), wheat (Laperche et al., 2006), rice (Cho et al., 2007; Tong et al., 2011; Wei et al. 2011, 2012), and maize (*Zea mays* L.; Agrama et al., 1999; Hirel et al., 2001; Gallais and Hirel, 2003; Liu et al., 2007). In barley, See et al. (2002) detected QTL for GPC in a bi-parental population (Karl x Lewis) on chromosomes 2H, 3H, and 6H. The low protein allele for the GPC QTL on 6H is derived from the cultivar Karl (Wesenberg et al., 1976; Burger et al., 1979; Sasaki et al., 1992) and affects nitrogen remobilization (Mickelson et al., 2003; Jukanti and Fischer, 2008). Distelfeld et al. (2008) determined that the 6H GPC locus in barley showed colinearity with the *Gpc-B1* locus in wheat. *Gpc-B1* had previously been discovered on the short arm of chromosome 6B in wheat (Joppa et al., 1997; Olmos et al., 2003) and was cloned and identified as a NAC transcription factor (Uauy et al, 2006b). The effects of *Gpc-B1* on GPC, grain yield, grain weight, protein yield, and senescence (Uauy et al., 2006a; Distelfeld et al., 2007; Brevis and Dubcovsky, 2010; Carter et al., 2012) indicate its importance in regulating

NUE in wheat. In barley, different alleles at this locus are associated with varying levels of GPC (Cai et al., 2013), grain yield, and grain weight (A. Sallam, personal communication, 2012), as well as plant development and whole-plant and leaf senescence (Jukanti et al., 2008; Lacerenza et al., 2010; Parrott et al., 2011). The large effect of this 6H QTL on grain yield and protein concentration related traits suggests that it may be useful in manipulating NUE in barley.

If specific QTL, such as the GPC QTL on 6H, are shown to affect NUE, then marker assisted selection (MAS), could be used to breed for this complex trait. Most of the previous studies investigated GPC but not NUE specifically. Mickelson et al. (2003) examined NUE in terms of nitrogen storage and remobilization, using a biparental mapping population generated from a cross between lines with marked differences in GPC. A limitation of mapping in biparental populations is that the loci identified may not have the same effect once introgressed into breeding materials due to differences in genetic background. Using association mapping (AM) in a set of elite breeding lines may aid in identifying additional alleles that are already present in adapted germplasm, which would increase the efficiency of introgressing these QTL into improved cultivars and, thereby, help breeders to respond quickly changes in the environment.

In this study, we investigated the genetic variation for NUE as defined by relevant traits and stress indices among two subsets of elite spring lines from US barley breeding programs that contributed to the Barley Coordinated Agricultural Project (BarleyCAP; Waugh et al., 2009; Hamblin et al., 2010). After determining which traits and stress indices showed significant genetic variation, we identified QTL for NUE using genome-wide association mapping (AM), and compared the results of AM in a two-row barley

panel to the results from a six-row barley panel. We identified a QTL for GPC on chromosome 6H, and knowing the importance of this locus from previous studies, investigated the marker haplotype classes at this locus.

Materials and Methods

Germplasm

Association mapping was conducted in two separate panels of barley lines chosen from the BarleyCAP collection, which is a set of 3,840 breeding lines from ten US barley breeding programs. The lines for the panels used here were chosen to represent genetic diversity as evaluated by neighbor joining tree maps, which were created using the ape package (Paradis et al., 2004) for R (R Core Team, 2015). Lines were removed before creating the tree maps if they were missing more than 10% of their genotypic data, exhibited more than 10% observed heterozygosity, or were unavailable due to low seed supplies. The tree maps were constructed based on 3,072 SNP markers using two Illumina GoldenGate Barley Oligonucleotide Pool Assays (BOPA1 and BOPA2; Close et al., 2009). after filtering out markers that were monomorphic, were missing more than 10% data, or exhibited more than 10% observed heterozygosity. The proportion of lines chosen from each breeding program for these panels is equal to the proportion of lines from each program in the entire BarleyCAP collection. The two-row barley AM panel consists of 252 spring two-row advanced breeding lines representing five US barley breeding programs—USDA-ARS-Aberdeen, Idaho; Busch Agricultural Resources, LLC.; Montana State University; North Dakota State University; and Washington State University ("Spring 2r AM panel" in the Triticeae Toolbox database; http://triticeaetoolbox.org; Blake et al., 2016). The six-row barley AM panel consists of

253 spring six-row advanced breeding lines representing five US barley breeding programs—USDA-ARS-Aberdeen, Idaho; Busch Agricultural Resources, LLC.; University of Minnesota; North Dakota State University; and Utah State University ("Spring 6r AM panel" in the Triticeae Toolbox database). Two lines from the two-row barley AM panel (Z068R055S and 06WA-472-28) and three lines from the six-row barley AM panel (FEG141-20, ND26017, and UT2170-15) were excluded from the analyses because they had more than 10% missing marker data.

Genotypic evaluation

The lines were advanced to at least the F_4 generation and genotyped with the 3,072 BOPA1 and BOPA2 SNP markers (Close et al., 2009). The estimated positions of the markers were based on the consensus linkage map generated by Muñoz-Amatriaín et al. (2011). The marker data for these lines and the genetic map are available in the Triticeae Toolbox database. Markers with a minor allele frequency of less than 5% (including monomorphic markers) or with more than 20% missing data were removed from the data set, leaving 1,780 markers for the two-row panel and 1,694 markers for the six-row panel. Linkage disequilibrium (LD) was estimated by using Haploview v4.2 (Barrett et al., 2005) to calculate the squared allele-frequency correlation (r^2) for all marker pairs on a per chromosome basis.

Phenotypic evaluation

The two- and six-row AM panels were each evaluated in four environments (Supplemental Table S1). In each environment, the lines were planted in two nitrogen fertilizer application treatments—one where nitrogen was limiting (referred to as "low nitrogen") and one where it was not (referred to as "normal nitrogen"). Soil nitrogen was

assessed at each location, and nitrogen fertilizer was applied to achieve the desired nitrogen level for each treatment. In the nitrogen-limiting treatment, nitrogen fertilizer was applied at a rate to achieve approximately 70% of target yield. Plot sizes ranged from 1.8 to 6.5 m^2, and seeding rate ranged from about 200 to 300 plants m^{-2} (Supplemental Table S1). The panels were planted as a single replication in each treatment in each environment. Except for one trial for the six-row AM panel that was planted as an augmented block design, all other trials were planted as a Type II Modified Augmented Design (Lin and Poushinsky, 1985). Five replicated checks were included in each trial to facilitate adjustments for spatial variation. The checks for the six-row AM panel were the cultivars Robust (PI 476976; Rasmusson and Wilcoxson, 1983), Lacey (PI 613603; Rasmusson et al., 2001), and Tradition (PI 612442; developed by Busch Agricultural Resources, Inc.), and two near isogenic lines (NILs) of Lacey—Gen2-036 and KLBC4-130i-KK. For the trial that used an augmented block design, the checks were replicated once in each of six blocks. For the trials using the Type II Modified Augmented Design, Tradition was the primary check and appeared once in each of the 21 blocks. The other four checks were used as secondary checks and were replicated in six of the blocks. The checks for the two-row AM panel were four cultivars: Harrington (Harvey and Rossnagel, 1984), Baronesse (PI 568246; developed by Nordsaat in Germany), Hockett (developed by Montana State University), and Pinnacle (PI 643354; North Dakota State University), and one well-adapted breeding line, MT090183 (GSHO 13039; developed by Montana State University), which has low GPC (T. Blake, personal communication, 2014). Harrington was used as the primary check and was replicated 21 times in the

Aberdeen, Idaho trials and 24 times in the Bozeman, MT trials. The other four checks were used as secondary checks and were replicated 6 times in each trial.

The six-row NILs have alternate alleles for the GPC locus on chromosome 6H. Gen2-036 has an allele from Chevron (PI 38061) that conditions high GPC relative to Lacey while KLBC4-130i-KK has an allele from Karl (CIho 15487; Wesenberg et al., 1976) that conditions low GPC relative to Lacey. The NILs were developed by the University of Minnesota barley breeding program using marker-assisted backcrossing for the desired allele from Chevron or Karl (Fig.1). The Gen2 family (high protein NILs) was derived from a series of crosses carrying the Chevron allele and then backcrosses to Lacey. First, Chevron was crossed to elite breeding line M69 to create a mapping population used to identify QTL for Fusarium head blight resistance and kernel discoloration (de la Pena et al., 1999) and, in a later study, for kernel discoloration and GPC (Canci et al., 2003). A progeny of this cross, MN92-299, was subsequently crossed to another breeding line, M81, to create a new mapping population to validate QTL detected for Fusarium head blight and kernel discoloration (Canci et al., 2004). Then, a progeny of that cross, FB11-113, was crossed to Lacey, and the F_1 progeny were backcrossed to Lacey three times. To create KLBC4-130i-KK, Karl was crossed to Lacey, and then the F_1 progeny were backcrossed to Lacey three times.

The AM panels and replicated checks were evaluated for several traits in each trial. Both panels were assessed for heading date (d after planting), plant height (cm), grain yield (kg ha^{-1}), plump grain (% by wt), test weight (g L^{-1}), and GPC (g kg^{-1}). Additionally, the six-row panel was assessed for spikes per meter, kernels per spike, and kernel weight (mg $kernel^{-1}$). Plant height data were not available for the trial conducted in

Montana in 2013 (Supplemental Table S1). Heading date was the number of days after planting when 50% of the spikes in a plot emerged half-way or more from the boot. Plant height was the distance from the soil surface to the tip of the spike excluding the awns. Spikes per meter referred to a count of spikes within one-half meter of one row of the plot and converted to spikes per one meter. After the plot ends were trimmed, each plot was harvested with a combine. Plump grain was the percentage of kernels by weight remaining on top of a 0.24 by 1.9 cm slotted screen after shaking the grain on a mechanical shaker. Grain protein content was measured by near infrared spectroscopy (NIRS; device details in Supplemental Table S1). The raw, plot-level phenotypic data are available in the Triticeae Toolbox database.

The phenotypic data were screened for outliers and adjusted for field spatial variation prior to statistical analysis and trait mapping. Outliers were identified by examining the Studentized deleted residuals (Kutner et al., 2004) obtained from linear models fitted with the terms genotype, location nested within nitrogen level, and nitrogen level. Then, the phenotypic data were adjusted for spatial variation according to procedures for their experimental design. For trials planted in the Type II Modified Augmented Design, three methods of adjustment—method I, method III (Lin and Poushinsky, 1985), and sliding window (Technow, 2012)—were investigated. For the trial planted in the Augmented Block Design, only the sliding window adjustment method was tested. For each trait-environment combination, the adjustment method with the highest relative efficiency ($RE = \frac{\sum_{i=1}^{c} \sum Var(unadjusted\ values\ of\ secondary\ checks)}{\sum_{i=1}^{c} \sum Var(adjusted\ values\ of\ secondary\ checks)} x100$ where c is the number of secondary checks; Lin et al., 1983) was used to adjust the data for further analysis. If no method improved the data based on relative efficiency (e.g.

$RE < 100$), the unadjusted data were used. Four stress indices—percent difference (PD), GM, STI, and SSI—were calculated for each trait in each location (Table 1). An analysis of variance (ANOVA) was conducted in R (R Core Team, 2015) for each trait and stress index to determine which factors had a significant effect. For the traits *per se*, the components of the linear model were line, nitrogen treatment, and environment nested within nitrogen treatment. For the stress indices for each trait, the linear model included line and environment. An ANOVA was also conducted for each trait in each environment individually to determine whether there were significant differences among lines. Pearson's correlation coefficients were calculated between each trait, between traits and the GM index, and between GM indices in R (R Core Team, 2015).

Association analysis

We conducted separate association analyses for the two- and six-row panels. A combined analysis of the two panels was not conducted in accordance with advice from Hamblin et al. (2010) and because the panels were evaluated in different locations without common checks. The phenotypic data and stress indices combined across all environments were analyzed in conjunction with the SNP marker data to identify significant maker-trait associations using the GWAS function in the rrBLUP package (Endelman, 2011) for R (R Core Team, 2015). To avoid spurious associations, population structure and relatedness among the panel lines must be accounted for using appropriate statistical models (Pritchard et al., 2000; Zhu et al., 2008). In a study using 1,803 of the BarleyCAP lines, Bradbury et al. (2011) established that using a mixed model that accounted for familial relatedness but not population structure performed as well as or better than all other models tested regardless of heritability level, number of QTL, and

sample size. Accordingly, we used an additive kinship matrix (K model; Yu et al., 2006) calculated based on the marker data to account for relatedness among the lines in each panel. The data were combined across environments in which genetic variation was significant for the trait being mapped by including environment as a fixed effect in the model, using the "fixed" argument in the GWAS function. We also conducted AM with the haplotype at the chromosome 6H GPC QTL as a fixed effect to determine whether more small-effect QTL could be identified for GPC. Statistical significance thresholds for associations were based on the simpleM method, which adjusts for multiple testing by considering the effective number of independent tests. This method is comparable to permutation-based correction methods but faster and less computationally intensive (Gao et al., 2008, 2010). The simpleM adjusted p-value threshold was 2.26×10^{-4} for the two-row panel and 2.45×10^{-4} for the six-row panel. After summarizing all the marker-trait associations for each trait, we identified QTL regions, which were defined as clusters of markers on the same chromosome and in high LD ($r^2 \geq 0.6$) with one another. The GM and STI showed similar QTL results, so we only report results for the GM here. Given the rationale that a plant performing well under low nitrogen is more efficient, we considered a QTL region to be associated with NUE (as opposed to the trait *per se*) if marker-trait associations were identified under the low nitrogen treatment and/or a stress index, but not under the normal nitrogen treatment.Nitrogen utilization efficiency is an important factor in overall NUE, especially in non-stressed treatments. However, in this experiment, for QTL detected under the normal nitrogen treatment, we could not distinguish between those associated with nitrogen utilization efficiency and those that were simply associated with the trait itself.

Haplotype definition

The GPC locus on chromosome 6H is collinear with the *Gpc-B1* region in wheat (Distelfeld et al., 2008), which has been well-characterized. Knowing the importance of this QTL in previous studies as detailed above, we investigated the marker haplotypes at this locus. To do this, we used Haploview to determine the extent of the haplotype block at this locus. Using its default settings, Haploview relies on an algorithm from Gabriel et al. (2002) to generate haplotype blocks when 95% of the informative comparisons between markers are considered to be in strong LD based on the D-prime value. Multiple sets of blocks are possible, so the program starts with the largest block and keeps adding blocks as long as they do not overlap with already declared blocks (Barrett et al., 2005). We confirmed the results from Haploview by using a customized Perl script (Cavanaugh et al., 2013) to calculate pairwise haplotype sharing (PHS; Toomajian et al., 2006). Pairwise haplotype sharing identifies a genomic segment that extends from a focal SNP and is shared among individuals within the population; the extent of a shared haplotype is normalized by genome-wide sharing between the individuals compared. The PHS score reports the length of the shared haplotype and its frequency in the population. In our analysis, the SNP with the highest –log*P* value for association with GPC was used as the focal SNP. Both Haploview and PHS showed that the haplotype block at this locus spans from about 49 to 65 cM in our panels.

To determine whether any of the GPC-associated markers were physically close to the GPC sequence, we used BLASTN to find which barley contig contains the GPC sequence reported by Distelfeld et al. (2008) (which is available on GenBank). Using BLASTN to search *Hordeum vulgare* within the EnsemblPlants database, we determined

that this sequence is on morex_contig_1574297 (Query length: 1453, Score: 1441, E-value: 0.0, %ID: 99.8), which is on the short arm of chromosome 6H. No BOPA SNP markers are present on this contig, so we were unable to determine physical proximity of any marker to the gene. Based on the Barley Reference v. 1.0, the sequence for the 6H GPC locus is located at 50,349,272-50,350,411 base pairs on chromosome 6H (Fig. 2; N. Stein, personal communication, 2016).

To define marker haplotypes, we chose four markers within this haplotype block that were significantly associated with GPC in our study: 11_11097, 12_30658, 12_30032, 12_31007 (Fig. 2). Other markers in the haplotype block were also associated with GPC but only provide redundant information. The AM panel lines and replicated checks were classified based on their marker haplotype at this locus. Then, Tukey's honest significant difference (HSD) test was used to determine whether the haplotype class means were significantly different.

Results

Genotypic marker data

We evaluated adjacent marker LD and the genetic length of regions of low LD to characterize the marker coverage across the genome. After filtering the genotypic marker data for minor allele frequency (including monomorphism) and missing data, 1,780 markers remained for the two-row barley AM panel. For this panel, mean r^2 for adjacent markers was 0.401 across the genome and ranged from 0.337 to 0.475 for individual chromosomes. Adjacent marker r^2 was less than 0.10 in 310 of 615 total marker intervals, which contained a total of 563 markers (Fig. 3a,c). Out of the 1137.3 cM map, these marker intervals represent 704.43 cM or 61.9% of the genome. For the six-row AM

panel, 1,694 markers remained after filtering. In this panel, mean r^2 for adjacent markers was 0.432 overall and ranged from 0.376 to 0.530 for individual chromosomes. Adjacent marker r^2 was less than 0.10 in 245 of 494 total marker intervals, which contained 429 markers, (Fig. 3b,d). Out of the 1137.3 cM map, these marker intervals represent 588.05 cM or 51.7% of the genome.

Phenotypic trait data

We assessed six phenotypic traits in the two-row trials (Table 2) and nine phenotypic traits in the six-row trials (Table 3) under low and normal nitrogen treatments. In the ANOVA across environments, the effects of nitrogen treatment and line were significant ($\alpha=0.05$) for all traits in both AM panels except test weight, which was unaffected by nitrogen level. For the within environment ANOVA, line did not have a significant effect in either nitrogen treatment for plant height in Minnesota in 2011; for grain yield in Minnesota in 2011; or for spikes per meter in North Dakota in 2012 (Supplemental Table S1). Accordingly, these trait-trial combinations were excluded from the AM analysis for traits *per se* and the indices. We used four stress indices to evaluate NUE; two of these, GM and STI, showed significant genetic variation ($p<0.0001$). For PD and SSI, line usually had a non-significant effect at the $\alpha=0.05$ level with exceptions for the PD of grain yield ($p=0.027$) and the PD of test weight ($p=0.002$). We calculated pairwise correlations between and among traits and stress indices (Table 4). The GM index of each trait was highly correlated with the trait *per se*. Grain protein content was negatively correlated with grain yield, especially in the two-row AM panel. The GM index of GPC and of grain yield were also negatively correlated. Unexpectedly, grain plumpness was negatively correlated with test weight in the two-row panel, but had an

equally high but positive correlation with test weight in the six-row panel. Grain plumpness also showed a negative correlation with GPC in the two-row panel, but a low positive correlation with GPC in the six-row panel. Similarly, grain yield showed a substantial negative correlation with test weight in the two-row panel but showed a low positive correlation with test weight in the six-row panel. Test weight and GPC showed substantial positive correlations in both panels. In the six-row panel, grain plumpness also showed substantial positive correlation with kernel weight.

QTL identified through association mapping

Of 57 QTL detected overall, only four were identified at the same location and for the same trait in both panels (Fig. 4a)—one for heading date on chromosome 2H and three for GPC on chromosome 6H (Fig. 5). Several other QTL mapped to the same location but for different traits in the two- and six-row panels: heading date in two-row and kernels per spike in six-row on 2H, protein in two-row and plant height in six-row on 5H, heading date and plant height in two-row and kernels per spike in six-row on 7H, and test weight and plump grain in two-row and grain yield in six-row on 7H (Fig. 5).

In the two-row panel, we detected 60 marker-trait associations, which were grouped into 25 QTL (Fig. 5a; Supplemental Table S2). For trait values under the low nitrogen treatment, 18 QTL were detected: four for heading date, one for plant height, one for grain yield, four for test weight, four for grain plumpness, and four for GPC. For trait values under the normal nitrogen treatment, 21 QTL were detected: three for heading date, two for plant height, two for grain yield, four for test weight, four for grain plumpness, and six for GPC. For the GM stress index, 21 QTL were detected: three for heading date, one for plant height, one for grain yield, four for test weight, five for grain

plumpness, and seven for GPC. Four of the 25 total QTL represented NUE (Fig. 5a; Table 5).

In the six-row panel, we detected 63 marker-trait associations, which were grouped into 36 QTL (Fig. 5b; Supplemental Table S2). For trait values under the low nitrogen treatment, 18 QTL were detected: two for heading date, one for plant height, one for grain yield, two for spikes per meter, two for kernels per spike, one for test weight, three for grain plumpness, one for kernel weight, and five for GPC. For trait values under the normal nitrogen treatment, 24 QTL were detected: three for heading date, two for plant height, three for grain yield, two for spikes per meter, two for kernels per spike, one for test weight, one for grain plumpness, two for kernel weight, and eight for GPC. For the GM stress index, 22 QTL were detected: four for heading date, three for plant height, one for grain yield, one for kernels per spike, one for test weight, two for grain plumpness, one for kernel weight, and nine for GPC. Twelve of the 36 total QTL represented NUE (Fig. 5b; Table 5).

By modeling the 6H GPC locus as a fixed effect, we detected one additional significant association with GPC under low nitrogen, two under normal nitrogen, and one for the GM in the six-row panel (Supplemental Fig. S1). None of the QTL were associated with NUE. In the two-row panel, we detected one additional significant association with GPC under low nitrogen, one under normal nitrogen, and none for the GM. The locus detected under low nitrogen was not detected in any other cases, so it was considered as associated with NUE. The locus detected under normal nitrogen had also been detected under low nitrogen in the regular model further complicating whether this QTL represents NUE or not.

Chromosome 6H GPC locus haplotypes

The GPC QTL detected on chromosome 6H was not representative of NUE based on our criteria (Fig. 5). Nevertheless, we chose to further investigate this locus because of its importance in previous studies. Based on four markers in the region of chromosome 6H that is associated with GPC, we identified four marker haplotypes, one of which was absent from the two-row panel (Fig. 6a). Haplotype CGCA was the most common in the six-row panel, while haplotype TACA was the most common in the two-row panel. Check lines Harrington, Baronesse, Hockett, and Gen2-036 had haplotype TACA; Tradition, MT090183, Pinnacle, and Lacey had haplotype CGCA; and KLBC4-130i-KK had haplotype CGTA. The haplotype of Robust was most similar to haplotype CGCA but differed at SNP 12_31007. Mean GPC among the haplotype classes was significantly different based on Tukey's HSD test at the $\alpha=0.05$ level (Fig. 6). Mean grain yield and mean kernel weight were not significantly different among the haplotype classes based on Tukey's HSD test at the $\alpha=0.05$ level (data not shown).

Discussion

Genetic variation and QTL for NUE based on stress indices

Nitrogen use efficiency is a complex trait and can be measured by many different experimental approaches that impose different nitrogen level treatments and evaluate different physiological traits. In this study, we quantified NUE by calculating four stress indices and then evaluated which indices demonstrated significant genetic variation to decide which ones to use in mapping. We observed genetic variation for NUE based on the GM and STI for each trait. The PD and SSI generally did not show genetic variation for the traits we evaluated. Studies using these stress indices in rapeseed found that

genetic variation was significant for seed yield, plant height and siliquae per plant (which is correlated with seed yield) and several stress indices for these traits. As in our study, GM and STI showed significant genetic variation, and in contrast to our study, SSI also showed significant genetic variation for these traits (Rameeh 2012, 2013, 2015).

The phenotypic variation observed and QTL identified for NUE provide an opportunity to improve this trait through phenotypic selection under nitrogen stressed conditions and through MAS. Because estimating NUE is imprecise and resource intensive, using MAS may be a more desirable strategy to breed for this trait. Introgressing one or more QTL through MAS is difficult, so choosing the best QTL to use in MAS is important. We considered a QTL to be associated with NUE (as opposed to the trait *per se*) when it was detected under low nitrogen and/or for the geometric mean index. Of the 25 QTL regions identified in the two-row AM panel, four represented NUE, and of the 36 QTL regions identified in the six-row AM panel, 12 represented NUE based on this criterion (Table 5). An additional NUE QTL was detected in the two-row panel when modeling the 6H GPC locus as a fixed effect (Supplemental Fig. S1). Two of the NUE QTL in the two-row panel and four in the six-row panel showed a near significant ($p > 0.001$) association under normal nitrogen (Table 5). The two-row NUE QTL for GPC was also identified under normal nitrogen when modeling the 6H GPC locus as a fixed effect. Because these QTL were detected in both low and normal nitrogen, they might be considered as associated with the trait *per* se. While these results complicate drawing clear conclusions about QTL for NUE, they underline the difficulty in defining and evaluating NUE. Still a total of 10 QTL clearly fit our criteria and could provide useful information for breeding. Considering which traits are most important to barley breeding

is another important aspect of choosing which QTL to focus on. Taking this all into consideration, the QTL for NUE based on the GM for yield detected on 7H at 88.06 cM in the six-row AM panel is an example of a QTL that would be useful for breeding malting barley with relatively low GPC and higher yields. Lines with the AA genotype for this marker have a mean grain yield that is 7.86% higher than the mean grain yield of lines with the BB genotype at this marker.

Mapping in a small subset of lines identifies some QTL from larger studies

Despite warnings against using populations smaller than 384 lines (Wang et al., 2012) and lack of power for QTL detection in small populations (Bradbury et al., 2011), we identified six QTL that were detected in studies that used a larger set of lines (Fig. 4)—three for GPC, one for heading date, and two for plant height. Our panels were designed as subsets of the whole set of 3,070 spring BarleyCAP lines. Compared to two previous studies using the larger sets of the BarleyCAP lines, our smaller panels of 250 lines found 21 non-NUE QTL in the two-row panel and 24 non-NUE QTL in the six-row panel. In a study using the full set of spring BarleyCAP lines, the authors conducted AM in the combined set of two- and six-row lines, which were evaluated in Bozeman, MT in dryland and irrigated trials. They identified 41 QTL for six of the traits that we studied—grain yield, plant height, heading date, grain plumpness, test weight, and grain protein (Pauli et al., 2014). That study used the genetic map generated by Close et al. (2009), so, to facilitate comparisons, we converted the map positions of significant markers to the genetic map positions from the consensus map by Muñoz-Amatriaín et al. (2011). Considering only the QTL that we identified for the traits *per* se, we identified four of the same loci as that study (Fig. 4a). For GPC in particular, we identified one of the same

QTL, the locus at 49.67 cM on chromosome 6H (Fig 1-B, D). In a study of malting quality data for BarleyCAP lines, AM was conducted separately for 938 spring two-row lines and the 764 spring six-row lines (Mohammadi et al., 2015). In this study, four QTL in the two-row panel and 10 QTL in the six-row panel were identified for three of the same traits that we studied—kernel weight, grain plumpness, and grain protein concentration. For these three traits, we found three of the same QTL (Fig. 4b). For GPC in particular, we detected three of the same QTL, again, the loci at 49.67-52.19 cM on chromosome 6H (Fig. 3d).

Overall, we identified common loci with these two previous studies for heading date, plant height, and GPC, but not for grain yield, grain plumpness, kernel weight, or test weight. Possible reasons for not detecting loci for some traits include lack of phenotypic variability for the trait, differences in environmental effects and genotype-by-environment interaction effects, and differences in minor allele frequencies for the QTL and markers among the panels. Trait heritability could also contribute to these differences, especially for grain yield, which typically has low heritability.

Uneven distribution of marker LD hinders QTL discovery

To better understand marker coverage across the genome, we calculated the LD of adjacent markers and investigated the genetic distance lying in regions of low LD. Previous studies using the same marker set as this study have relied on LD decay (Hamblin et al., 2010), the average LD of adjacent markers (Mohammadi et al., 2015), or the density of SNP markers per cM (Zhou et al., 2012; Zhou and Steffenson, 2013a; Zhou and Steffenson, 2013b; Zhou et al., 2014; Mohammadi et al., 2015) as indicators of marker coverage. Massman et al. (2011) used the BOPA I set of 1,536 SNPs and reported

both average extent of LD in cM and the percentage of adjacent SNPs with $r^2 > 0.2$, but did not report the genetic distance lying between markers in low LD. These metrics give an incomplete picture of LD across the genome because the distribution of markers is uneven (Hamblin et al., 2010).

In this study, the average LD of adjacent markers was $r^2 = 0.401$ in the two-row panel (Fig. 3a) and $r^2 = 0.432$ in the six-row panel (Fig. 3c), which is similar to the average LD of adjacent markers reported in an AM study using 1,862 BarleyCAP lines (Mohammadi et al., 2015). However, we found that 61.9% (704.43 cM; two-row panel) and 51.7% (588.05 cM; six-row panel) of the genome lie in areas of low LD interspersed among areas of high LD (Fig. 3b, d). This potentially limited our ability to detect QTL that lie in these marker intervals of low LD. Though the marker platform we used includes 3,072 SNPs, after filtering only 1,694 (six-row panel) and 1,780 (two-row panel) markers remained. Upon factoring in the uneven distribution of these markers, we see that marker coverage is lacking in some regions. With new marker platforms, such as genotyping-by-sequencing, many more SNP markers are generated, which should improve marker coverage throughout the genome. These new marker platforms will be useful for conducting better genome-wide AM studies and for further investigating and validating QTL that have been identified in this study and previous ones.

Genetic architecture differs between two- and six-row panels

Six-row barley originated from a mutation in wild barley (*Hordeum vulgare* ssp. *spontaneum*), which has the two-row spike morphology (Komatsuda et al., 2007). Early cultivators selected for the six-row phenotype, which produced three times as many seeds per spike and, accordingly, higher yield (Zohary et al., 2012; Helbaek, 1959; Harlan,

1968). Following domestication, the two spike types were separated geographically for millennia (Zohary et al., 2012; Helbaek, 1959, Fischbeck, 2002), allowing them time to diverge into subpopulations. The separation of these germplasm groups has been reinforced by the tendency to limit germplasm exchange between geographically dispersed breeding programs, which have differing breeding objectives.

A study of a subset of the barley accessions in the USDA National Small Grains Collection, known as the informative Core or iCore, estimated population structure using the software STRUCTURE (Pritchard et al., 2000) and by principal components analysis using TASSEL (Bradbury et al., 2007). The results showed that spike row number was a principal determinant of population structure within the iCore (Muñoz-Amatriaín et al., 2014). In another study, lines from 10 US barley breeding programs that participated in the BarleyCAP were characterized using principal components analysis, and the authors found again that spike row number is a primary cause of population structure (Poets et al., 2015). Three earlier analyses of subsets of the BarleyCAP lines also demonstrated that spike row number explains population structure in these materials (Cuesta-Marcos et al., 2010; Hamblin et al., 2010; Wang et al., 2012). Differences in allele frequency and LD between the two- and six-row subpopulations could explain why we observe few QTL that are detected in both subpopulations. Different patterns of LD in the subpopulations could mean that a marker that was significantly associated with a trait in one subpopulation may not be detected in the other because it is in low LD with the causal gene. Different allele frequencies in the two subpopulations could also cause us not to detect QTL. Not only will a fixed marker or gene cause us to overlook a QTL, but also markers or genes with low minor allele frequency are unlikely to be detected

especially if the linked gene's effect is not of large effect or if the linkage between the marker and the gene is not tight.

In this study, we observed vastly different genetic architecture in the two- and six-row panels—only four out of 57 QTL were common to both AM panels (Fig. 5). A number of other AM studies in the BarleyCAP lines have shown similar results. In an AM study of the first half of lines submitted to the BarleyCAP project for Fusarium head blight resistance (Massman et al., 2011), just three of 13 QTL were detected in both the two- and six-row lines. In an AM study of food quality traits in the spring BarleyCAP lines (Mohammadi et al., 2014), only three out of 29 marker-trait associations were identified in both the two-row and six-row mapping panels. In an AM study for malt quality traits in the spring BarleyCAP lines (Mohammadi et al., 2015) only two of 72 marker trait associations were common to the two- and six-row mapping panels. Based on our results for agronomic and yield-component traits and these previous studies of AM for various types of traits (i.e., quality, disease resistance), we can conclude that the two- and six-row subpopulations in barley are quite differentiated. Because of this, evaluating each subpopulation separately is important for genetic studies. On the other hand, breeding can exploit QTL or alleles available in one sub-population in breeding for the other.

Allelic series for GPC QTL on chromosome 6H

We identified four haplotypes based on four markers on chromosome 6H, which were significantly associated with GPC (Fig. 5). The six-row NILs—Gen2-036, Lacey, and KLBC4-130i-KK—have significantly different protein levels (Table 3) and belonged to the high, mid, and low protein GPC haplotypes as expected. Another study looking at

these three NILs among many others also found that GPC is significantly different among them (L. Yin, personal communication, 2016). Pinnacle has low GPC and has the six-row low protein line Karl in its pedigree (J. Franckowiak, personal communication, 2016). Unexpectedly, it does not have the same haplotype as KLBC4-130i-KK, which is a NIL with the Karl allele at the 6H GPC locus. Further investigation is needed to confirm or refine this result. We separated the AM panel lines into classes based on their haplotypes at this region. In the two-row barley AM panel, only three haplotypes were present, one of which—haplotype CGTA—had a small sample size ($n=7$). One of the haplotype classes, TACA, was significantly different for GPC from the other two classes (Fig. 6a). In the six-row barley AM panel, we found that three of the four classes were significantly different in their GPC levels (Fig. 6b), indicating the possibility of an allelic series at this locus.

While these haplotype classes were significantly different for GPC, they were not significantly different for grain yield in either panel. This result is congruent with those of Brevis and Dubcovsky (2010) and Carter et al. (2012), which demonstrated that the functional *Gpc-B1* allele did not significantly affect grain yield in wheat. Additionally, another study looking at these NILs found that grain yield was not significantly different among them (L. Yin, personal communication, 2016).While grain yield is not significantly different among the haplotype classes, grain yield is significantly different between Gen2-036, which has the high-protein Chevron allele and the other NILs, Lacey and KLBC4-130i-KK, which have mid and low-protein alleles (Table 3). This discrepancy is possibly explained by other loci contributing grain yield in the AM panel lines.

In the six-row AM panel, kernel weight did not differ significantly by haplotype class, differing from the findings of Brevis and Dubcovsky (2010) and Carter et al. (2012), which showed that the functional allele of *Gpc-B1* was associated with significantly lower grain weight. As with grain yield, we observed significant differences among the six-row NILs but not the haplotype classes for this trait. Again, other loci present in the AM panel lines may contribute to kernel weight, which may explain why the NILs but not the haplotype classes show significant differences.

Harrington had higher GPC than Pinnacle but did not show a statistically significant difference for this trait (Table 2). However, the two lines belonged to haplotype classes with significantly different mean GPC (Fig. 6a). The six-row NILs—Gen2-036, Lacey, and KLBC4-130i-KK—have high, medium, and low GPC, respectively (Table 3) and correspond to high, medium, and low haplotype classes, respectively (Fig. 6b). Cai et al. (2013) conducted a similar haplotype analysis of this locus and identified three haplotypes in cultivated barley and four haplotypes in Tibetan wild barley—two of the haplotypes were common to both germplasm groups (though which haplotypes were held in common was not distinguished). Over two field seasons, they detected consistent albeit non-significant differences in GPC among these haplotypes. Because the authors do not distinguish which of their haplotypes were present in Tibetan wild barley lines versus cultivated lines, we could not to draw further comparisons between their results and ours.

As a genetically complex trait involving many physiological processes, NUE is difficult to characterize and impose selection upon for breeding. Here, we observed genetic variation for stress indices, which may be useful in approximating NUE without the need to measure biomass components. The phenotypic variation observed and QTL

identified for NUE provide an opportunity to improve this trait through phenotypic selection under nitrogen stressed conditions and through MAS. Because estimating NUE is imprecise and labor intensive, using MAS may be a better strategy to breed for this trait. Introgressing one or more QTL through MAS is difficult, so choosing the best QTL to consider for MAS is important and could involve validating the QTL effect in another population (e.g. Navara and Smith, 2014). Many QTL were identified in these sets of elite breeding lines, and the differences in genetic architecture between the two- and six-row lines provide an opportunity to capitalize on loci detected in one subpopulation when breeding for the other. Additionally, the allelic series at the 6H GPC locus could be useful in manipulating protein levels to suit industry standards without affecting grain yield. Finally, considering the limitations of AM to detect small effect loci and the difficulty of stacking useful alleles, genomic selection should be investigated as a means to improve this trait.

Table 1. Stress indices, their abbreviations, calculations, and references.

Stress index	Abbreviation	Formula†	Reference
Percent difference	PD	$\frac{Y_p - Y_s}{2}$	
Mean productivity	MP	$\frac{Y_s + Y_p}{2}$	Rosielle and Hamblin, 1981
Geometric mean	GM	$\sqrt{Y_s \times Y_p}$	Fernandez, 1992
Stress tolerance index	STI	$\frac{Y_p \times Y_s}{\bar{Y}_p^2}$	Fernandez, 1992
Stress susceptibility index	SSI	$\frac{1 - \left(\frac{Y_s}{Y_p}\right)}{1 - (\bar{Y}_s / \bar{Y}_p)}$	Fischer and Maurer, 1978

† Y_p is yield under non-stress conditions or yield potential; Y_s is yield under stress conditions; $\bar{Y}_p$ refers to the mean yield of all genotypes in the non-stress treatment; $\bar{Y}_s$ refers to the mean yield of all genotypes in the stress treatment.

Table 2. Phenotypic means under each nitrogen treatment for each trait for two of the two-row checks and AM panel.

		Pinnacle†	Harrington	AM Panel
Grain protein ($g\ kg^{-1)}$	Low	105.1 **a** ‡	119.8 **a**	118.7
	Normal	116.6 **a**	131.9 **a**	130.5
Grain yield ($kg\ ha^{-1}$)	Low	5993 **b**	6240 **a**	6144
	Normal	6171 **b**	6461 **a**	6232
Plant height (cm)	Low	83.3 **a**	80.4 **b**	78.4
	Normal	81.1 **a**	78.1 **b**	78.0
Heading date (DAP)	Low	62.3 **b**	63.7 **a**	63.0
	Normal	61.7 **b**	63.7 **a**	63.1
Grain plumpness (%)	Low	88.4 **a**	80.2 **b**	83.6
	Normal	95.9 **a**	84.0 **b**	87.6
Test weight ($g\ L^{-1}$)	Low	664.1 **a**	654.1 **b**	659.1
	Normal	658.9 **a**	653.3 **b**	659.5

† Pinnacle represents the Karl allele.

‡ Values followed by the same letter in the same row signifies that the means are not significantly different (t-test, $\alpha=0.05$).

Table 3. Phenotypic means under each nitrogen treatment for each trait for the six-row near isogenic lines and AM panel.

		Gen2-036†	Lacey	KLBC4-130i-KK	AM Panel
Grain protein ($g\ kg^{-1}$)	Low	142.2 **a**‡	130.1 **b**	105.1 **c**	127.1
	Normal	156.0 **a**	136.2 **b**	115.4 **c**	134.3
Grain yield ($kg\ ha^{-1}$)	Low	4065 **b**	4656 **a**	4604 **a**	4205
	Normal	4681 **b**	5544 **a**	5321 **a**	4959
Plant height (cm)	Low	65.8 **a**	67.3 **a**	62.5 **b**	65.5
	Normal	78.7 **a**	76.1 **b**	73.5 **c**	76.5
Heading date (DAP)	Low	53.2 **a**	52.5 **b**	52.2 **b**	53.0
	Normal	53.0 **a**	51.9 **b**	52.5 **a**	52.4
Grain plumpness (%)	Low	75.8 **b**	80.9 **a**	77.9 **ab**	79.1
	Normal	73.5 **b**	78.5 **a**	75.4 **ab**	74.5
Test weight ($g\ L^{-1}$)	Low	630.6 **a**	634.3 **a**	628.4 **a**	626.1
	Normal	633.1 **ab**	638.6 **a**	629.0 **b**	625.9
Kernel weight ($mg\ kernel^{-1}$)	Low	3.26 **c**	3.48 **a**	3.40 **b**	3.46
	Normal	3.28 **b**	3.46 **a**	3.35 **b**	3.39
Kernels per spike	Low	54.36 **a**	55.47 **a**	55.40 **a**	52.54
	Normal	55.79 **b**	55.13 **b**	58.29 **a**	54.22
Spikes per m	Low	90.1 **a**	90.4 **a**	92.3 **a**	94.1
	Normal	107.5 **a**	111.8 **a**	115.2 **a**	111.7

† Gen2-036 represents the Chevron allele, and KLBC4-130i-KK represents the Karl allele.
‡ Values followed by the same letter in the same column signifies that the means are not significantly different (HSD, $\alpha=0.05$)

Table 4. Pearson's correlation coefficients of each trait and the geometric mean of each trait for the six-row AM panel (upper right triangle) and the two-row AM panel (lower left triangle). Magnitudes of correlation were color-coded from most negative (red) to most positive (green).

	Grain protein	Grain yield	Plant height	Heading date	Grain plumpness	Test weight	Kernel weight	Kernels per spike	Spikes per meter	Grain protein-GM	Grain yield-GM	Plant height-GM	Heading date-GM	Grain plumpness-GM	Test weight-GM	Kernel weight-GM	Kernels per spike-GM	Spikes per meter-GM
Grain protein		-0.11	0.36	0.11	0.14	0.41	0.16	0.10	-0.16	0.96	-0.20	0.37	0.06	0.13	0.41	0.15	0.11	-0.20
Grain yield	-0.54		0.05	-0.25	0.24	0.24	0.06	-0.07	0.25	-0.14	0.89	-0.02	-0.26	0.23	0.25	0.01	-0.04	0.17
Plant height	0.18	0.00		0.03	0.00	0.30	0.13	0.09	-0.09	0.33	-0.02	0.92	0.03	0.00	0.31	0.15	0.10	-0.09
Heading date	0.30	0.12	0.34		-0.17	-0.11	-0.16	0.32	-0.07	0.10	-0.16	0.06	0.97	-0.14	-0.11	-0.13	0.30	-0.02
Grain plumpness	-0.43	0.39	-0.06	-0.31		0.46	0.62	-0.12	-0.15	0.18	0.24	-0.01	-0.19	0.97	0.42	0.59	-0.10	-0.22
Test weight	0.54	-0.46	0.06	0.16	-0.46		0.11	0.01	-0.05	0.45	0.20	0.31	-0.14	0.45	0.96	0.06	0.03	-0.14
Kernel weight								-0.07	-0.27	0.14	0.05	0.09	-0.19	0.59	0.09	0.96	-0.02	-0.30
Kernels per spike									-0.28	0.09	-0.08	0.14	0.33	-0.09	0.05	-0.04	0.93	-0.29
Spikes per meter										-0.17	0.23	-0.13	-0.03	-0.16	-0.05	-0.30	-0.27	0.77
Grain protein-GM	0.95	-0.52	0.16	0.32	-0.39	0.54					-0.21	0.36	0.06	0.16	0.45	0.13	0.10	-0.18
Grain yield-GM	-0.57	0.94	0.03	0.12	0.36	-0.49				-0.58		-0.05	-0.20	0.23	0.20	0.01	-0.05	0.22
Plant height-GM	0.18	-0.04	0.94	0.33	-0.04	0.07				0.15	0.02		0.06	-0.01	0.33	0.11	0.14	-0.11
Heading date-GM	0.20	0.16	0.37	0.96	-0.28	0.16				0.23	0.16	0.37		-0.16	-0.13	-0.15	0.29	-0.01
Grain plumpness-GM	-0.38	0.33	-0.07	-0.31	0.97	-0.47				-0.34	0.31	-0.05	-0.28		0.41	0.59	-0.08	-0.25
Test weight-GM	0.57	-0.43	0.08	0.19	-0.45	0.98				0.56	-0.45	0.09	0.18	-0.46		0.05	0.06	-0.13
Kernel weight-GM																	0.00	-0.34
Kernels per spike-GM																		-0.27
Spikes per meter-GM																		

Table 5. Locations (chromosome and genetic position) of QTL for NUE and the –log*P* value and marker effect of the most significant marker in each QTL region.

				Low N		GM index		Normal N‡	
	Trait	Chromosome	Position†	-log*P* value	Marker effect	-log*P* value	Marker effect	-log*P* value	Marker effect
Two-row	Heading date	1H	73.13	3.687§	1.27	--	--	--	--
	Heading date	5H	132.32	4.210	0.15	--	--	--	--
	Grain protein conc.	7H	2.13	4.297	8.46	3.788	8.68	3.382	8.62
	Grain plumpness	2H	93.26	3.696	4.09	3.763	4.12	3.316	3.99
Six-row	Heading date	7H	134.10	--	--	3.786	0.31	3.444	0.31
	Plant height	4H	28.00	--	--	3.864	1.94	3.242	1.99
	Grain yield	7H	88.06	3.750	154.48	--	--	--	--
	Spikes per m	5H	63.93	3.703	3.83	--	--	--	--
	Spikes per m	7H	44.12	3.804	5.35	--	--	--	--
	Kernels per spike	1H	45.20	3.664	1.56	--	--	--	--
	Kernels per spike	3H	127.26-132.62	3.984	1.17	--	--	--	--
	Test weight	6H	11.68	4.352	11.08	4.051	10.93	3.437	11.48
	Grain plumpness	4H	94.07	3.851	4.12	--	--	--	--
	Grain plumpness	6H	86.96	4.422	3.95	3.945	4.27	--	--
	Kernel weight	6H	53.54	4.181	0.05	3.788	0.05	--	--
	Grain protein conc.	6H	52.19	--	--	3.696	3.89	3.312	3.90

† Map positions are based on Muñoz-Amatriaín et al. (2011).

‡For normal N, –log*P* values are only given in the case that of a nearly significant association at this locus under normal N.

§For QTL regions with multiple significant SNPs, the –log*P* value of the most significantly associated SNP is given.

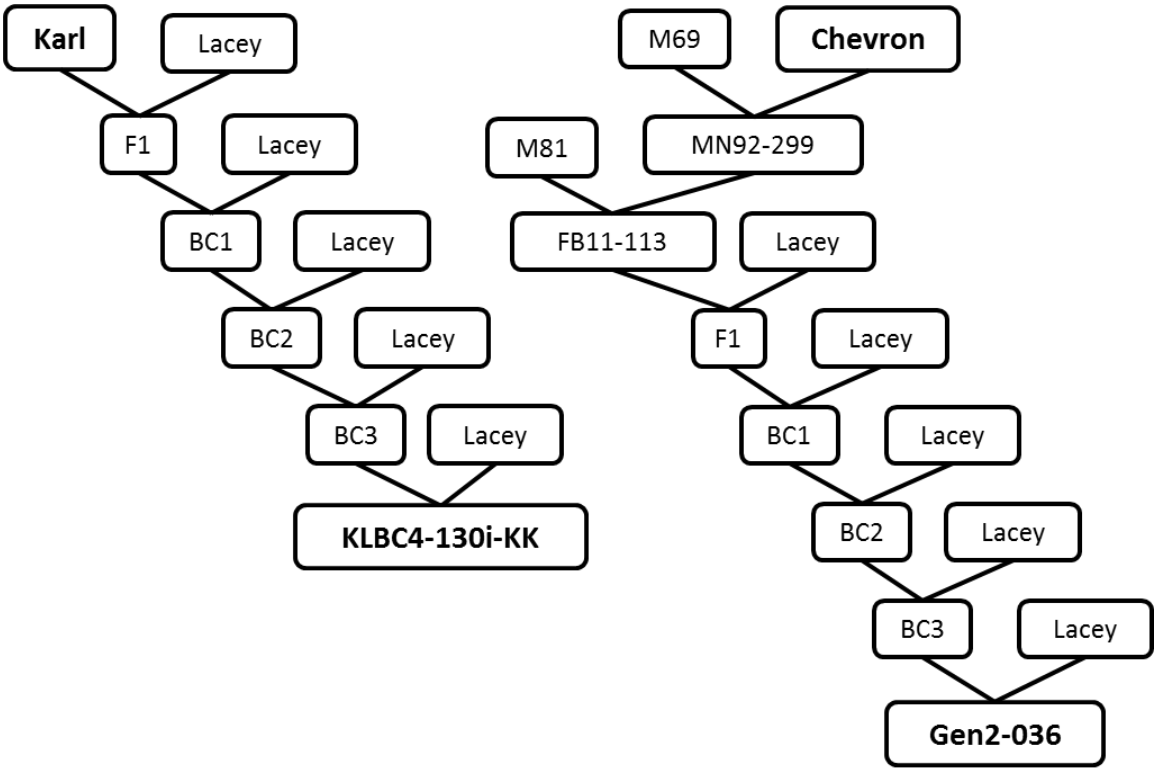


Figure 1. Diagram of the marker-assisted backcrossing scheme for creation of near isogenic lines with different alleles at 6H grain protein concentration locus. KLBC4-130i-KK has a low protein allele from Karl introgressed into the background of Lacey. Gen2-036 has a high protein allele originally from Chevron introgressed into the background of Lacey.

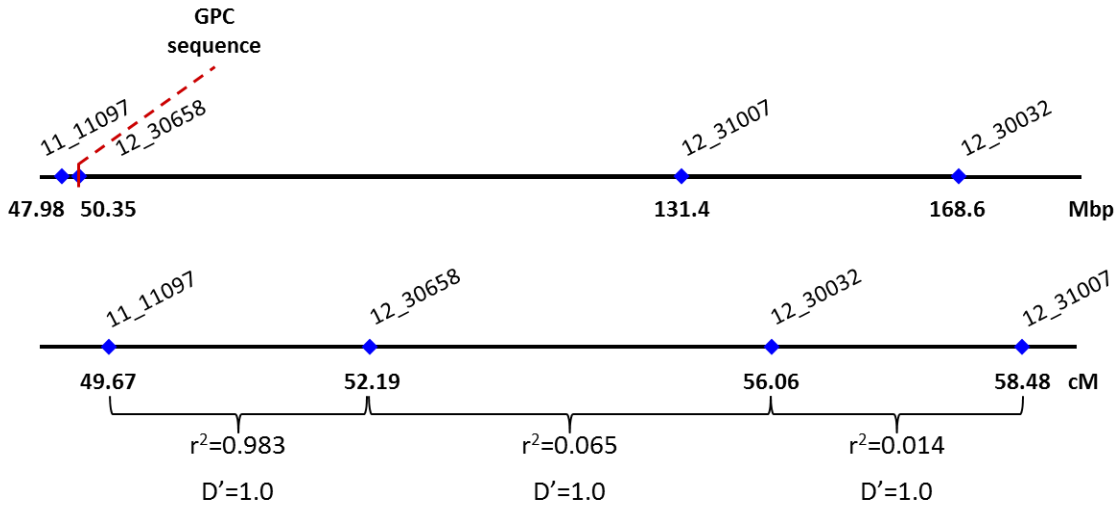


Figure 2. Physical (Mbp) and genetic (cM) map positions for the four markers used to determine the haplotypes at the 6H GPC locus. The physical position of the GPC sequence from Distelfeld et al. (2008) is indicated in red. Below the genetic positions, genetic positions, r^2 values and *D'* values from the six-row panel for each pair of markers are given.

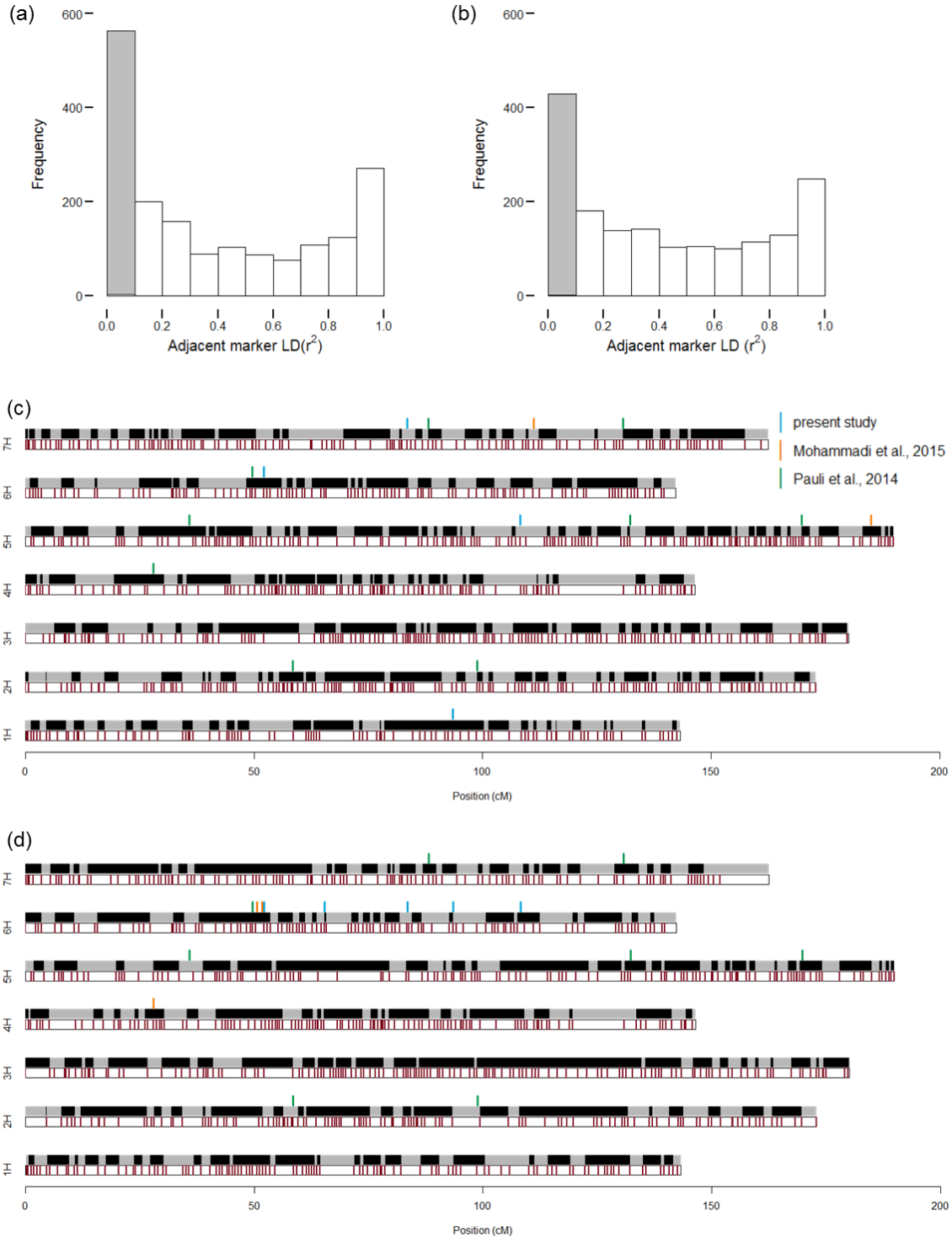

(a)
Frequency
Adjacent marker LD(r^2)
(b)
Frequency
Adjacent marker LD (r^2)
(c)
present study
Mohammadi et al., 2015
Pauli et al., 2014
7H
6H
5H
4H
3H
2H
1H
Position (cM)
(d)
Position (cM)

Figure 3. Histogram and chromosome representations of adjacent marker linkage disequilibrium values for the two-row panel (a, c) and the six-row panel (b, d). The bottom bar for each chromosome shows the position of the SNP markers (red lines). The top bar for each chromosome shows intervals of low LD ($r^2 < 0.1$; light gray). Above the bars for each chromosome, colored line segments (see legend) show the locations of QTL for grain protein concentration from three association mapping studies. In (d), there are overlapping marker-trait associations on chromosome 6H for all three studies.

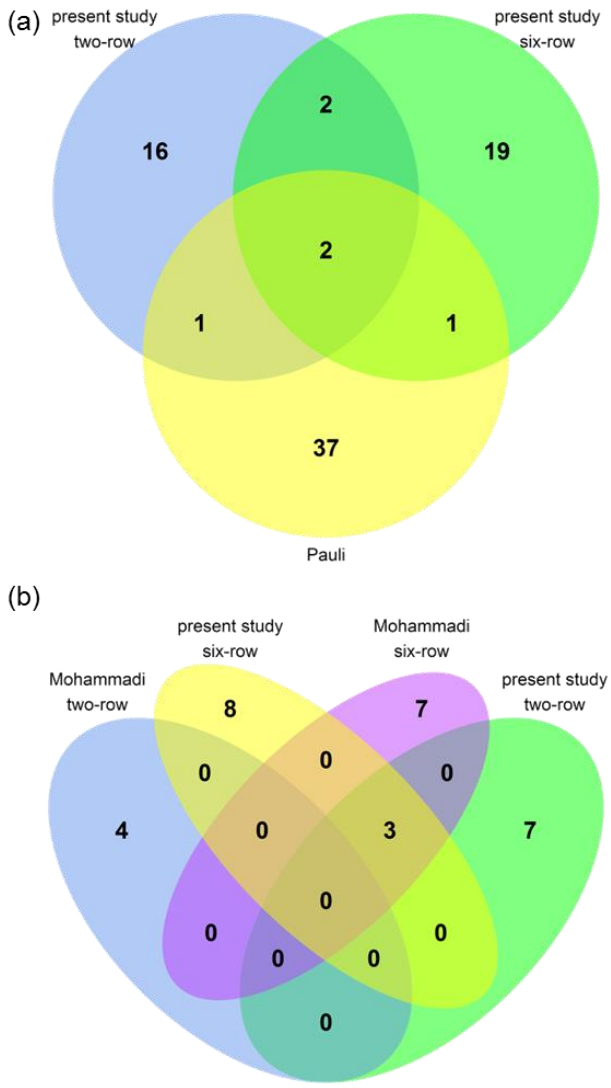


Figure 4. Venn diagrams illustrating the number of QTL shared or unique to the specified studies. (a) Six traits were common between the present study and the study by Pauli et al. (2014)—heading date, plant height, grain yield, test weight, grain plumpness, grain protein concentration. (b) Three traits were common between the present study and the study by Mohammadi et al. (2015)—kernel weight, grain plumpness, and grain protein concentration.

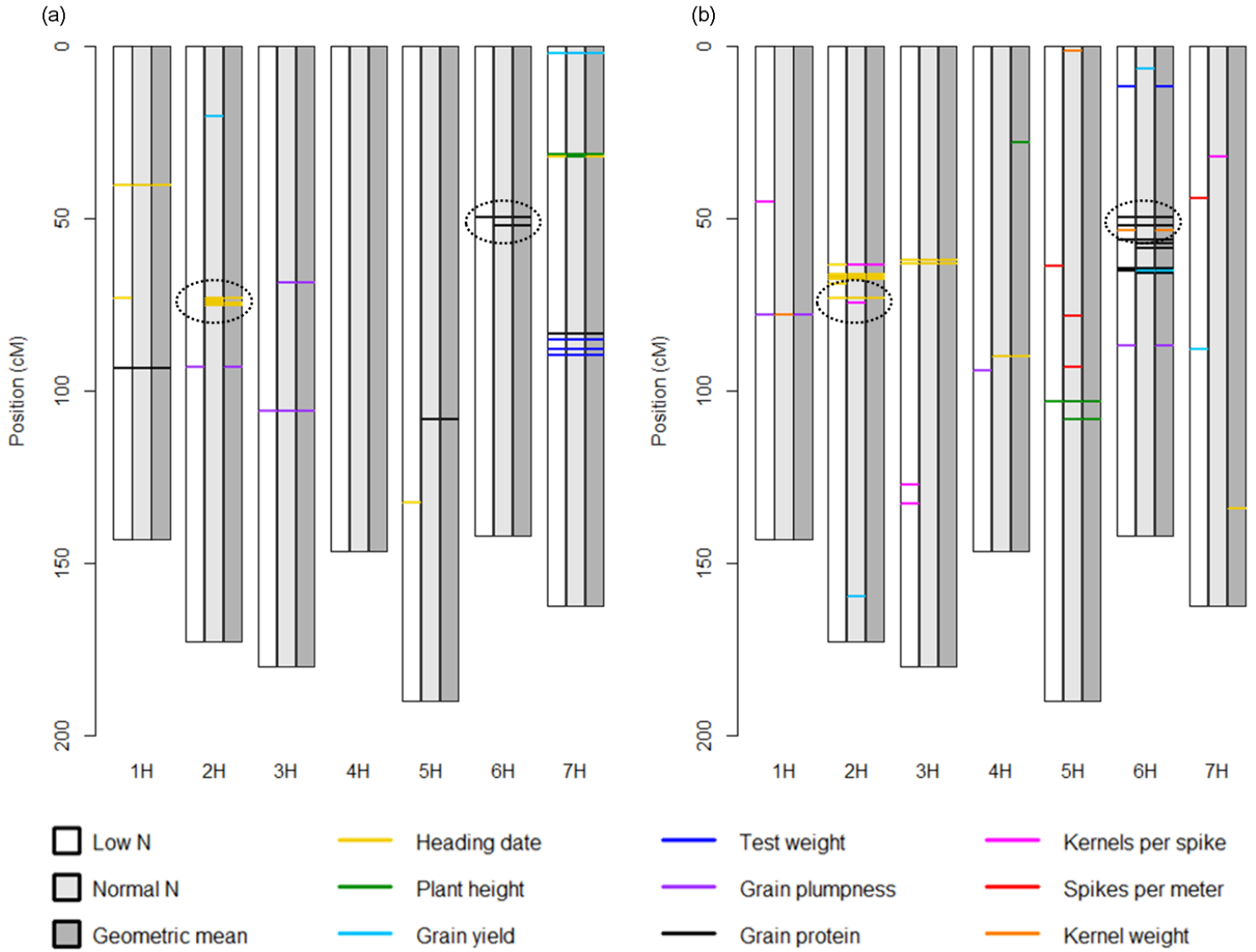

(a)
(b)
Position (cM)
0
50
100
150
200
1H
2H
3H
4H
5H
6H
7H
Low N
Normal N
Geometric mean
Heading date
Plant height
Grain yield
Test weight
Grain plumpness
Grain protein
Kernels per spike
Spikes per meter
Kernel weight

Figure 5. Significant marker-trait associations for the low and normal nitrogen treatments and the geometric mean stress index in the two-row panel (a) and the six-row panel (b). The circled (dotted line) heading date locus on chromosome 2H and the grain protein loci on chromosome 6H were the only loci detected in both AM panels. In each panel, some marker-trait associations are overlapping for two traits. Two-row panel: under low nitrogen, grain yield overlapping grain protein at 2.13 cM on chromosome 7H, test weight overlapping grain plumpness at 85.28 cM and at 88.06 cM on chromosome 7H; under normal nitrogen, plant height overlapping heading date at 32.13 cM on chromosome 7H, test weight overlapping grain plumpness at 85.28 cM and at 88.06 cM on chromosome 7H; for the geometric mean index, grain yield overlapping grain protein at 2.13 cM on chromosome 7H, test weight overlapping grain plumpness at 85.28 cM and at 88.06 cM on chromosome 7H. Six-row panel: under normal nitrogen, kernel weight overlapping grain plumpness at 77.92 cM on chromosome 1H, kernels per spike overlapping heading date at 63.55 cM on chromosome 2H, grain yield overlapping grain protein at 65.29 cM on chromosome 6H, grain protein overlapping test weight at 56.06 cM on chromosome 6H; for the geometric mean index, kernels per spike overlapping heading date at 63.55 cM on chromosome 2H, grain yield overlapping grain protein at 65.29 cM on chromosome 6H.

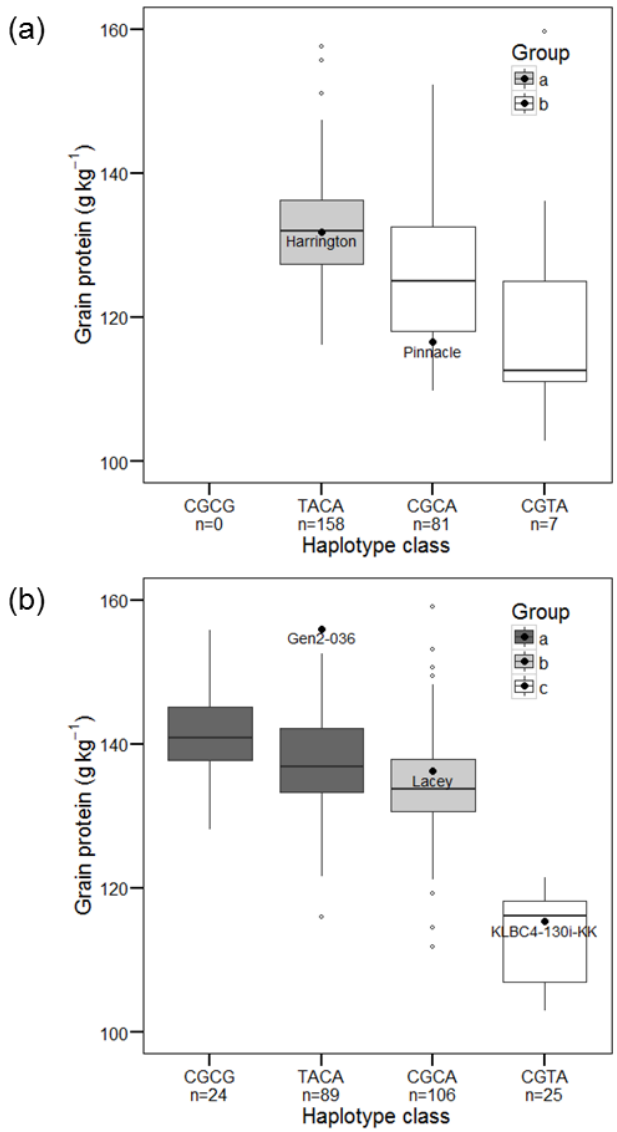


Figure 6. Mean grain protein for the four haplotype classes in the two-row AM panel (A) and the six-row AM panel (b). Box plots show median values (solid horizontal lines), 50th percentile values (box outline), and 90th percentile values (whiskers). The number of entries in each haplotype class is given under the label for that class; note that haplotype class CGTA in the two-row panel has a small sample size (*n=7*). Box fill colors indicate significant differences among the haplotype classes (HSD test, $p \leq 0.05$). Markers used to define haplotype classes at the grain protein locus on chromosome 6H were 11_11097, 12_30658, 12_30032, and 12_31007. The mean of each near-isogenic line or cultivar is marked on the box for the haplotype class to which it belongs.

References

Agrama, H.A.S., A.G. Zakaria, F.B. Said, and M. Tuinstra. 1999. Identification of quantitative trait loci for nitrogen use efficiency in maize. Mol. Breed. 5:187-195.

Barrett, J.C., B. Fry, J. Maller, and M.J. Daly. 2005. Haploview: Analysis and visualization of LD and haplotype maps. Bioinformatics 21:263-265.

Berger, G.L., S. Liu, M.D. Hall, W.S. Brooks, S. Chao, G.J. Muehlbauer, B. Baik, B. Steffenson, and C.A. Griffey. 2013. Marker-trait associations in Virginia Tech winter barley identified using genome-wide mapping. Theor. Appl. Genet. 126:693-710.

Blake, V.C., C. Birkett, D.E. Matthews, D.L. Hane, P. Bradbury, and J. Jannink. 2016. The Triticeae Toolbox: Combining phenotype and genotype data to advance small-grains breeding. The Plant Genome 9:2.

Bradbury, P., T. Parker, M.T. Hamblin, and J. Jannink. 2011. Assessment of power and false discovery rate in genome-wide association studies using the BarleyCAP germplasm. Crop Sci. 51:52-59.

Bradbury, P.J., Z. Zhang, D.E. Kroon, T.M. Casstevens, Y. Ramdoss, and E.S. Buckler. 2007. TASSEL: Software for association mapping of complex traits in diverse samples. Bioinformatics 23:2633-2635.

Brevis, J.C., and J. Dubcovsky. 2010. Effects of the chromosome region including the *Gpc-B1* locus on wheat grain and protein yield. Crop Sci. 50:93-104.

Burger, W., D. Wesenberg, J. Carden, and P. Pawlisch. 1979. Protein content and composition of Karl and related barleys. Crop Sci. 19:235-238.

Cai, S., G. Yu, X. Chen, Y. Huang, X. Jiang, G. Zhang, and X. Jin. 2013. Grain protein content variation and its association analysis in barley. BMC Plant Biol. 13(35). doi:10.1186/1471-2229-13-35.

Canci, P.C., L.M. Nduulu, R. Dill-Macky, G.J. Muehlbauer, D.C. Rasmusson, and K.P. Smith. 2003. Genetic relationship between kernel discoloration and grain protein concentration in barley. Crop Sci. 43:1671-1679.

Canci, P.C., L.M. Nduulu, G.J. Muehlbauer, R. Dill-Macky, D.C. Rasmusson, and K.P. Smith. 2004. Validation of quantitative trait loci for fusarium head blight and kernel discoloration in barley. Molecular Breeding 14:91-104.

Carter, A.H., D.K. Santra, and K.K. Kidwell. 2012. Assessment of the effects of the *Gpc-B1* allele on senescence rate, grain protein concentration and mineral content in hard red spring wheat (*Triticum aestivum* L.) from the Pacific Northwest Region of the USA. Plant Breed. 131:62-68.

Cavanagh, C.R., S. Chao, S. Wang, B.E. Huang, S. Stephen, S. Kiani, K. Forrest, C. Saintenac, G.L. Brown-Guedira, A. Akhunova, D. See, G. Bai, M. Pumphrey, L. Tomar, D. Wong, S. Kong, M. Reynolds, M.L. da Silva, H. Bockelman, L. Talbert, J.A. Anderson, S. Dreisigacker, S. Baenziger, A. Carter, V. Korzun, P.L. Morrell, J. Dubcovsky, M.K. Morell, M.E. Sorrells, M.J. Hayden, and E. Akhunov. 2013. Genome-wide comparative diversity uncovers multiple targets of selection for improvement in hexaploid wheat landraces and cultivars. Proc. Natl. Acad. Sci. USA 110:8057-8062.

Cho, Y., W. Jiang, J. Chin, Z. Piao, Y. Cho, S.R. McCouch, and H. and Koh. 2007. Identification of QTLs associated with physiological nitrogen use efficiency in rice. Mol. Cells 23:72-79.

Close, T.J., P.R. Bhat, S. Lonardi, Y. Wu, N. Rostoks, L. Ramsay, A. Druka, N. Stein, J.T. Svensson, S. Wanamaker, S. Bozdag, M.L. Roose, M.J. Moscou, S. Chao, R.K. Varshney, P. Szűcs, K. Sato, P.M. Hayes, D.E. Matthews, A. Kleinhofs, G.J. Muehlbauer, J. DeYoung, D.F. Marshall, K. Madishetty, R.D. Fenton, P. Condamine, A. Graner, and R. Waugh. 2009. Development and implementation of high-throughput SNP genotyping in barley. BMC Genomics 10(582). doi:10.1186/1471-2164-10-582.

Cuesta-Marcos, A., P. Szűcs, T.J. Close, T. Filichkin, G.J. Muehlbauer, K.P. Smith, and P.M. Hayes. 2010. Genome-wide SNPs and re-sequencing of growth habit and inflorescence genes in barley: Implications for association mapping in germplasm arrays varying in size and structure. BMC Genomics 11(707). doi:10.1186/1471-2164-11-707.

de la Pena, R., K. Smith, F. Capettini, G. Muehlbauer, M. Gallo-Meagher, R. Dill-Macky, D. Somers, and D. Rasmusson. 1999. Quantitative trait loci associated with resistance to fusarium head blight and kernel discoloration in barley. Theor. Appl. Genet. 99:561-569.

Delogu, G., L. Cattivelli, N. Pecchioni, D. De Falcis, T. Maggiore, and A.M. Stanca. 1998. Uptake and agronomic efficiency of nitrogen in winter barley and winter wheat. Eur. J. Agron. 9:11-20.

Distelfeld, A., A. Korol, J. Dubcovsky, C. Uauy, T. Blake, and T. Fahima. 2008. Colinearity between the barley grain protein content (GPC) QTL on chromosome arm 6HS and the wheat *Gpc-B1* region. Mol. Breed. 22:25-38.

Distelfeld, A., I. Cakmak, Z. Peleg, L. Ozturk, A.M. Yazici, H. Budak, Y. Saranga, and T. Fahima. 2007. Multiple QTL-effects of wheat *Gpc-B1* locus on grain protein and micronutrient concentrations. Physiol. Plant. 129:635-643.

Endelman, J.B. 2011. Ridge regression and other kernels for genomic selection with R package rrBLUP. Plant Gen. 4:250-255.

Fernandez, G.C.J. 1992. Effective selection criteria for assessing stress tolerance. In: C.G. Kuo, editor, Proceedings of the International Symposium on "Adaptation of Vegetables and Other Food Crops in Temperature and Water Stress", Tainan, Taiwan. 13-16 Aug 1991. AVRDC, Shanhua, Taiwan. p. 257-270.

Fischbeck, G. 2002. Contribution of barley to agriculture: A brief overview. In: G.A. Slafer, J.L. Molina-Cano, R. Savin, J.L. Araus, and I. Romagosa, editors, Barley science: Recent advances from molecular biology to agronomy of yield and quality. The Haworth Press, Binghamton, NY. p. 1-14.

Fischer, R.A., and R. Maurer. 1978. Drought resistance in spring wheat cultivars. I. Grain yield responses. Aust. J. Agric. Res. 29:897-917.

Gabriel, S.B., S.F. Schaffner, H. Nguyen, J.M. Moore, J. Roy, B. Blumenstiel, J. Higgins, M. DeFelice, A. Lochner, M. Faggart, S.N. Liu-Cordero, C. Rotimi, A. Adeyemo, R. Cooper, R. Ward, E.S. Lander, M.J. Daly, and D. Altshuler. 2002. The structure of haplotype blocks in the human genome. Science 296:2225-2229.

Gallais, A., and M. Coque. 2005. Genetic variation and selection for nitrogen use efficiency in maize: A synthesis. Maydica 50:531-547.

Gallais, A., and B. Hirel. 2003. An approach to the genetics of nitrogen use efficiency in maize. J. Exp. Bot. 55:295-306.

Gao, X., J. Starmer, and E.R. Martin. 2008. A multiple testing correction method for genetic association studies using correlated single nucleotide polymorphisms. Genet. Epidemiol. 32:361.

Gao, X., L.C. Becker, D.M. Becker, J.D. Starmer, and M.A. Province. 2010. Avoiding the high Bonferroni penalty in genome-wide association studies. Genet. Epidemiol. 34:100-105.

Gastal, F., G. Lemaire, J. Durand, and G. Louarn. 2015. Quantifying crop responses to nitrogen and avenues to improve nitrogen-use efficiency. In: V.O. Sadras, and D.E. Calderini, editors, Crop physiology: Applications for genetic improvement and agronomy. Elsevier Inc., Waltham, MA; San Diego, CA. p. 161-206.

Górny, A., and S. Garczyński. 2008. Nitrogen and phosphorus efficiency in wild and cultivated species of wheat. J. Plant Nutr. 31:263-279.

Górny, A.G. 2001. Variation in utilization efficiency and tolerance to reduced water and nitrogen supply among wild and cultivated barleys. Euphytica 117:59-66.

Górny, A.G., Z. Banaszak, B. Ługowska, and D. Ratajczak. 2011. Inheritance of the efficiency of nitrogen uptake and utilization in winter wheat (*Triticum aestivum* L.) under diverse nutrition levels. Euphytica 177:191-206.

Hamblin, M.T., T.J. Close, P.R. Bhat, S. Chao, J.G. Kling, K.J. Abraham, T. Blake, W.S. Brooks, B. Cooper, and C.A. Griffey. 2010. Population structure and linkage disequilibrium in U.S. barley germplasm: Implications for association mapping. Crop Sci. 50:556-566.

Harlan, J.R. 1968. On the origin of barley. In: G.A. Wiebe, editor, Barley: Origin, botany, culture, winter-hardiness, genetics, utilization, pests. Agriculture Handbook No. 338. U.S. Department of Agriculture, Washington, DC. p. 9-31.

Harvey, B.L., and B.G. Rossnagel. 1984. Harrington barley. Can. J. Plant Sci. 64:193-194.

Helback, H. 1959. Domestication of food plants in the Old World: Joint efforts by botanists and archeologists illuminate the obscure history of plant domestication. Science 130:365-372.

Hirel, B., P. Bertin, I. Quilleré, W. Bourdoncle, C. Attagnant, C. Dellay, A. Gouy, S. Cadiou, C. Retailliau, M. Falque, and A. Gallais. 2001. Towards a better understanding of the genetic and physiological basis for nitrogen use efficiency in maize. Plant Physiol. 125:1258-1270.

Joppa, L.R., C. Du, G.E. Hart, and G.A. Hareland. 1997. Mapping gene(s) for grain protein in tetraploid wheat (*Triticum turgidum* L.) using a population of recombinant inbred chromosome lines. Crop Sci. 37:1586-1589.

Jukanti, A.K., and A.M. Fischer. 2008. A high-grain protein content locus on barley (*Hordeum vulgare*) chromosome 6 is associated with increased flag leaf proteolysis and nitrogen remobilization. Physiol. Plant. 132:426-439.

Jukanti, A.K., N.M. Heidlebaugh, D.L. Parrott, I.A. Fischer, K. McInnerney, and A.M. Fischer. 2008. Comparative transcriptome profiling of near-isogenic barley (*Hordeum vulgare*) lines differing in the allelic state of a major grain protein content locus identifies genes with possible roles in leaf senescence and nitrogen reallocation. New Phytol. 177:333-349.

Kimani, J., P. Tongoona, J. Derera. 2011. Genetic mechanisms controlling soil phosphorus and nitrogen tolerance as determined by leaf and seed content in the F_2 and F_3 rice populations. In: J. Tenywa, G. Taulya, G. Kawube, R. Kawuki, M. Namugwanya and L. Santos, editors, 10th African Crop Science Conference Proceedings, Maputo, Mozambique. 10-13 October 2011, African Crop Science Society, Maputo, Mozambique. p. 553-568.

Komatsuda, T., M. Pourkheirandish, C. He, P. Azhaguvel, H. Kanamori, D. Perovic, N. Stein, A. Graner, T. Wicker, A. Tagiri, U. Lundqvist, T. Fujimura, M. Matsuoka, T. Matsumoto, and M. Yano. 2007. Six-rowed barley originated from a mutation in a homeodomain-leucine zipper I-class homeobox gene. Proc. Natl. Acad. Sci. USA 104:1424-1429.

Kutner, M.H., C.J. Nachtsheim, J. Neter, and W. Li. 2004. Applied linear statistical models, 4th ed. McGraw-Hill, Boston, MA.

Lacerenza, J.A., D.L. Parrott, and A.M. Fischer. 2010. A major grain protein content locus on barley (*Hordeum vulgare* L.) chromosome 6 influences flowering time and sequential leaf senescence. J. Exp. Bot. 61:3137-3149.

Laperche, A., F. Devienne-Barret, O. Maury, J. Le Gouis, and B. Ney. 2006. A simplified conceptual model of carbon/nitrogen functioning for QTL analysis of winter wheat adaptation to nitrogen deficiency Theor. Appl. Genet. 113:1131-1146.

Le Gouis, J., O. Delebarre, D. Beghin, E. Heumez, and P. Pluchard. 1999. Nitrogen uptake and utilisation efficiency of two-row and six-row winter barley cultivars grown at two N levels. Eur. J. Agron. 10:73-79.

Le Gouis, J., D. Béghin, E. Heumez, and P. Pluchard. 2000. Genetic differences for nitrogen uptake and nitrogen utilisation efficiencies in winter wheat. Eur. J. Agron. 12:163-173.

Lin, C.S., and G. Poushinsky. 1985. A modified augmented design (type 2) for rectangular plots. Can. J. Plant Sci. 65:743-749.

Lin, C., G. Poushinsky, and P. Jui. 1983. Simulation study of three adjustment methods for the modified augmented design and comparison with the balanced lattice square design. J. Agric. Sci. 100:527-534.

Liu, Z., J. Tang, X. Wei, C. Wang, G. Tian, Y. Hu, and W. Chen. 2007. QTL mapping of ear traits under low and high nitrogen conditions in maize. Sci. Agric. Sin. 40:2409-2417.

Massman, J., B. Cooper, R. Horsley, S. Neate, R. Dill-Macky, S. Chao, Y. Dong, P. Schwarz, G. Muehlbauer, and K. Smith. 2011. Genome-wide association mapping of Fusarium head blight resistance in contemporary barley breeding germplasm. Mol. Breed. 27:439-454.

Mickelson, S., D. See, F.D. Meyer, J.P. Garner, C.R. Foster, T.K. Blake, and A.M. Fischer. 2003. Mapping of QTL associated with nitrogen storage and remobilization in barley (*Hordeum vulgare* L.) leaves. J. Exp. Bot. 54:801-812.

Mohammadi, M., T.K. Blake, A.D. Budde, S. Chao, P.M. Hayes, R.D. Horsley, D.E. Obert, S.E. Ullrich, and K.P. Smith. 2015. A genome-wide association study of malting quality across eight U.S. barley breeding programs. Theor. Appl. Genet. 128:705-721.

Mohammadi, M., J.B. Endelman, S. Nair, S. Chao, S.S. Jones, G.J. Muehlbauer, S.E. Ullrich, B. Baik, M.L. Wise, and K.P. Smith. 2014. Association mapping of grain hardness, polyphenol oxidase, total phenolics, amylose content, and β-glucan in U.S. barley breeding germplasm. Mol. Breed. 34:1229-1243.

Moll, R.H., E.J. Kamprath, and W.A. Jackson. 1982. Analysis and interpretation of factors which contribute to efficiency of nitrogen utilization. Agron. J. 74:562-564.

Muñoz-Amatriaín, M., A. Cuesta-Marcos, J.B. Endelman, J. Comadran, J.M. Bonman, H.E. Bockelman, S. Chao, J. Russell, R. Waugh, and P.M. Hayes. 2014. The USDA Barley Core Collection: Genetic diversity, population structure, and potential for genome-wide association studies. PLoS One 9(4): e94688. doi:10.1371/journal.pone.0094688

Muñoz-Amatriaín, M., M.J. Moscou, P.R. Bhat, J.T. Svensson, J. Bartoš, P. Suchánková, H. Šimková, T.R. Endo, R.D. Fenton, S. Lonardi, A.M. Castillo, S. Chao, L. Cistué, A. Cuesta-Marcos, K.L. Forrest, M.J. Hayden, P.M. Hayes, R.D. Horsley, K. Makoto, D. Moody, K. Sato, M.P. Vallés, B.B.H. Wulff, G.J. Muehlbauer, J. Doležel, and T.J. Close. 2011. An improved consensus linkage map of barley based on flow-sorted chromosomes and single nucleotide polymorphism markers. Plant Gen. 4:238-249.

Olmos, S., A. Distelfeld, O. Chicaiza, A.R. Schlatter, T. Fahima, V. Echenique, and J. Dubcovsky. 2003. Precise mapping of a locus affecting grain protein content in durum wheat. Theor. Appl. Genet. 107:1243-1251.

Paradis, E., J. Claude, and K. Strimmer. 2004. APE: Analyses of phylogenetics and evolution in R language. Bioinformatics 20:289-290.

Parrott, D.L., E.P. Downs, and A.M. Fischer. 2012. Control of barley (*Hordeum vulgare* L.) development and senescence by the interaction between a chromosome six grain protein content locus, day length, and vernalization. J. Exp. Bot. 63:1329-1339.

Pauli, D., G.J. Muehlbauer, K.P. Smith, B. Cooper, D. Hole, D.E. Obert, S.E. Ullrich, and T.K. Blake. 2014. Association mapping of agronomic QTLs in U.S. spring barley breeding germplasm. Plant Gen. 7(3). doi: 10.3835/plantgenome2013.11.0037

Poets, A.M., M. Mohammadi, K. Seth, H. Wang, T.J. Kono, Z. Fang, G.J. Muehlbauer, K.P. Smith, and P.L. Morrell. 2015. The effects of both recent and long-term selection and genetic drift are readily evident in North American barley breeding populations. G3 6(3):609-622. doi: 10.1534/g3.115.024349.

Pritchard, J.K., M. Stephens, and P. Donnelly. 2000. Inference of population structure using multilocus genotype data. Genetics 155:945-959.

R Core Team. 2015. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. Available at: https://www.R-project.org/. 2015.

Rameeh, V. 2015. Nitrogen deficiency stress indices of seed yield in rapeseed (*Brassica napus* L.) genotypes. Cercet. Agron. in Moldova 48(1):89-96.

Rameeh, V. 2013. Combining ability of nitrogen deficiency stress indices for plant height in rapeseed varieties. J. Agric. Sci. (Belgrade) 58:19-30.

Rameeh, V. 2012. Genetic parameters assessment of siliquae associated with stress indices in rapeseed cultivars. Annales Universitatis Mariae Curie Sklodowska Lublin-Polonia 17(4):35-44.

Rasmusson, D.C., and R.D. Wilcoxson. 1983. Registration of 'Robust' barley. Crop Sci. 23:1216.

Rasmusson, D.C., K.P. Smith, R. Dill-Macky, E.L. Schiefelbein, and J.V. Wiersma. 2001. Registration of 'Lacey' barley. Crop Sci. 41:1991.

Rosielle, A.A., and J. Hamblin. 1981. Theoretical aspects of selection for yield in stress and non-stress environments. Crop Sci. 21:943-946.

Sasaki, A., M. Kiryu, T. Kato, and A. Kaminaga. 1992. Accumulation of dry matter and nitrogen in low protein barley [*Hordeum vulgare*] cv. Karl and its offsprings. Jpn. J. Breed. 42:853-862.

Schum, A., and G. Jansen. 2014. *In vitro* method for early evaluation of nitrogen use efficiency associated traits in potato. J. Appl. Bot. Food Qual. 87:256-264.

See, D., V. Kanazin, K. Kephart, and T. Blake. 2002. Mapping genes controlling variation in barley grain protein concentration. Crop Sci. 42:680-685.

Sinebo, W., R. Gretzmacher, and A. Edelbauer. 2004. Genotypic variation for nitrogen use efficiency in Ethiopian barley. Field Crops Res. 85:43-60.

Technow, F. 2012. R package for moving grid adjustment in plant breeding field trials. Available at: http://artax.karlin.mff.cuni.cz/r-help/library/mvngGrAd/html/00Index.html. 2015.

Tilman, D., K.G. Cassman, P.A. Matson, R. Naylor, and S. Polasky. 2002. Agricultural sustainability and intensive production practices. Nature 418:671-677.

Tong, H., L. Chen, W. Li, H. Mei, Y. Xing, X. Yu, X. Xu, S. Zhang, and L. Luo. 2011. Identification and characterization of quantitative trait loci for grain yield and its components under different nitrogen fertilization levels in rice (*Oryza sativa* L.). Mol Breed. 28:495-509.

Toomajian, C., T.T. Hu, M.J. Aranzana, C. Lister, C. Tang, H. Zheng, K. Zhao, P. Calabrese, C. Dean, and M. Nordborg. 2006. A nonparametric test reveals selection for rapid flowering in the *Arabidopsis* genome. PLoS Biol. 4(5): e137. doi:10.1371/journal.pbio.0040137

Uauy, C., J.C. Brevis, and J. Dubcovsky. 2006a. The high grain protein content gene *Gpc-B1* accelerates senescence and has pleiotropic effects on protein content in wheat. J. Exp. Bot. 57:2785-2794.

Uauy, C., A. Distelfeld, T. Fahima, A. Blechl, and J. Dubcovsky. 2006b. A NAC gene regulating senescence improves grain protein, zinc, and iron content in wheat. Science 314:1298-1301.

Wang, H., K.P. Smith, E. Combs, T. Blake, R.D. Horsley, and G.J. Muehlbauer. 2012. Effect of population size and unbalanced data sets on QTL detection using genome-wide association mapping in barley breeding germplasm. Theor. Appl. Genet. 124:111-124.

Waugh, R., J. Jannink, G.J. Muehlbauer, and L. Ramsay. 2009. The emergence of whole genome association scans in barley. Curr. Opin. Plant Biol. 12:218-222.

Wei, D., K. Cui, G. Ye, J. Pan, J. Xiang, J. Huang, and L. Nie. 2012. QTL mapping for nitrogen-use efficiency and nitrogen-deficiency tolerance traits in rice. Plant Soil 359:281-295.

Wei, D., K. Cui, J. Pan, G. Ye, J. Xiang, L. Nie, and J. Huang. 2011. Genetic dissection of grain nitrogen use efficiency and grain yield and their relationship in rice. Field Crops Res. 124:340-346.

Wesenberg, D., R. Hayes, N. Standridge, W. Burger, E. Goplin, and F. Petr. 1976. Registration of Karl barley. Crop Sci. 16:737.

Yu, J., G. Pressoir, W.H. Briggs, I. Vroh Bi, M. Yamasaki, J.F. Doebley, M.D. McMullen, B.S. Gaut, D.M. Nielsen, J.B. Holland, S. Kresovich, and E.S. Buckler. 2006. A unified mixed-model method for association mapping that accounts for multiple levels of relatedness. Nat. Genet. 38:203-208.

Zhou, H., G. Muehlbauer, and B. Steffenson. 2012. Population structure and linkage disequilibrium in elite barley breeding germplasm from the United States. J. Zhejiang Univ., Sci., B 13:438-451.

Zhou, H., B. Steffenson, G. Muehlbauer, R. Wanyera, P. Njau, and S. Ndeda. 2014. Association mapping of stem rust race TTKSK resistance in US barley breeding germplasm. Theor. Appl. Genet. 127:1293-1304.

Zhou, H., and B.J. Steffenson. 2013a. Association mapping of Septoria speckled leaf blotch resistance in U.S. barley breeding germplasm. Phytopathology 103:600-609.

Zhou, H., and B. Steffenson. 2013b. Genome-wide association mapping reveals genetic architecture of durable spot blotch resistance in US barley breeding germplasm. Mol. Breed. 32:139-154.

Zhu, C.G., M. Buckler, and S.Y. Edward. 2008. Status and prospects of association mapping in plants. Plant Gen. 1(1):5-20. doi: 10.3835/plantgenome2008.02.0089.

Zohary, D., M. Hopf, and E. Weiss. 2012. Domestication of plants in the Old World: The origin and spread of domesticated plants in Southwest Asia, Europe, and the Mediterranean Basin. Oxford University Press Inc., New York.

Chapter 2: Evaluating the effectiveness of genomic selection to initiate a winter barley breeding program

Genomic selection utilizes genome-wide marker data to predict the phenotype of individuals. With a focus on winter hardiness in barley (*Hordeum vulgare*), we aimed to assess the utility of genomic selection in the context of initiating a breeding program. Our specific objectives were to 1) empirically measure gain from selection and change in phenotypic variation per cycle; 2) examine changes in marker allele frequency; and 3) investigate how the population shifted overall with selection. We conducted two cycles of genomic selection for a selection index that included multiple traits (low temperature tolerance, malt extract, grain yield, plant height, and heading date), which were each given different weights. We also selected lines by phenotypic selection in the first cycle and at random in both cycles. The sets of selected lines were assessed in field trials for the selection index traits plus 10 others. Between cycles 0 and 2, genomic selection improved low temperature tolerance and malt extract while maintaining the other selection index traits. Phenotypic variance fluctuated but did not change significantly from cycle 0 to cycle 2. Three markers linked to winter hardiness traits shifted in genotypic frequency over the cycles of selection. Based on all marker data, the population shifted toward similarity with the winter growth-type parent lines after two cycles of genomic selection. Overall, this study demonstrated that genomic selection is an effective method for improving trait values in a population at the initiation of a breeding program.

Introduction

Genomic selection (GS) uses marker data to predict the phenotype of individuals. In contrast to marker assisted selection (MAS), which relies on a few markers that are estimated to have significant effects, GS estimates all marker effects across the entire genome simultaneously to calculate genomic predictions (also called genomic estimated breeding values; Meuwissen et al., 2001). A model trained using genotypic and phenotypic data from a "training population" is used to calculate predictions in conjunction with genotypic data for a "selection candidate population." Then, individuals are selected for advancement in the breeding cycle or for use as parents based on their predicted values (Meuwissen et al., 2001).

Simulation and cross-validation studies have explored how best to implement GS in terms of number of markers, size and composition of the training population, prediction model, and other factors (Bernardo and Yu, 2007; Heffner et al., 2009;Jannink, 2010; reviewed in Jannink et al., 2010 and Lorenz et al., 2011; Lorenzana and Bernardo, 2009; Crossa et al., 2010; Asoro et al., 2011; Heffner et al., 2011; Heslot et al., 2012; Lorenz et al., 2012; Combs and Bernardo, 2013; Massman, et al., 2013; Riedelsheimer et al., 2013; Beaulieu et al., 2014; Guo et al., 2014; Grenier et al., 2015; Isidro et al., 2015; Sallam et al., 2015; Lorenz and Smith, 2015). Empirical studies have demonstrated that gains from selection achieved by GS are equal to or greater than those achieved through other breeding strategies, including phenotypic selection (Combs and Bernardo, 2013;

Asoro et al., 2013; Rutkoski et al., 2015) and MAS (Massman et al., 2013; Asoro et al., 2013; Rutkoski et al., 2015; Beyene et al., 2016).

In comparison to phenotypic selection or MAS, GS reduces the breeding cycle time, particularly for quantitative traits. GS can be conducted in earlier generations than phenotypic selection since it does not require large amounts of seed to plant replicated trials in multiple environments. Predictions can be generated quickly and multiple times per year, meaning GS can increase the gain per unit time (Heffner et al., 2010). Genomic selection also allows the breeder to make selections in breeding generations when trait heritability is low or trait data cannot be collected (e.g. in off-season nurseries or greenhouses). Several studies have shown that implementing GS could increase gains per year and reduce costs for a breeding program (Lorenzana and Bernardo, 2009; Schaeffer, 2006; König et al., 2009, Heffner et al., 2010).

Genomic selection is especially appropriate for quantitative traits, for which phenotype is often a poor predictor of breeding value for a number of reasons including low heritability, high levels of genotype-by-environment interaction, and epistatic effects. Additionally, phenotyping quantitative traits can be difficult and costly. In the case of winter hardiness, which we consider here, evaluation is difficult because some winters are too mild, allowing most lines to survive, while other winters are too harsh, killing most lines. Since quantitative traits are affected by so many loci of both large and small effects, attempting to pyramid desirable alleles using MAS is ineffective (Dekkers and Hospital, 2002; Kearsey and Farquhar, 1998). GS, on the other hand, uses all marker

information including small effect loci that would be overlooked by mapping studies, to improve the population.

Winter hardiness in barley is a complex trait involving low temperature tolerance (LTT), photoperiod (PPD) sensitivity, and vernalization (VRN) sensitivity (Hayes et al., 1993). PPD and VRN sensitivity relate to LTT by regulating the timing of the transition from vegetative to reproductive growth, which must occur after the risk of cold temperatures has diminished to improve chances of survival (Fowler et al., 2001; von Zitzewitz et al., 2005). PPD sensitivity delays the transition under short days (in the fall) and promotes it under long days (in the spring; Pan et al., 1994; Cuesta-Marcos et al., 2008). VRN sensitivity delays the transition until the plant has experienced a sufficiently long cold period. Barley growth habit is classified into three categories. Spring growth-types do not have LTT, do not require vernalization, and are insensitive to short day PPD. Winter growth-types are low temperature tolerant, photoperiod sensitive, and vernalization responsive. Facultative growth-types do not require vernalization, but are low temperature tolerant like winter varieties and may be photoperiod sensitive (von Zitzewitz et al., 2005). Facultative and winter growth types show comparable variation in LTT, indicating that VRN sensitivity is unnecessary for maximum LTT (Rizza et al., 2011).

Previous studies have identified a number of QTL that affect winter hardiness in barley. Two QTL influence PPD sensitivity: *PPD-H1 and PPD-H2*. In spring barley, the recessive allele of *PPD-H1* results in insensitivity to long-day conditions, which allows

for a longer growing period, and therefore higher grain yield (Turner et al., 2005). Individuals that are sensitive to short-day conditions (i.e. remain vegetative) have a deletion of or within *PPD-H2* (Faure et al., 2007; Kikuchi et al., 2009). This locus also affects flowering time under short photoperiods and in fall-sown experiments (Pan et al. 1994; Cuesta-Marcos et al., 2008).

Three QTL, which interact in an epistatic manner, contribute to VRN sensitivity: *VRN-H1*, *VRN-H2*, and *VRN-H3*. *VRN-H1* promotes flowering after a period of cold temperatures. *VRN-H2* encodes a flowering repressor that is down regulated by VRN (Yan et al., 2004). Long days induce expression of *VRN-H3*, which may mediate long-day flowering response (Turner et al., 2005). Individuals with the winter growth-type (i.e. those that require vernalization to transition to reproductive growth) have the genotype *Vrn-H2_/vrn-H1vrn-H1/vrn-H3vrn-H3*. Individuals with any other allele combination are insensitive to vernalization (Szűcs et al., 2007). Facultative individuals have a winter allele at the *VRN-H1* locus and a complete deletion of *VRN-H2* (Karsai et al., 2005; von Zitzewitz et al., 2005; Szűcs et al. 2007).

At least three major QTL affect LTT: *Frost Resistance-1* (*FR-H1*), *Frost Resistance-2* (*FR-H2*; Francia et al., 2004; Skinner et al., 2005; Galiba et al., 2009) and *Frost Resistance-3* (*FR-H3*; Fisk et al., 2013). The likely candidate gene for *FR-H1* is *HvBM5A* (Fu et al., 2005; von Zitzewitz et al., 2005), which was also identified as the main source of allelic variation for *VRN-1* in the *Triticeae* family (Danyluk et al., 2003; Trevaskis et al., 2003; Yan et al., 2003; von Zitzewitz et al., 2005). The *VRN-H1* and *FR-*

H1 QTL may be pleotropic effects of this gene (Dhillon et al., 2010; Limin et al., 2007). In an association mapping study by von Zitzewitz et al. (2011), *FR-H1* and *FR-H2* explained just 25% of the variation in LTT. No other loci were detected but numerous regions were near significant levels of association with this trait. In the Fisk et al. study (2013), *FR-H2* and *FR-H3* explained 40 or 64% of the observed variation depending on the environment. Other population- and environment-specific QTL that had smaller effects were also identified. These results, in addition to those from numerous previous studies (Skinner et al., 2006; Chen et al., 2009a, 2009b; Reinheimer et al., 2004), indicate that other minor effect loci are contributing to LTT. Because mapping and accumulating these minor effect loci into a single line would be beyond the scope of QTL mapping and MAS, GS may be a better method for fixing the favorable LTT alleles in a breeding population.

Winter barley could be a useful cover crop in many regions, but current varieties are not hardy enough for certain climates. As a cover crop, winter barley provides a number of ecosystem services. It is more water-use efficient since it utilizes moisture from spring snow thaw (von Zitzewitz et al., 2005; Szűcs et al., 2007). Winter barley also sequesters carbon, improves nutrient cycling, reduces erosion, builds organic matter in the soil, suppresses weeds (Clark, 2008) and provides animal habitat. Fall-sown barley may also avoid certain diseases by growing and maturing earlier than spring-planted barley. This is especially important for contending with the fungal disease Fusarium head blight, which has contributed to the decrease in spring barley production in Minnesota

over the past 25 years. Unlike many other cover crops, winter barley can potentially be sold at a profit to the malting and brewing industries, making it an attractive option for producers.

In this study, we sought to initiate a winter malting barley breeding program that would produce varieties adapted to Minnesota and surrounding regions. Accordingly, our goals were different than those one might see in a mature and active breeding program. An active breeding program for winter barley would likely already have fixed the major LTT loci. In our case, increasing the frequency of the desired alleles of the LTT QTL was yet to be accomplished. To do this, while also maintaining or improving the values of other traits, we used a selection index that combined several traits. The combination of a selection index and GS is advantageous over phenotypic selection where traits are assessed in different trials and at different and often late stages of the breeding program. Since this study was conducted within the context of conducting real-time breeding, a number of parameters were changed between the first and second cycle of selection. Though this limits the strength and scope of our conclusions, it is reflective of actual choices that breeders might make in order to maximize gain and is therefore informative to applied situations.

To assess the utility of GS in the context and timeline of an actual breeding program, we investigated the use of this method to establish a winter barley breeding program. In this study, our objectives were to 1) empirically measure gain from selection and change in phenotypic variation per cycle; 2) determine whether marker allele

frequencies shift over cycles of selection; and 3) investigate how the population overall shifts with selection.

Materials and methods

Germplasm

The germplasm evaluated in this study was composed of breeding lines from three cycles: parents, cycle 1 (C1), and cycle 2 (C2; Fig. 1). Selections were made as described below in the C1 and C2 lines to develop a total of five selected sets. The set of parents consisted of 47 six-row barley lines from the Oregon State University (OSU) and University of Minnesota (UMN) breeding programs. The OSU lines were all winter or facultative growth types, while UMN contributed five spring lines, which are adapted to the Upper Midwest in terms of agronomic traits and disease resistance. Crosses were made among the 47 parent lines to create 64 families of 16 full-sibs each. These F_1s were selfed and the F_2 generation and planted in the field in the spring. Sixteen of the 64 families were dropped based on their performance in this spring-planted trial (including the removal of true winter families, which did not transition to reproductive growth having not been vernalized) and based on performance of the parents in previous LTT evaluations leaving 48 families of 16 lines each. These 768 lines were then selfed to the F_3 generation (C1). Facultative lines were used for this project because 1) without the need for vernalization, cycling is more rapid and 2) facultative accessions are as (or more) cold tolerant as winter accessions (von Zitzewitz et al., 2011). From the 768 C1 lines, three sets of 100 lines each were selected. One set was selected at random to serve

as a control (C1-R). Another set was chosen by genomic selection (C1-GS), and another set was chosen phenotypically based on visual screening of winter survival, heading date, and maturity in a field trial of $F_{3:4}$ lines (C1-PS). Because each parent line was not used in an equal number of crosses (i.e., parental lines have different contributions to C1), C1-R is a better representation of the baseline population before selection. Thus, we refer to C1-R as C0 for the rest of the phenotypic results. To create cycle 2, crosses were made at random (but avoiding crosses between lines from the same family) among the C1-GS lines to create 64 families of 12 full-sibs each for a total of 768 facultative lines. These 64 F_1s were selfed and selections (C2-R and C2-GS) were made in the F_2 generation Phenotypic selections were not made in this cycle.

Genomic selections

Genomic selections were made on a selection index that combined predictions for multiple traits. In C1, the index was calculated as

$$y = 0.55\ winter\ survival + 0.2\ malt\ extract + 0.1\ grain\ yield - 0.1\ plant\ height - 0.05\ heading\ date$$

. In C2, the index was calculated as

$y = 0.55\ winter\ survival + 0.3\ malt\ extract - 0.15\ plant\ height$. The weight given to each trait was based on two factors. First, we considered the priority of the trait in our breeding scheme(e.g. improving winter survival was the most important goal, so it was given the highest weight in both selection cycles). We also considered the correlations among the traits in the training population trials (data not shown). For instance, LTT was

positively correlated with grain yield but negatively correlated with malt extract in the training population data. Thus, to bolster our chances of improving malt extract, it was given a higher weight while we depended on the correlation of grain yield with LTT to achieve improvements in grain yield. Genomic predictions were made for each trait based on an additive model using the "kinship.BLUP" function in the rrBLUP package (Endelman, 2011) for R (R Core Team, 2015). In the most recent version of the rrBLUP packge, "kin.BLUP" has the same functionality. Genomic selection was imposed on the lines based on their selection index value calculated from the predictions for each trait.

Genotyping

The training population lines were chosen from the BarleyCAP lines (see details in the "Training population" section below), which were previously genotyped with 3,072 SNP markers using two Illumina GoldenGate Barley Oligonucleotide Pool Assays (BOPA1 and BOPA2; Close et al., 2009). The 47 parent lines were also genotyped with the 3,072 BOPA SNP markers. The C1 and C2 lines were genotyped with a custom Veracode assay of 384 of the BOPA SNPs (Supplemental Table 1). Seven of the SNPs have previously been demonstrated to show significant association with various winter hardiness QTL (Supplemental Table 2). The remaining 377 SNPS were polymorphic among the parent lines (as indicated by the polymorphic information content value) and were chosen at intervals of about 15 cM where possible (i.e., in some cases a polymorphic SNP was not available at 15cM from the last chosen SNP). For the C1 lines, genetic positions based on the map generated by Close et al. (2009) for these markers and

an additional 950 BOPA1 markers for which the parents were genotyped were used to project parent marker states onto their progeny. The probabilities of inheriting parental alleles at the unobserved markers in the progeny were calculated using the "calc.genoprob" function from the R package "qtl" (Broman et al., 2003). These probabilities were combined with the parental marker scores to calculate allele dosages for the progeny at the 950 untyped loci. All genotypic data can be downloaded from the Triticeae Toolbox database (https://triticeaetoolbox.org/; Blake et al. 2016).

Training population

The training population varied for each trait based on what data were available in the Triticeae Toolbox database when the predictions were made. For C1, for LTT, the training population was comprised of 148 of the BarleyCAP I and II lines, which were used for association mapping for LTT by von Zitzewitz et al. (2011). Nineteen of these training population lines were also used as parents. This training population was evaluated for LTT in four field trials (Pendleton, OR 2006; Fort Collins, CO 2006; St. Paul, MN 2009 and 2011) and one controlled environment test conducted in Hungary in 2006. To make predictions for C2, LTT data collected for the C1 lines in a fall-planted trial in St. Paul, MN in 2011-12 were added to the training model.

In C1, for the other traits in the index (malt extract, grain yield, plant height, and heading date), the lines in the training population were chosen as follows. Based on the genotypic marker data, the average Euclidean distance between each BarleyCAP line from five breeding programs (designated as "AB", "BA", "MN", "N6", and "OR" in the

T3 database) and the set of C1 progeny was calculated. BarleyCAP lines were retained to be in the training set if they were in the closest 33% to the C1 progeny (i.e., two thirds of the BarleyCAP lines were eliminated). BarleyCAP trials conducted between 2006 and 2009 that contained training set lines were analyzed. The total number of trials analyzed varied by trait: 92 trials for grain yield, 91 for plant height, 88 for heading date, and 77 for malt extract. For C2, for the other traits in the index (malt extract and plant height), all BarleyCAP lines from the same five breeding programs were included.

Phenotypic evaluation of selected sets

To evaluate the progress from selection, the parent lines and 50 of 100 randomly chosen individuals from each selected set (C1-R, C1-GS, C1-PS, C2-R, C2-GS) were assessed in field trials in 2014 and 2015 (Supplemental Table 3). For malt quality, 25 individuals selected at random from each selected set were evaluated.

The six sets of lines were evaluated for heading date (Julian days), plant height (cm), grain yield (kg ha^{-1}), winter survival (percent of plot), Fusarium head blight (FHB) severity (percent diseased kernels), and nine malt quality traits (Supplemental Table 3). Winter survival was evaluated visually to estimate the percent of the plot that survived. In the St. Paul and Lamberton, MN trials, the winter survival was normalized by the percent of the plot that had germinated in the fall; fall germination was not considered in the Mead, NE trial. Heading date was the Julian date when 50% of the spikes in a plot emerged half-way or more from the boot. Plant height was the distance from the soil surface to the tip of the spike excluding the awns. In yield trials, after the plot ends were

trimmed, each plot was harvested with a combine. Grain yield was converted from g $plot^{-1}$ to kg ha^{-1} by dividing the weight of the grain by the plot area. Fusarium head blight (FHB) severity was evaluated using a previously described method (Steffenson, 2003) in single-row disease nurseries. A full description of the methods used for malt quality measurements is detailed in Budde et al. (2010). Each sample was analyzed for kernel weight (mg), kernel plumpness (%), malt extract (%), grain protein concentration (g kg^{-1}), wort protein (%), soluble over total protein ratio (abbreviated as S/T), diastatic power (°ASBC), alpha-amylase (20°DU), and beta-glucan (ppm). The trial data are available in the Triticeae Toolbox database. The phenotypic data were screened for outliers by examining the Studentized deleted residuals (Kutner et al., 2004) obtained from linear models fitted with the terms line and environment. Each data point that qualified as an outlier was investigated. Data points that looked to be typographical errors were checked with written records to be corrected or were removed if written records were unavailable. The remaining data points were biologically reasonable, so they were retained for the analysis. Then, for all traits except winter survival and the malting quality traits, we adjusted the data for field spatial variation. We investigated three methods of adjustment—method I, method III (Lin and Poushinsky, 1985), and sliding window (Technow, 2012). For each trait-environment combination, the adjustment method with the highest relative efficiency ($RE = \frac{\sum_{i=1}^{c} \sum Var(unadjusted\ values\ of\ secondary\ checks)}{\sum_{i=1}^{c} \sum Var(adjusted\ values\ of\ secondary\ checks)} x100$ where *c* is the number of secondary checks; Lin et al., 1983) was used to adjust data for further analysis. If no method improved the data based on relative efficiency (e.g.

$RE < 100$), the unadjusted data were used. For each line, a selection index value was calculated from the observed phenotype values based on the C1 index equation and based on the C2 index equation.To combine trait data for each line across environments, best linear unbiased predictors were calculated from a model where line, environment, and the interaction between line and environment were fitted as random effects.

Data analysis

An analysis of variance (ANOVA) was conducted for each trait across environments to determine whether line and environment had significant effects. An ANOVA was also conducted for each trait in each individual environment to determine whether there were significant differences among lines. Pearson's correlation coefficients were calculated between each pair of traits. We tested for difference among the means of the selected sets using Tukey's honest significant difference (HSD) test at the α=0.05 level. To compare phenotypic variances between cycles, an *F*-test was calculated using the var.test function for R (R Core Team, 2015); *F*-tests were considered significant at the α=0.05 level. Progeny-based prediction accuracy ($r_{G,\hat{G}}$) was calculated for each trait as the Pearson correlation between the predicted genomic estimated breeding values ($\hat{G}$) with the "true" breeding values as estimated from the phenotypic data (G). All statistical analyses were conducted in R (R Core Team, 2015).

Shifts in the population were analyzed by visual observation of a plot of the first two principle components, which were calculated based on all marker data. To examine the degree of differentiation among the cycles of selection, we calculated the mean F_{ST}

for all pairwise comparisons: parents versus C1, C1 versus C2, and parents versus C2. Shifts in the genotypic frequency were examined using a scatterplot of the frequency of the AA genotype in C1 versus its frequency in C2 for each marker. To quantify the changes in allele frequency, we used the Weir and Cockerham (1984) measure of F_{ST} referred to as θ, as implemented in the package hierfstat (Goudet, 2005) for R (R Core Team, 2015). Heterozygous loci were treated as missing data. An empirical genome-wide threshold for the top 5% of F_{ST} values was used to identify SNPs with large differences in frequency relative to the genome-wide average.

Results

Phenotypic trait data

Across environments, line and environment showed significant effects (α=0.05) for all traits. For each environment individually, all traits showed significant variance among lines with one exception: grain protein concentration in Corvallis, OR Fall 2013. Twelve pairs of traits exhibited strong positive correlations (>0.4): wort protein and FAN, wort protein and S/T, S/T and FAN, wort protein and alpha-amylase, S/T and alpha-amylase, alpha-amylase and FAN, kernel weight and grain plumpness, malt extract and S/T, wort protein and diastatic power, grain protein concentration and wort protein, diastatic power and FAN, heading date and FHB severity, and grain protein concentration and diastatic power. Five pairs of traits exhibited strong negative correlations (<-0.4): S/T and beta-glucan, beta-glucan and FAN, alpha-amylase and beta-glucan, heading date and grain protein concentration, and malt extract and grain protein concentration (Table 1).

Genetic gain and variation in phenotypic variance

Gain from selection varied by trait (Fig. 2). The mean of the selection index value—calculated using the weights used in C1—improved with the first cycle of selection but decreased with second cycle so that it was statistically the same as the base population. Using the weights used in C2, the mean of the selection index value did not change significantly across the cycles of selection.Four traits—winter survival, malt extract, FAN, and S/T—improved significantly from C0 to C2. Grain yield improved in C1 and then declined in C2 such that it was not significantly improved overall. Ten traits did not change over cycles: grain protein concentration, plant height, and heading date, diastatic power, wort protein, beta-glucan, FHB severity, kernel weight, grain plumpness, and alpha-amylase. Prediction accuracy calculated over both cycles of selection was 0.21 for winter survival, 0.42 for malt extract, 0.02 for grain yield, 0.36 for plant height, and 0.29 for heading date.

In C1, we had the opportunity to conduct phenotypic selection based mainly on winter survival while also considering heading date and maturity. We observed that the mean value of C2-GS was not significantly different from the mean of C1-PS for winter survival and both were improved over the C1-R (data not shown). Besides an improvement in winter survival, we also noticed an improvement in the selection index and grain yield for C1-PS. However, C1-PS was not improved for malt extract, plant height, or heading date.

For the index trait and 13 individual traits, phenotypic variance did not vary significantly between the cycles of selection. For heading date, we did observe a significant reduction in phenotypic variance from C0 to C1, but from C1 to C2, phenotypic variance increased significantly. Overall, the change from C0 to C2 overall was not significant. Kernel weight showed a similar pattern in phenotypic variance changes. It was significantly reduced from C0 to C1; significantly increased from C1 to C2; and not significantly different overall from C0 to C2.

Germplasm differentiation

To characterize the structure of the population, we conducted a principle components analysis using all the genotypic marker data. The first two principle components explained 8.93 and 8.25% of the total variation (Fig. 3). The parent lines (black symbols) and C1 lines (red symbols) show the widest variation. The C2 lines (blue symbols) exhibit less variation than the parent lines and the C1 lines. Additionally, the C2 lines cluster to the right in the figure where we also observe many of the parent lines of the winter growth type ('w' symbol). Most of the spring growth-type parent lines ('s' symbol) are far from the C2 lines (Fig. 3). We also examined the distribution of F_{ST} for the cycles of selection to determine the degree of differentiation between them. Mean values of F_{ST} were 0.035 for the parent lines compared with C1, 0.072 for C1 compared with C2, and 0.114 for the parent lines compared with C2.

Change in allele frequencies

To make initial observations about changes in allele frequency, we plotted the frequency of the AA genotype for each SNP in the 384 marker panel in C1 versus their frequency in C2 (Fig. 4a). The seven SNP markers that are linked to winter hardiness moved toward fixation. To quantify the changes in allele frequency, we calculated F_{ST} for C1 versus C2 for each SNP marker. For two of the seven LTT-related SNP markers (12_30889 and 11_31326), we could not calculate F_{ST} because data were missing for all lines in at least one of the cycles. For the remaining five LTT-related SNP markers, three have an F_{ST} value above the 95th percentile threshold (12_30872, 12_30854, 11_11080), while two have low F_{ST} values (12_30883, 11_20126; Fig. 4b).

Discussion

Observed gain from selection

Genomic selection has the greatest opportunity to improve breeding efficiency when it is implemented in stages of the breeding program where the trait heritability is low (e.g. in an off-season nursery or greenhouse) and therefore phenotypic selection is ineffective (Bernardo and Yu, 2007). Likewise, genomic selection can reduce cost when genotyping is less expensive than phenotyping (Heffner et al., 2010). In this study, we implemented and examined GS to improve LTT, grain yield, and malting quality—costly traits that were either impossible or difficult to phenotype in the early generations of breeding. While the selection index (as calculated using the weights established for C1) improved with one cycle of selection and then declined with the second cycle, we made

gains in winter survival and malt extract while also maintaining grain yield, plant height, and heading date.

For producers to grow winter malting barley as a viable and profitable cover crop, breeders need to achieve high levels of survival in varied climates. As such, winter survival was the most important trait to our objectives and was accordingly given the largest weight (0.55 in both C1 and C2) in the index. Winter survival is difficult to phenotype and has low heritability because it is greatly influenced by the environment—namely winter weather including temperature and snow cover—making it a good candidate for genomic selection. If temperatures are too low or if there is little snow cover to insulate the plants and soil, most lines will die. If temperatures are too warm or there is a lot of insulating snow cover, most lines will live. In either case, we cannot collect useful survival data to distinguish among lines. Mean winter survival reached a level of 14.8% in C2 (Supplemental Table 4; Fig. 2). While this is an improvement over the base population, greater gains in this trait—closer to 100% survival—are needed to make winter barley a feasible cover crop in many climates. Winter conditions vary each year and by locations, so additional testing of these lines will provide more insight into their winter hardiness.

In breeding malting barley, we must consider the malt quality criteria set forth by maltsters and brewers. A summary of these specifications was mostly recently updated by the American Malting Barley Association (AMBA) in June 2014 and is available online (http://ambainc.org/content/63/guidelines, verified 6 May 2016). While most large-scale

U.S. malting and brewing companies agree on these criteria, some brewers may prefer barley with slight differences. For certain traits, like malt extract, higher values are better while for other traits, like diastatic power or alpha-amylase, a particular range of values is best and may differ among brewers using different adjuncts. Malt quality is costly to measure, so it is usually only evaluated in lines that have demonstrated good agronomic performance and disease resistance over multiple years. Malt extract is the most important trait affecting the quantity of beer that can be produced. As such, this trait was given the second highest weight (0.2 in C1 and 0.3 in C2) in our selection index. Mean malt extract reached a level of 78.71% in C2 (Supplemental Table 4; Fig. 2). Though this is a significant improvement over the base population, the criteria set forth by AMBA specify malt extract levels of greater than 79.0%. Maximum malt extract was 80% (Supplemental Table 4), so continued improvement should be possible.

Grain yield is the most important trait for producers, but was given a low weight (0.1 in C1; not considered in C2) in our selection index. Our main goal in this breeding project was to improve lines for winter survival, which was favorably correlated (r=0.61) with grain yield in the training population data; thus, improving LTT should also improve grain yield. Though it is not difficult to measure, as a highly quantitative trait, grain yield must be evaluated in many environments to accurately approximate its breeding value. Due to its low heritability, selecting for this trait based on phenotype or genotype often only produces small or negligible gains. In a study of the University of Minnesota spring, six-row barley breeding program, genetic gains were made at a rate of just 0.40% per

year by using phenotypic selection (Condon et al., 2009). By including this trait with a low weight in our selection index, we maintained mean grain yields of 4762 to 4939 kg ha^{-1} (Supplemental Table 4; Fig. 2) in the population. Besides having a low index weight, the lack of improvement in grain yield may also be due to its low progeny-based prediction accuracy, which was 0.02 overall.

Plant height was also given a low weight in our index at -0.1 in C1 and -0.15 in C2. The weight was negative in this case since shorter, not taller, plants are desirable. This trait helps to preventing lodging and to limit the resources that the plant is putting into vegetative growth so that they may be used in reproductive growth (kernels) instead. Plant height is inexpensive to measure and has mid-level heritability, so it is not the best use of GS. Plant height exhibited moderate prediction accuracy at 0.36 overall. Though we sought to decrease plant height, we observed a slight but non-significant increase in height (Supplemental Table 4; Fig. 2). To select for shorter plants, future breeding efforts should place more weight on this trait. Alternatively, since this trait can be phenotyped at low cost, it could be improved through phenotypic selection in a population already improved for winter survival.

The final trait in our selection index was heading date, which was given the lowest weight, -0.05 in C1 (not considered in C2). Early heading date correlates with earlier maturity, which allows the producer to harvest in time to plant a second crop in a double cropping system. Earlier heading date may also help winter barley to escape certain disease pressures, especially FHB infection, which showed moderate correlation

with heading date in this study (Table 1) and has shown strong relationships with heading date in previous studies in spring barley (de la Pena et al., 1999; Mesfin et al., 2003; Dahleen et al., 2003; Horsley et al., 2006; Massman et al., 2010). In our population, heading date became later, though not significantly, by C2 (Supplemental Table 4; Fig. 2). As with plant height, it may be useful to increase the weight of selection on this trait in future breeding efforts to achieve desired values. Heading date showed an overall prediction accuracy of 0.29. To achieve greater accuracy, future GS for this trait in fall-planted barley should rely on data from fall-planted trials for the training population data. Since this trait has high heritability and can be phenotyped at low cost, it could also be improved via phenotypic selection.

We evaluated a number of traits that were not included in our selection index. In the field, we evaluated FHB severity. This disease has greatly influenced barley breeding goals especially in the Midwest where it caused devastating yield losses in the early 1990s, leading to a decline in barley production in this region. The spring parent lines were included to incorporate FHB resistance into this population. Fall-sown barley tends to head earlier than spring-sown barley (von Zitzewitz et al., 2011), which could mitigate its vulnerability to this disease. Quest, which was a member of the parent population, is a spring, six-row, malting barley cultivar with enhanced FHB resistance (Smith et al., 2013). It had a best linear unbiased prediction value of 33.31% diseased kernels in this experiment. Considering that the selected lines had mean levels of about 40% diseased kernels (Supplemental Table 4; Fig. 2), this trait should be improved further in this winter

barley population. Since FHB resistance requires a lot of time and labor to evaluate phenotypically and has low heritability due to its quantitative nature, this trait is a great candidate for GS (Rutkoski et al., 2012; Lorenz et al., 2012) and could be targeted in future GS efforts.

The other traits measured were all components of malt quality. Grain plumpness and grain protein concentration are particularly important because they are measured at the grain elevator to determine overall grain quality and, therefore, whether the producer will receive the premium price for malting barley. Grain plumpness did not change over cycles of selection, maintaining a mean value of about 85% (Supplemental Table 4; Fig. 2), which is above the AMBA requirement of at least 80% plump kernels. Kernel weight is related to grain plumpness and is also a yield component (Schwarz and Horsley, 1995). In this study, these two traits show high positive correlation (Table 1). Like grain plumpness, kernel weight remained constant over cycles of selection, maintaining a value of about 34 mg (Supplemental Table 4; Fig. 2).

Grain protein concentration is influenced by environmental factors as well as nitrogen fertilizer use (Bertholdsson, 1998). Fertilizer application is necessary to increase yield, but producers also need to maintain moderate protein levels to achieve acceptable malt quality. Thus, lines with lower grain protein concentration are desired. In this experiment, grain protein concentration dropped slightly, but not significantly after two cycles of selection. Mean protein levels were about 120 g kg^{-1} (Supplemental Table 4; Fig. 2), which meets the AMBA criterion of less than or equal to 13%. However, lower

grain protein levels are desirable to allow room for environmental and nitrogen-application effects. Related to grain protein concentration, nitrogen use efficiency could also play a role in winter barley. One of the services provided by winter cover crops is the uptake of nitrogen that would otherwise leach into the groundwater and move into aquatic ecosystems (Clark, 2008). This is especially relevant because nitrogen fertilizer is typically applied to the field in the fall before planting. In malting barley, where low grain protein is desirable, it is preferable that the plant directs additional nitrogen to increased grain yield. Therefore, to develop winter malting barley that is most useful as a cover crop, future breeding efforts should seek to incorporate alleles detected in previous studies for nitrogen use efficiency as it pertains to increased grain yield (See Chapter 1).

Besides malt extract, a number of other traits are assessed in the malt. Two of these are diastatic power and alpha-amylase activity, which both affect the conversion of starch to fermentable sugars in the malting process. Fermentable sugars are essential for fermentation in the brewing process. In this study, we observed that alpha-amylase stayed the same across cycles of selection at a value of about 62 to 66 DU (Supplemental Table 4; Fig. 2). These values are well above the AMBA minimum requirement of 50 DU. Diastatic power increased, albeit not statistically, after two cycles of selection. In our population, mean diastatic power ranged from about 142 to 154 °ASBC (Supplemental Table 4; Fig. 2), while the AMBA minimum requirement is 150 °ASBC for adjunct brewers.

Low levels of beta-glucan in the wort are desirable since high levels indicate low malt modification, resulting in lower conversion of starch to fermentable sugars. In this experiment, mean beta-glucan levels decreased but did not change statistically over cycles of selection. The mean beta-glucan levels were between 311 and 348 ppm (Supplemental Table 4; Fig. 2), which is much higher than the desired maximum of 120 ppm. To achieve acceptable malting quality in this population, future breeding efforts would need to consider beta-glucan.

Three traits inform us about the amount of protein being broken down into soluble proteins and free amino acids in the wort, which are essential to yeast nutrition during brewing: wort protein, also called soluble protein; S/T; and free amino nitrogen (FAN). Wort protein increased but not significantly so after two cycles of selection. Mean wort protein values were around 4.5 to 4.8% (Supplemental Table 4; Fig. 2), which is lower than the AMBA recommended range of 5.2 to 5.7%. The soluble over total protein ratio increased significantly after two cycles of selection to 41.4% (Supplemental Table 4; Fig. 2), which is just below the AMBA recommended range of 42-47%. Both of these The training population varied for each trait based on what data were available in the Triticeae Toolbox database when the predictions were made. For C1, for LTT, the training population was comprised of 148 of the BarleyCAP I and II lines, which were used for association mapping for LTT by von Zitzewitz et al. (2011). Nineteen of these training population lines were also used as parents. This training population was evaluated for LTT in four field trials (Pendleton, OR 2006; Fort Collins, CO 2006; St. Paul, MN 2009

and 2011) and one controlled environment test conducted in Hungary in 2006. To make predictions for C2, LTT data collected for the C1 lines was added to the training model.

In C1, for the other traits in the index (malt extract, grain yield, plant height, and heading date), the lines in the training population were chosen as follows. Based on the genotypic marker data, the average Euclidean distance between each BarleyCAP line from five breeding programs (designated as "AB", "BA", "MN", "N6", and "OR" in the T3 database) and the set of C1 progeny was calculated. BarleyCAP lines were retained to be in the training set if they were in the closest 33% to the C1 progeny (i.e., two thirds of the BarleyCAP lines were eliminated). BarleyCAP trials conducted between 2006 and 2009 that contained training set lines were analyzed. The total number of trials analyzed varied by trait: 92 trials for grain yield, 91 for plant height, 88 for heading date, and 77 for malt extract. For C2, for the other traits in the index (malt extract and plant height), all BarleyCAP lines from the same five breeding programs were included.

Three traits inform us about the amount of protein being broken down into soluble proteins and free amino acids in the wort, which are essential to yeast nutrition during brewing: wort protein, also called soluble protein; S/T; and free amino nitrogen (FAN). Wort protein increased but not significantly so after two cycles of selection. Mean wort protein values were around 4.5 to 4.8% (Supplemental Table 4; Fig. 2), which is lower than the AMBA recommended range of 5.2 to 5.7%. The S/T ratio increased significantly after two cycles of selection to 41.4% (Supplemental Table 4; Fig. 2), which is just below the AMBA recommended range of 42-47%. Both of these traits need to be improved to

achieve acceptable malting quality. FAN increased significantly over two cycles of selection to a mean level of about 225 ppm (Supplemental Table 4; Fig. 2). The desired level of FAN is highly dependent on the brewing style—all-malt brewers prefer lower FAN while adjunct-brewers prefer higher FAN. Thus, the increase in FAN from C0 to C2 may be favorable or unfavorable depending on the end-use of the barley.

Trait relationships

In some cases, the relationships among the traits that we measured were favorable for breeding. That is to say, the traits were positively correlated and we desired to achieve higher values in both traits or lower values in both traits OR the traits were negatively correlated and we desired higher values in one trait and lower values in the other. Considering those correlations that have an absolute value greater than 0.4, favorable relationships occurred between six pairs of traits: alpha-amylase and FAN, diastatic power and FAN, heading date and FHB severity, beta-glucan and FAN, alpha-amylase and beta-glucan, kernel weight and grain plumpness, and malt extract and grain protein concentration. The last three pairs of traits were found to be similarly correlated (same direction and larger than 0.4 in magnitude) in a genome-wide association study of malting quality traits (Mohammadi et al., 2015). Unfavorable relationships occurred between two pairs of traits: heading date and grain protein concentration and grain protein concentration and diastatic power. The relationship between grain protein concentration and diastatic power was also present in the Mohammadi et al. study (2015). Finally, a number of relationships were not clearly favorable or unfavorable because we

wanted to achieve mid-range values of one or both traits. Favorably correlated traits are easier to breed for because an improvement in one trait usually coincides with improvement in the other. On the other hand, unfavorably correlated traits are difficult to breed for simultaneously because gains in one trait usually equate to setbacks in the other.

For the traits that were part of our trait index, strong correlations could have affected the response of the correlated traits. Though no trait was strongly correlated (absolute value of correlation greater than 0.4) with LTT, the most strongly correlated trait was S/T (r=-0.31). With this negative correlation, we would expect the traits to move in opposite directions, but actually we observed that the value for both traits increased with selection (Fig. 2). This may be due to the fact that the correlation between these two traits was not exceedingly high. All of the other traits that we measured showed weak correlations with LTT.

Malt extract showed high correlations with grain protein concentration (r=-0.41) and S/T (r=0.53). We observed that malt extract increased significantly in the population (Fig. 2). With the negative correlation between malt extract and grain protein concentration, we expected these traits to change in opposite directions and indeed, we observed that grain protein concentration decreased though not significantly (Fig. 2). Since malt extract and S/T were positively correlated, we expected them to move in the same direction, and S/T did increase with malt extract (Fig. 2). The positive correlation

between malt extract and S/T could explain why S/T increased despite its moderate negative correlation with LTT.

The other traits in the selection index—grain yield, plant height, and heading date—did not change significantly between C0 and C2 (Fig. 2). Thus, we did not expect changes in the traits that were correlated with them and not under direct selection. Grain yield was moderately correlated with grain protein concentration (-0.36) and wort protein (-0.28), neither of which changed significantly. Plant height showed moderate correlations with grain yield (0.32) and grain protein concentration (-0.37), which did not change significantly. Heading date was moderately correlated with plant height (0.37), and strongly correlated with FHB severity (0.42) and grain protein concentration (-0.43), none of which changed significantly.

Effects of selection: gain in trait mean and changes in phenotypic variance

Based on the gains we achieved in the two most highly weighted traits (winter survival and malt extract) of the selection index, we have shown that genomic selection can improve traits that are under selection. While the other three traits in our index did not show significant improvement, they also did not decline significantly. Including a trait in the selection index but giving it a low weight may function to remove lines that are very poor without prioritizing the trait, allowing gains to be made for other traits (Combs and Bernardo, 2013). Based on histograms for grain yield, plant height, and heading date, we did not observe that pattern in this study (data not shown), which may indicate that the assigned weights were too low to influence these traits at all.

In two cases, traits that were not included in the selection index showed significant change with cycles of selection: FAN and S/T. These gains may be due to correlation of FAN and S/T with traits that were under selection. S/T is highly correlated (r=0.53) with malt extract, which was under selection, and FAN is highly correlated with S/T (r=0.75). Alternately, loci for FAN and S/T might be physically linked in coupling phase to loci for one or more traits that were under selection, making it possible for them to be selected together. Another possibility is that genetic drift influenced the change in value for these traits. The remaining traits that we evaluated did not change with cycles of selection. This is not unexpected since the traits were not under direct selection. Additional reasons for the lack of change in these traits include low correlation with the traits under selection and low variation in the base population.

Maintaining genetic variation is imperative to making long-term gains from selection. Theoretical and simulation studies have shown that genetic variance is better maintained using GS compared to selection based on breeding values estimated using pedigree data because GS results in less inbreeding in each selection cycle (Daetwyler et al., 2007; Jannink et al., 2010). This theory was confirmed in an empirical study of GS for beta-glucan in oat (Asoro et al., 2013). However, traditional plant breeding typically relies on phenotype, not pedigree, data to make selections. Genomic selection may decrease genetic variation more rapidly than phenotypic selection by increasing inbreeding more rapidly than phenotypic selection and by rapidly losing favorable QTL (reviewed in Jannink et al., 2010). Rutkoski et al. (2015) observed that GS did indeed

decrease genetic variation more rapidly that phenotypic selection. Another study found that whether genotypic variance increased or decreased differed for different traits (Tiede, personal communication, 2016). From C0 to C2, we did not observe significant changes in the phenotypic variation in any trait, indicating that the population did not become more phenotypically uniform with cycles of selection. For the traits not under selection, it is unsurprising that phenotypic variance remained relatively constant. For the traits that were part of the selection index, we did not observe a reduction in phenotypic variance possibly as a result of selecting on more than one trait simultaneously. One can imagine that selecting on multiple traits allows the maintenance of variation since selection is not as strict for any particular trait. At the same time, we observed that the genotypic variation in C2 was lower than in the parents and C1 (Fig. 3), and that some markers moved toward fixation with selection (Fig. 4). One strategy to explicitly maintain genetic variance in GS is to weight alleles based on the inverse of their frequency so that low frequency alleles are given more consideration (Goddard, 2009; Hayes et al., 2009). A simulation study in barley showed that this strategy reduced the number of favorable alleles that were lost from the population, leading to higher long-term gain (Jannink, 2010). Another strategy is to use genomewide markers to predict the additive variance among progeny of a bi-parental cross in order to select populations that have not only high mean performance but also high variance (Bernardo, 2014; Mohammadi et al., 2015; Lian et al. 2015; Tiede et al., 2015). Empirical testing of these strategies is necessary to determine their effectiveness in actual breeding programs.

Change in allele frequencies and germplasm differentiation

A proposed advantage of GS over MAS is that it selects lines based on all available marker data without setting an arbitrary statistical cutoff to decide which markers to include. However, breeders may question whether the large-effect markers that they would normally use in MAS are being selected for with GS. To this end, we examined allele frequency changes for the 384 markers in our custom SNP assay, which included seven markers known to be linked to winter hardiness traits. We plotted the frequency of the AA genotype for each SNP in C1 versus their frequency in C2 (Fig. 4a) and observed that the seven SNP markers for winter hardiness traits moved toward fixation of the desired genotype. To further quantify the changes, we calculated F_{ST} for each SNP marker in the custom assay. Two of the seven winter hardiness linked markers (12_31236 and 12_30889) were missing all data for one of the cycles, so we could not calculate F_{ST} for them. Of the remaining five, three markers, were above the 95th percentile for F_{ST} values (Fig. 4b). Marker 11_11080 is linked to a VRN-H1/FR-H1 gene (Hayes, personal communication, 2011) and the frequency of its AA genotype changed from 0.57 in C1 to 0.97 in C2 (Fig. 4a). Marker 12_30872, which is the causal polymorphism in Ppd-H1, changed in frequency for the AA genotype from 0.61 in C1 to 1.00 in C2 (Fig. 4a). Marker 12_30854, which demonstrated a highly significant association with LTT and is thought to be linked to FR-H2 (Hayes, personal communication; 2011) showed a frequency change of 0.52 in C1 to 0.18 in C2 for the AA genotype (Fig. 4a). The other two markers had low F_{ST} values (Fig. 4b). Marker

12_30883 is an insertion/deletion polymorphism in the first intron of HvBM5A, which is the candidate gene for the VRN-H1/FR-H1 QTL (Hayes, personal communication, 2011). Marker 11_20126 shows a highly significant association with LTT and is believed to be linked to VRN-H3 (Hayes, personal communication, 2011). Marker 12_30883 likely has low F_{ST} because it was already nearly fixed in C1 (Fig. 4a). The frequency of marker 11_20126 changed only slightly from C1 to C2, which explains its low F_{ST} value (Fig. 4b). Three additional markers with F_{ST} values above the 95th percentile threshold were linked to markers that have previously been identified as significantly associated with frost tolerance (Visioni et al., 2013)—11_10094, 12_30872, and 11_11200. Overall, the frequency of large effect QTL and markers that are tightly linked to them can be moved toward fixation due to indirect selection via GS.

Effects of selecting based on index versus individual traits

By selecting on an index, we aimed to make gains in several traits simultaneously, which is a challenge in traditional breeding where different traits are evaluated at different stages. For example, malt quality traits are usually only evaluated in lines that have already been extensively tested for their agronomic and disease resistance qualities. By using a selection index, we were able to consider malt extract at the same time as winter survival and agronomic traits. Previous research has demonstrated that use of a selection index is more efficient than the use of independent culling levels or tandem selection for improving multiple traits. However, as the number of traits under consideration increases, the improvement in any one trait decreases relative to the

improvement that could be achieved by selection for only that trait (Hazel and Lush, 1942). By using GS on a selection index, we improved the two traits with the heaviest weights in the index—winter survival and malt extract. However, the selection index itself was not improved, nor were the other traits in the index. This result contrasts that of Massman et al., (2013), which achieved improvements in the selection indices used, but not the individual component traits. We compared C1-PS with C1-GS to investigate the differences resulting from selection on the index trait versus individual traits. While the selection index incorporated winter survival, malt extract, yield, plant height, and heading date; the C1-PS set was selected based mainly on winter survival while also considering heading date and maturity. We observed that mean winter hardiness in C1-PS was statistically the same as winter hardiness in C2-GS and both were improved from C1R (C0-base population), indicating that two cycles of GS resulted in a net gain similar to one cycle of phenotypic selection. Further cycles of phenotypic selection could determine whether this pattern continues. Besides the improvement for winter survival, C1-PS was also improved for the selection index and grain yield despite the fact that these were not under direct selection. The other traits considered in the selection index—malt extract, plant height, and heading date—were not improved in C1-PS. The lack of gain in malt extract and plant height for C1-PS is not surprising since we did not apply phenotypic selection for these traits. Heading date was considered in phenotypic selection but only secondarily to survival. By selecting for an index trait in our GS, we were able to

improve both winter survival and malt extract—two traits that would not usually be considered at the same stage of breeding if using phenotypic selection.

Our results support the use of GS to initiate a breeding program. We took advantage of available phenotype and genotype data to train a GS model without creating new populations or conducting new trials. The parameters of our GS scheme changed between C1 and C2 as would be expected in a breeding program where the ultimate goal is to maximize gain. GS enabled us to change the marker allele frequencies for markers linked to winter hardiness traits without selecting directly upon them like in MAS. We also observed that the population shifted toward increased genetic similarity to the winter growth-type parents while we also selected for the facultative growth-type. Most importantly, through GS we were able to significantly improve winter survival and malt extract, the two traits that were most crucial to our breeding goals, in just two cycles of selection, while also maintaining other relevant traits.

Table 1. Pearson's correlation coefficients for each pair of traits. Magnitudes of correlation were color-coded from most negative (red) to most positive (green).

	Winter survival	Plant height	Grain yield	FHB severity	Kernel weight	Grain plumpness	Malt extract	Grain protein conc	Wort protein	Sol/total protein	Alpha-amylase	Diastatic power	Beta-glucan	Free amino nitrogen
Heading date	0.07	0.37	0.12	0.42	-0.09	-0.09	0.14	-0.43	-0.21	0.09	-0.08	-0.20	0.16	-0.08
Winter survival		0.10	-0.03	0.02	-0.05	0.06	-0.14	0.17	-0.17	-0.31	-0.17	-0.12	0.21	-0.12
Plant height			0.32	-0.04	0.24	0.07	0.25	-0.37	-0.12	0.16	-0.01	-0.06	-0.08	0.03
Grain yield				0.00	0.21	0.21	0.17	-0.36	-0.28	-0.03	-0.10	-0.21	0.03	-0.19
FHB severity					-0.12	-0.02	0.07	-0.21	-0.15	-0.01	0.00	0.00	0.00	-0.12
Kernel weight						0.66	0.14	-0.06	-0.08	-0.02	-0.14	-0.17	-0.03	0.01
Grain plumpness							0.11	0.19	-0.03	-0.16	-0.18	-0.02	0.08	0.00
Malt extract								-0.41	0.22	0.53	0.27	0.10	-0.28	0.29
Grain protein conc									0.43	-0.25	0.11	0.40	0.12	0.30
Wort protein										0.76	0.73	0.52	-0.39	0.89
Sol/total protein											0.70	0.27	-0.48	0.75
Alpha-amylase												0.38	-0.44	0.69
Diastatic power													-0.26	0.43
Beta-glucan														-0.45

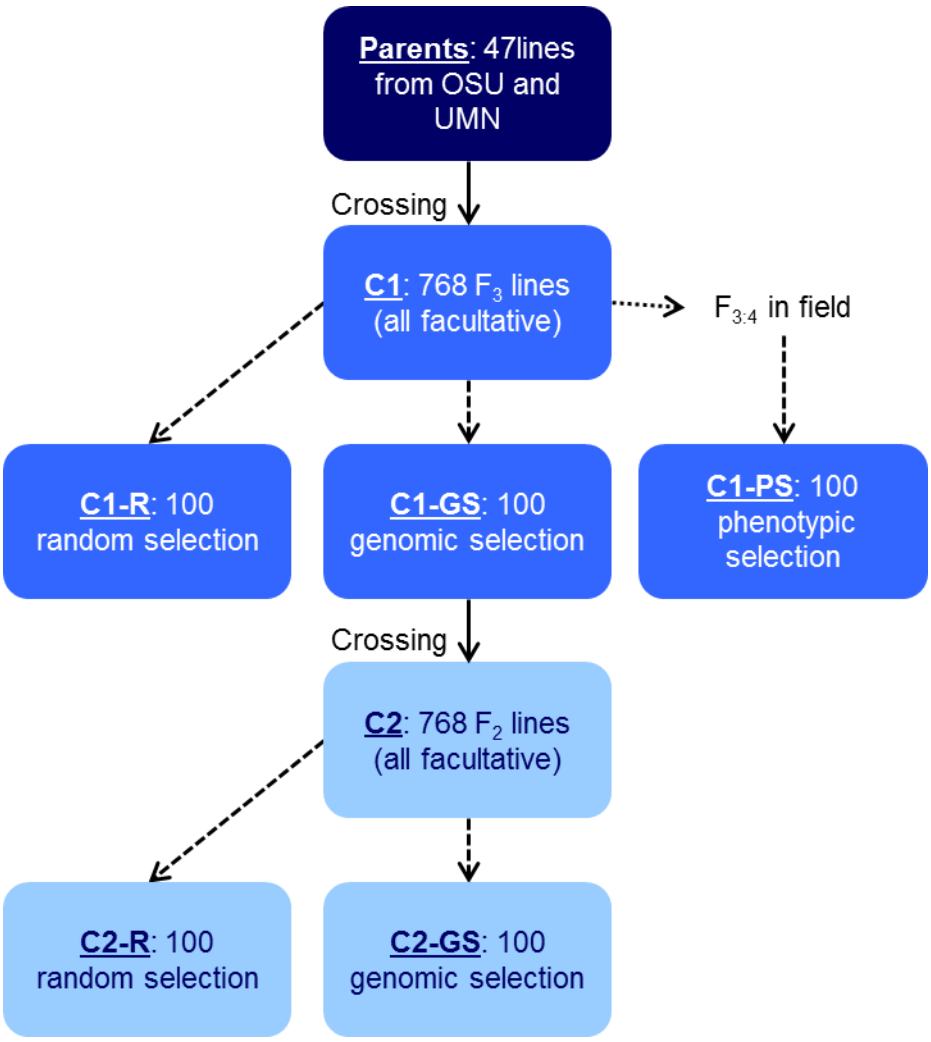


Figure 1. Selection scheme: Initial population consisted of 47 lines, which were crossed to create 768 progeny. From these, 100 lines were selected at random (R), 100 were selected based on GS, and 100 were selected based on phenotypic selection (PS). The 100 lines chosen based on genomic selection were crossed to generate another 768 progeny, and from these 100 lines were chosen at random and 100 were chosen based on genomic selection.

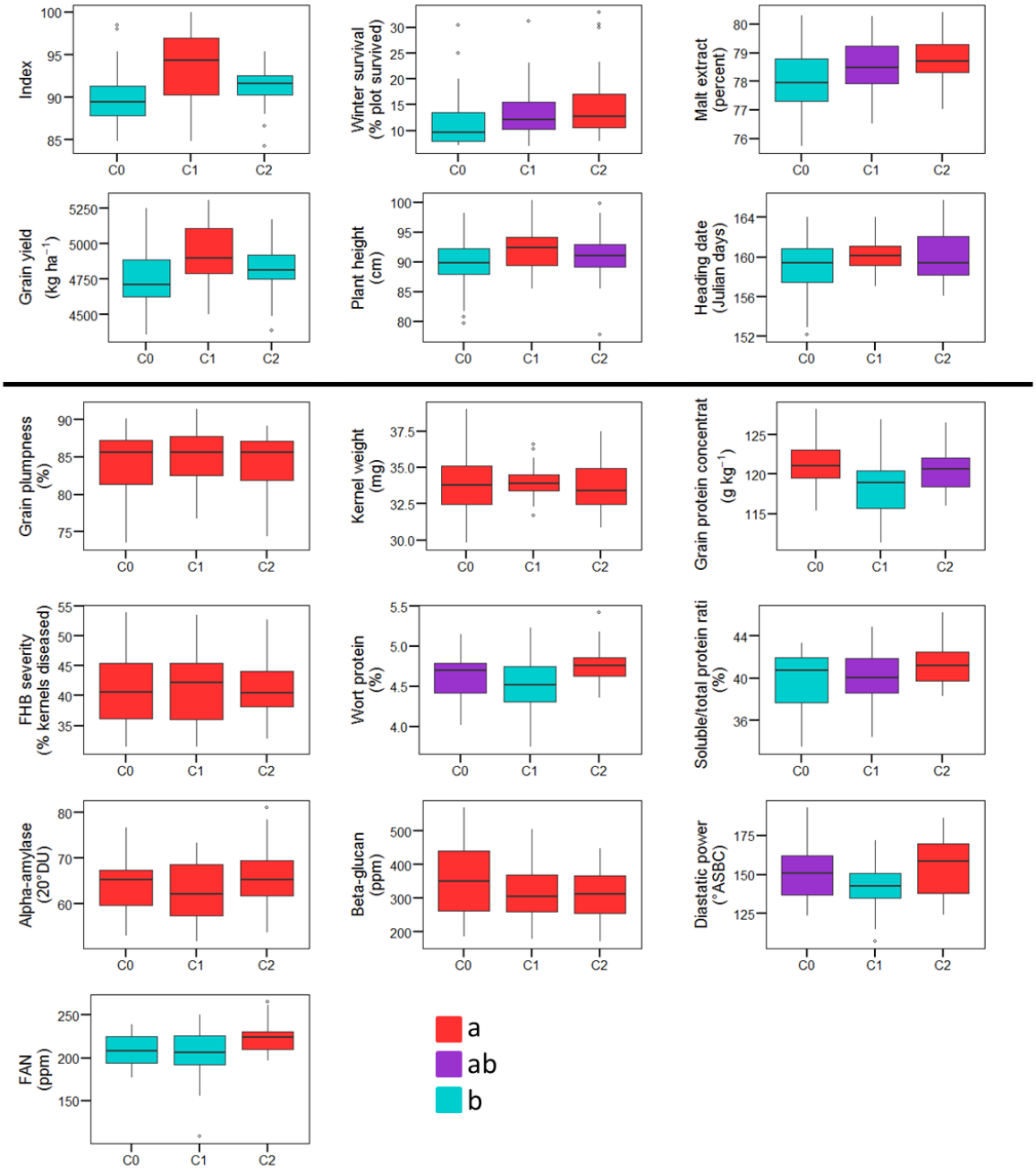


Figure 2. Box plot of selected sets for each trait. Traits with plots above the line were part of the selection index in at least one cycle of selection. Box colors indicate which group the set is in based on Tukey's HSD test at $\alpha=0.05$.

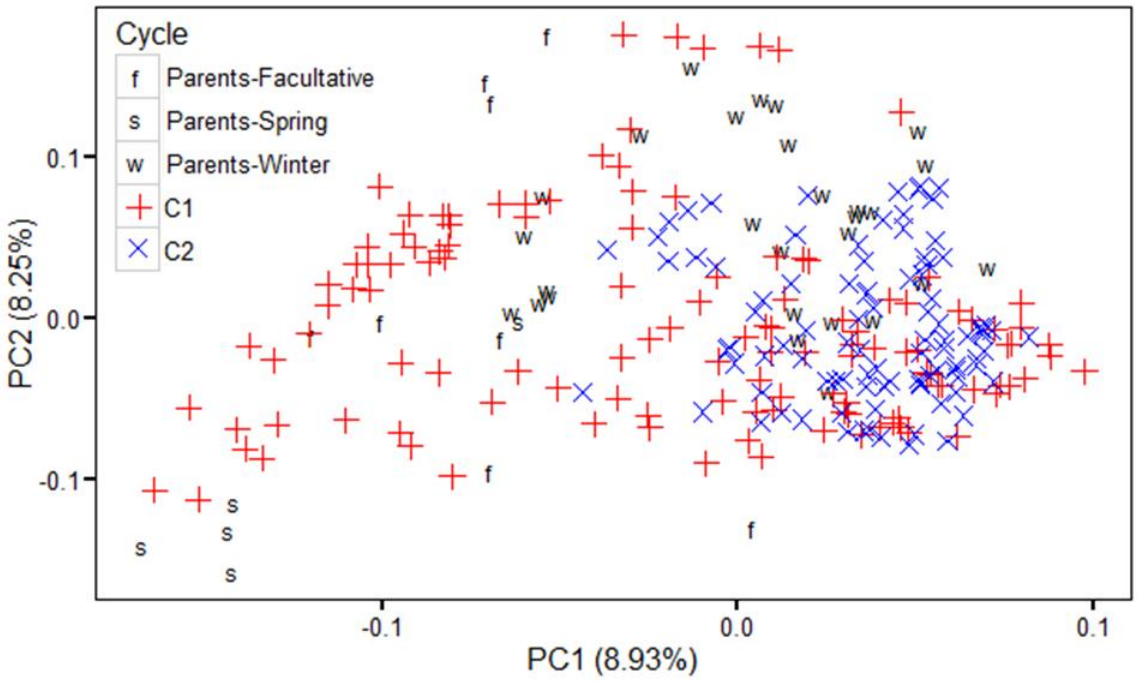


Figure 3. Scatterplot of the first two principle components based on genotype data. Colors of symbols represent Cycle. For C0 (parents) the letter used as a symbol represents the growth habit of that line (see legend).

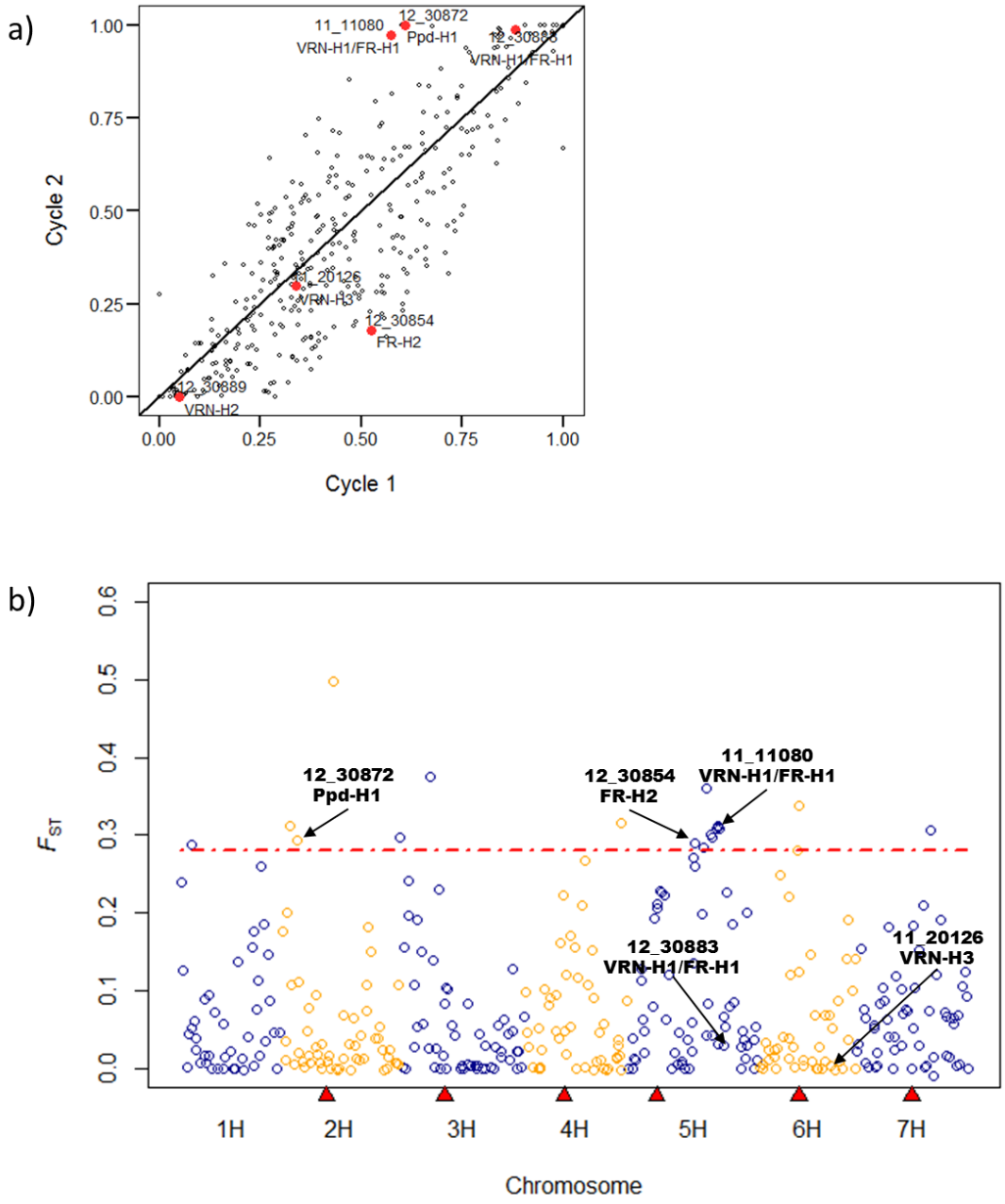


Figure 4. Marker allele frequency change. a) Scatterplot of frequency of AA genotype in Cycle 1 versus in Cycle 2. b) F_{ST} plot: Allele frequency differentiation between Cycle 1 and Cycle 2. Triangles indicate the genetic position of centromeres (Muñoz-Amatriaín et al., 2011). Dotted line corresponds to the 95th percentile of the F_{ST} values distribution. Linkage groups are shown in alternating colors.

References

Asoro, F.G., M.A. Newell, W.D. Beavis, M.P. Scott, and J. Jannink. 2011. Accuracy and training population design for genomic selection on quantitative traits in elite North American oats. The Plant Genome 4:132-144.

Asoro, F.G., M.A. Newell, W.D. Beavis, M.P. Scott, N.A. Tinker, and J. Jannink. 2013. Genomic, marker-assisted, and pedigree-BLUP selection methods for β-glucan concentration in elite oat. Crop Sci. 53:1894-1906.

Beaulieu, J., T. Doerksen, S. Clément, J. MacKay, and J. Bousquet. 2014. Accuracy of genomic selection models in a large population of open-pollinated families in white spruce. Heredity 113:343-352.

Bernardo, R. 2014. Genomewide selection of parental inbreds: Classes of loci and virtual biparental populations. Crop Sci. 54:2586-2595.

Bernardo, R., and J. Yu. 2007. Prospects for genomewide selection for quantitative traits in maize. Crop Sci. 47:1082-1090.

Bertholdsson, N. 1998. Selection methods for malting barley consistently low in protein concentration. Eur. J. Agron. 9:213-222.

Beyene, Y., K. Semagn, J. Crossa, S. Mugo, G.N. Atlin, A. Tarekegne, B. Meisel, P. Sehabiague, B.S. Vivek, and S. Oikeh. 2016. Improving maize grain yield under drought stress and non-stress environments in sub-Saharan Africa using marker-assisted recurrent selection. Crop Sci. 56:344-353.

Blake, V.C., C. Birkett, D.E. Matthews, D.L. Hane, P. Bradbury, and J. Jannink. 2016. The Triticeae Toolbox: Combining phenotype and genotype data to advance small-grains breeding. The Plant Genome 9:2.

Broman, K.W., H. Wu, S. Sen, and G.A. Churchill. 2003. R/qtl: QTL mapping in experimental crosses. Bioinformatics 19:889-890.

Budde, A.D., C. Martens, and Staff. 2010. Mississippi valley regional spring barley Nursery—2009 preliminary quality report. (Technical Report), Available online at: http://www.ars.usda.gov/SP2UserFiles/Place/36551000/barleyreports/2009MVNfinal.pdf

Chen, A., L.V. Gusta, A. Brûlé-Babel, R. Leach, U. Baumann, G.B. Fincher, and N.C. Collins. 2009a. Varietal and chromosome 2H locus-specific frost tolerance in reproductive tissues of barley (*Hordeum vulgare* L.) detected using a frost simulation chamber. Theor. Appl. Genet. 119:685-694.

Chen, A., J. Reinheimer, A. Brûlé-Babel, U. Baumann, M. Pallotta, G.B. Fincher, and N.C. Collins. 2009b. Genes and traits associated with chromosome 2H and 5H regions controlling sensitivity of reproductive tissues to frost in barley. Theor. Appl. Genet. 118:1465-1476.

Clark, A. 2008. Managing cover crops profitably. DIANE Publishing.

Close, T.J., P.R. Bhat, S. Lonardi, Y. Wu, N. Rostoks, L. Ramsay, A. Druka, N. Stein, J.T. Svensson, S. Wanamaker, S. Bozdag, M.L. Roose, M.J. Moscou, S. Chao, R.K. Varshney, P. Szűcs, K. Sato, P.M. Hayes, D.E. Matthews, A. Kleinhofs, G.J. Muehlbauer, J. DeYoung, D.F. Marshall, K. Madishetty, R.D. Fenton, P. Condamine, A. Graner, and R. Waugh. 2009. Development and implementation of high-throughput SNP genotyping in barley. BMC Genomics 10:582.

Combs, E., and R. Bernardo. 2013. Accuracy of genomewide selection for different traits with constant population size, heritability, and number of markers. The Plant Genome 6:.

Condón, F., D.C. Rasmusson, E. Schiefelbein, G. Velasquez, and K.P. Smith. 2009. Effect of advanced cycle breeding on genetic gain and phenotypic diversity in barley breeding germplasm. Crop Sci. 49:1751-1761.

Crossa, J., L. Campos Gde, P. Perez, D. Gianola, J. Burgueno, J.L. Araus, D. Makumbi, R.P. Singh, S. Dreisigacker, J. Yan, V. Arief, M. Banziger, and H.J. Braun. 2010. Prediction of genetic values of quantitative traits in plant breeding using pedigree and molecular markers. Genetics 186:713-724.

Cuesta-Marcos, A., E. Igartua, P. Codesal, J.R. Russell, J.L. Molina-Cano, M. Moralejo, P. Szűcs, M.P. Gracia, J.M. Lasa, and A.M. Casas. 2008. Heading date QTL in a spring × winter barley cross evaluated in Mediterranean environments. Mol. Breed. 21:455-471.

Daetwyler, H.D., B. Villanueva, P. Bijma, and J.A. Woolliams. 2007. Inbreeding in genome-wide selection. J. Anim. Breed. Genet. 124:369-376.

Dahleen, L., H. Agrama, R. Horsley, B. Steffenson, P. Schwarz, A. Mesfin, and J. Franckowiak. 2003. Identification of QTLs associated with fusarium head blight resistance in zhedar 2 barley. Theor. Appl. Genet. 108:95-104.

Danyluk, J., N.A. Kane, G. Breton, A.E. Limin, D.B. Fowler, and F. Sarhan. 2003. TaVRT-1, a putative transcription factor associated with vegetative to reproductive transition in cereals. Plant Physiol. 132:1849-1860.

de la Pena, R., K. Smith, F. Capettini, G. Muehlbauer, M. Gallo-Meagher, R. Dill-Macky, D. Somers, and D. Rasmusson. 1999. Quantitative trait loci associated with resistance to Fusarium head blight and kernel discoloration in barley. Theor. Appl. Genet. 99:561-569.

Dekkers, J.C.M., and F. Hospital. 2002. The use of molecular genetics in the improvement of agricultural populations. Nat. Rev. Genet. 3:22-32.

Dhillon, T., S.P. Pearce, E.J. Stockinger, A. Distelfeld, C. Li, A.K. Knox, I. Vashegyi, A. Vagujfalvi, G. Galiba, and J. Dubcovsky. 2010. Regulation of freezing tolerance and flowering in temperate cereals: The VRN-1 connection. Plant Physiol. 153:1846-1858.

Dubcovsky, J., C. Chen, and L. Yan. 2005. Molecular characterization of the allelic variation at the VRN-H2 vernalization locus in barley. Mol. Breed. 15:395-407.

Endelman, J.B. 2011. Ridge regression and other kernels for genomic selection with R package rrBLUP. Plant Gen. 4:250-255.

Faure, S., J. Higgins, A. Turner, and D.A. Laurie. 2007. The FLOWERING LOCUS T-like gene family in barley (*Hordeum vulgare*). Genetics 176:599-609.

Fisk, S.P., A. Cuesta-Marcos, L. Cistué, J. Russell, K.P. Smith, S. Baenziger, Z. Bedo, A. Corey, T. Filichkin, and I. Karsai. 2013. FR-H3: A new QTL to assist in the development of fall-sown barley with superior low temperature tolerance. Theor. Appl. Genet. 126:335-347.

Fowler, D.B., G. Breton, A.E. Limin, S. Mahfoozi, and F. Sarhan. 2001. Photoperiod and temperature interactions regulate low-temperature-induced gene expression in barley. Plant Physiol. 127:1676-1681.

Francia, E., F. Rizza, L. Cattivelli, A. Stanca, G. Galiba, B. Toth, P. Hayes, J. Skinner, and N. Pecchioni. 2004. Two loci on chromosome 5H determine low-temperature

tolerance in a ‘Nure’(winter) × ‘Tremois’(spring) barley map. Theor. Appl. Genet. 108:670-680.

Fu, D., P. Szűcs, L. Yan, M. Helguera, J.S. Skinner, J. Von Zitzewitz, P.M. Hayes, and J. Dubcovsky. 2005. Large deletions within the first intron in VRN-1 are associated with spring growth habit in barley and wheat. Molecular Genetics and Genomics 273:54-65.

Galiba, G., A. Vágújfalvi, C. Li, A. Soltész, and J. Dubcovsky. 2009. Regulatory genes involved in the determination of frost tolerance in temperate cereals. Plant Science 176:12-19.

Gianola, D., R.L. Fernando, and A. Stella. 2006. Genomic-assisted prediction of genetic value with semiparametric procedures. Genetics 173:1761-1776.

Goddard, M. 2009. Genomic selection: Prediction of accuracy and maximisation of long term response. Genetica 136:245-257.

Goudet, J. 2005. Hierfstat, a package for R to compute and test hierarchical *F*-statistics. Molecular Ecology Notes 5:184-186.

Grenier, C., T. Cao, Y. Ospina, C. Quintero, M.H. Châtel, J. Tohme, B. Courtois, and N. Ahmadi. 2015. Accuracy of genomic selection in a rice synthetic population developed for recurrent selection breeding. PloS One 10:e0136594.

Guo, Z., D.M. Tucker, C.J. Basten, H. Gandhi, E. Ersoz, B. Guo, Z. Xu, D. Wang, and G. Gay. 2014. The impact of population structure on genomic prediction in stratified populations. Theor. Appl. Genet. 127:749-762.

Han, F., J. Clancy, B. Jones, D. Wesenberg, A. Kleinhofs, and S. Ullrich. 2004. Dissection of a malting quality QTL region on chromosome 1 (7H) of barley. Mol. Breed. 14:339-347.

Han, F., S. Ullrich, A. Kleinhofs, B. Jones, P. Hayes, and D. Wesenberg. 1997. Fine structure mapping of the barley chromosome-1 centromere region containing malting-quality QTLs. Theor. Appl. Genet. 95:903-910.

Hayes, B., P. Bowman, A. Chamberlain, and M. Goddard. 2009. Invited review: Genomic selection in dairy cattle: Progress and challenges. J. Dairy Sci. 92:433-443.

Hayes, P.M., T. Blake, T.H.H. Chen, S. Tragoonrung, F. Chen, A. Pan, and B. Liu. 1993. Quantitative trait loci on barley (*Hordeum vulgare* L.) chromosome-7 associated with components of winterhardiness. Genome 36:66-71.

Hazel, L., and J.L. Lush. 1942. The efficiency of three methods of selection. J. Hered. 33:393-399.

Heffner, E.L., J. Jannink, and M.E. Sorrells. 2011. Genomic selection accuracy using multifamily prediction models in a wheat breeding program. The Plant Genome 4:65-75.

Heffner, E.L., M.E. Sorrells, and J. Jannink. 2009. Genomic selection for crop improvement. Crop Sci. 49:1-12.

Heffner, E.L., A.J. Lorenz, J. Jannink, and M.E. Sorrells. 2010. Plant breeding with genomic selection: Gain per unit time and cost. Crop Sci. 50:1681-1690.

Heslot, N., H. Yang, M.E. Sorrells, and J. Jannink. 2012. Genomic selection in plant breeding: A comparison of models. Crop Sci. 52:146-160.

Horsley, R., D. Schmierer, C. Maier, D. Kudrna, C. Urrea, B. Steffenson, P. Schwarz, J. Franckowiak, M. Green, and B. Zhang. 2006. Identification of QTLs associated with fusarium head blight resistance in barley accession CIho 4196. Crop Sci. 46:145-156.

Isidro, J., J. Jannink, D. Akdemir, J. Poland, N. Heslot, and M.E. Sorrells. 2015. Training set optimization under population structure in genomic selection. Theor. Appl. Genet. 128:145-158.

Jannink, J.L. 2010. Dynamics of long-term genomic selection. Genet. Sel. Evol. 42:35-9686-42-35.

Jannink, J.L., A.J. Lorenz, and H. Iwata. 2010. Genomic selection in plant breeding: From theory to practice. Brief Funct. Genomics 9:166-177.

Karsai, I., P. Szűcs, K. Mészáros, T. Filichkina, P. Hayes, J. Skinner, L. Láng, and Z. Bedő. 2005. The vrn-H2 locus is a major determinant of flowering time in a facultative × winter growth habit barley (*Hordeum vulgare* L.) mapping population. Theor. Appl. Genet. 110:1458-1466.

Kearsey, M., and A. Farquhar. 1998. QTL analysis in plants: Where are we now? Heredity 80:137-142.

Kikuchi, R., H. Kawahigashi, T. Ando, T. Tonooka, and H. Handa. 2009. Molecular and functional characterization of PEBP genes in barley reveal the diversification of their roles in flowering. Plant Physiol. 149:1341-1353.

Konig, S., H. Simianer, and A. Willam. 2009. Economic evaluation of genomic breeding programs. J. Dairy Sci. 92:382-391.

Kutner, M.H., C.J. Nachtsheim, J. Neter, and W. Li. 2004. Applied linear statistical models, 4th ed. McGraw-Hill, Boston, MA.

Levitt, J. 1980. Response of plants to environmental stresses. Academic Press, New York.

Lian, L., A. Jacobson, S. Zhong, and R. Bernardo. 2015. Prediction of genetic variance in biparental maize populations: Genomewide marker effects versus mean genetic variance in prior populations. Crop Sci. 55:1181-1188.

Limin, A., A. Corey, P. Hayes, and D.B. Fowler. 2007. Low-temperature acclimation of barley cultivars used as parents in mapping populations: Response to photoperiod, vernalization and phenological development. Planta 226:139-146.

Lin, C.S., and G. Poushinsky. 1985. A modified augmented design (type 2) for rectangular plots. Can. J. Plant Sci. 65:743-749.

Lin, C., G. Poushinsky, and P. Jui. 1983. Simulation study of three adjustment methods for the modified augmented design and comparison with the balanced lattice square design. The Journal of Agricultural Science 100:527-534.

Lorenz, A.J., and K.P. Smith. 2015. Adding genetically distant individuals to training populations reduces genomic prediction accuracy in barley. Crop Sci. 55:2657-2667.

Lorenz, A.J., S. Chao, F.G. Asoro, E.L. Heffner, T. Hayashi, H. Iwata, K.P. Smith, M.E. Sorrells, and J. Jannink. 2011. Genomic selection in plant breeding: Knowledge and prospects. Adv Agron 110:77-123.

Lorenz, A., K. Smith, and J. Jannink. 2012. Potential and optimization of genomic selection for fusarium head blight resistance in six-row barley. Crop Sci. 52:1609-1621.

Lorenzana, R.E., and R. Bernardo. 2009. Accuracy of genotypic value predictions for marker-based selection in biparental plant populations. Theor. Appl. Genet. 120:151-161.

Massman, J., B. Cooper, R. Horsley, S. Neate, R. Dill-Macky, S. Chao, Y. Dong, P. Schwarz, G. Muehlbauer, and K. Smith. 2011. Genome-wide association mapping of Fusarium head blight resistance in contemporary barley breeding germplasm. Mol. Breed. 27:439-454.

Massman, J.M., H.G. Jung, and R. Bernardo. 2013. Genomewide selection versus marker-assisted recurrent selection to improve grain yield and stover-quality traits for cellulosic ethanol in maize. Crop Sci. 53:58-66.

Mesfin, A., K. Smith, R. Dill-Macky, C. Evans, R. Waugh, C. Gustus, and G. Muehlbauer. 2003. Quantitative trait loci for fusarium head blight resistance in barley detected in a two-rowed by six-rowed population. Crop Sci. 43:307-318.

Meuwissen, T.H.E., B.J. Hayes, and M.E. Goddard. 2001. Prediction of total genetic value using genome-wide dense marker maps. Genetics 157:1819-1829.

Mohammadi, M., T. Tiede, and K.P. Smith. 2015. PopVar: A genome-wide procedure for predicting genetic variance and correlated response in biparental breeding populations. Crop Sci. 55:2068-2077.

Muñoz-Amatriaín, M., M.J. Moscou, P.R. Bhat, J.T. Svensson, J. Bartoš, P. Suchánková, H. Šimková, T.R. Endo, R.D. Fenton, S. Lonardi, A.M. Castillo, S. Chao, L. Cistué, A. Cuesta-Marcos, K.L. Forrest, M.J. Hayden, P.M. Hayes, R.D. Horsley, K. Makoto, D. Moody, K. Sato, M.P. Vallés, B.B.H. Wulff, G.J. Muehlbauer, J. Doležel, and T.J. Close. 2011. An improved consensus linkage map of barley based on flow-sorted chromosomes and single nucleotide polymorphism markers. Plant Gen. 4:238-249.

Pan, A., P. Hayes, F. Chen, T. Chen, T. Blake, S. Wright, I. Karsai, and Z. Bedö. 1994. Genetic analysis of the components of winterhardiness in barley (*Hordeum vulgare* L.). Theor. Appl. Genet. 89:900-910.

R Core Team. 2015. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. Available at: https://www.R-project.org/. 2015.

Reinheimer, J.L., A.R. Barr, and J.K. Eglinton. 2004. QTL mapping of chromosomal regions conferring reproductive frost tolerance in barley (*Hordeum vulgare* L.). Theor. Appl. Genet. 109:1267-1274.

Riedelsheimer, C., J.B. Endelman, M. Stange, M.E. Sorrells, J.L. Jannink, and A.E. Melchinger. 2013. Genomic predictability of interconnected biparental maize populations. Genetics 194:493-503.

Rizza, F., D. Pagani, M. Gut, I. Prášil, C. Lago, A. Tondelli, L. Orru, E. Mazzucotelli, E. Francia, and F. Badeck. 2011. Diversity in the response to low temperature in representative barley genotypes cultivated in Europe. Crop Sci. 51:2759-2779.

Rutkoski, J., J. Benson, Y. Jia, G. Brown-Guedira, J. Jannink, and M. Sorrells. 2012. Evaluation of genomic prediction methods for fusarium head blight resistance in wheat. The Plant Genome 5:51-61.

Rutkoski, J., R. Singh, J. Huerta-Espino, S. Bhavani, J. Poland, J. Jannink, and M. Sorrells. 2015. Efficient use of historical data for genomic selection: A case study of stem rust resistance in wheat. The Plant Genome 8:1.

Sallam, A., J. Endelman, J. Jannink, and K. Smith. 2015. Assessing genomic selection prediction accuracy in a dynamic barley breeding population. The Plant Genome 8:1.

Schaeffer, L.R. 2006. Strategy for applying genome-wide selection in dairy cattle. J. Anim. Breed. Genet. 123:218-223.

Schwarz, P., and R. Horsley. 1995. Malt quality improvement in North American six-rowed barley cultivars since 1910. Journal of the American Society of Brewing Chemists 53:14-18.

Skinner, J.S., J. von Zitzewitz, P. Szűcs, L. Marquez-Cedillo, T. Filichkin, K. Amundsen, E.J. Stockinger, M.F. Thomashow, T.H. Chen, and P.M. Hayes. 2005. Structural, functional, and phylogenetic characterization of a large CBF gene family in barley. Plant Mol. Biol. 59:533-551.

Skinner, J.S., P. Szűcs, J. von Zitzewitz, L. Marquez-Cedillo, T. Filichkin, E.J. Stockinger, M.F. Thomashow, T.H. Chen, and P.M. Hayes. 2006. Mapping of barley homologs to genes that regulate low temperature tolerance in *Arabidopsis*. Theor. Appl. Genet. 112:832-842.

Smith, K., A. Budde, R. Dill-Macky, D. Rasmusson, E. Schiefelbein, B. Steffenson, J. Wiersma, J. Wiersma, and B. Zhang. 2013. Registration of ‘Quest’ spring malting barley

with improved resistance to fusarium head blight. Journal of Plant Registrations 7:125-129.

Steffenson, B. 2003. Fusarium head blight of barley: Impact, epidemics, management, and strategies for identifying and utilizing genetic resistance. p. 241-295. In K. Leonard, and W. Bushnell (eds.) Fusarium head blight of wheat and barley. APS Press, St. Paul, MN.

Szűcs, P., J.S. Skinner, I. Karsai, A. Cuesta-Marcos, K.G. Haggard, A.E. Corey, T.H. Chen, and P.M. Hayes. 2007. Validation of the VRN-H2/VRN-H1 epistatic model in barley reveals that intron length variation in VRN-H1 may account for a continuum of vernalization sensitivity. Mol. Genet. Genomics 277:249-261.

Technow, F. 2012. R package for moving grid adjustment in plant breeding field trials. Available at: Http://artax.karlin.mff.cuni.cz/r-help/library/mvngGrAd/html/00Index.html. 2015:.

Tiede, T., L. Kumar, M. Mohammadi, and K.P. Smith. 2015. Predicting genetic variance in bi-parental breeding populations is more accurate when explicitly modeling the segregation of informative genomewide markers. Mol. Breed. 35:1-13.

Trevaskis, B., D.J. Bagnall, M.H. Ellis, W.J. Peacock, and E.S. Dennis. 2003. MADS box genes control vernalization-induced flowering in cereals. Proc. Natl. Acad. Sci. U. S. A. 100:13099-13104.

Turner, A., J. Beales, S. Faure, R.P. Dunford, and D.A. Laurie. 2005. The pseudo-response regulator ppd-H1 provides adaptation to photoperiod in barley. Science 310:1031-1034.

von Zitzewitz, J., P. Szűcs, J. Dubcovsky, L. Yan, E. Francia, N. Pecchioni, A. Casas, T.H.H. Chen, P.M. Hayes, and J.S. Skinner. 2005. Molecular and structural characterization of barley vernalization genes. Plant Mol Biol 59:449-467.

von Zitzewitz, J., A. Cuesta-Marcos, F. Condon, A.J. Castro, S. Chao, A. Corey, T. Filichkin, S.P. Fisk, L. Gutierrez, K. Haggard, I. Karsai, G.J. Muehlbauer, K.P. Smith, O. Veisz, and P.M. Hayes. 2011. The genetics of winterhardiness in barley: Perspectives from genome-wide association mapping. The Plant Genome 4:76-91.

Weir, B.S., and C.C. Cockerham. 1984. Estimating F-statistics for the analysis of population structure. Evolution1358-1370.

Yan, L., A. Loukoianov, G. Tranquilli, M. Helguera, T. Fahima, and J. Dubcovsky. 2003. Positional cloning of the wheat vernalization gene VRN1. Proc. Natl. Acad. Sci. U. S. A. 100:6263-6268.

Yan, L., A. Loukoianov, A. Blechl, G. Tranquilli, W. Ramakrishna, P. SanMiguel, J.L. Bennetzen, V. Echenique, and J. Dubcovsky. 2004. The wheat VRN2 gene is a flowering repressor down-regulated by vernalization. Science 303:1640-1644.

Yan, L., D. Fu, C. Li, A. Blechl, G. Tranquilli, M. Bonafede, A. Sanchez, M. Valarik, S. Yasuda, and J. Dubcovsky. 2006. The wheat and barley vernalization gene VRN3 is an orthologue of FT. Proc. Natl. Acad. Sci. U. S. A. 103:19581-19586.

Chapter 3: Future directions

In the first chapter of my thesis, we aimed to identify quantitative trait loci (QTL) associated with nitrogen use efficiency (NUE) in two-row and six-row barley panels. A number of the QTL that we identified fit our definition of NUE association. Additionally, we detected a locus for grain protein concentration on chromosome 6H that has been mapped previously in barley and is collinear with the well-characterized Gpc-B1 locus in wheat. We saw that marker haplotype classes at this locus exhibited significant differences in grain yield in both panels. Overall, our results indicated that potentially effective breeding strategies for NUE include selection based on stress indices, marker assisted selection for desirable alleles, and genomic selection to capture small effect loci. Given our results and issues we encountered, the following are ideas for potential follow-up work:

1. Because NUE is difficult to measure, we calculated stress indices as a proxy. These stress indices were originally created for water use efficiency and have been used in relatively few studies for NUE. While we observed genetic variation for two of the stress indices in our AM panels, we do not know whether they correlate with other measures of NUE. Additional investigation into the use of these stress indices for NUE is needed. Specifically stemming from this research, it would be useful to compare the values of the stress indices for the NILs with other measurements of NUE such as determining the amount of nitrogen taken up from the soil and moved

into the grain by measuring nitrogen content in the vegetative and reproductive tissues.

2. Before targeting any of these QTL for marker assisted selection, it is necessary to validate their effects. Validation could be achieved using heterogeneous inbred families which are sets of progeny that are near isogenic with different alleles at the QTL of interest. To create these families, we would need to first identify lines that were heterozygous for a marker associated with the QTL in question. We would then self the lines and plant a number of their progeny in separate pots in the greenhouse. The progeny would be genotyped and would be expected to show a 1:2:1 segregation ratio at the marker that was heterozygous in the parent line. The families of near isogenic lines would be planted in the field and phenotyped to observe differences between sets of near isogenic lines.
3. The two-row cultivar Pinnacle has low GPC and has the six-row low protein line Karl in its pedigree (J. Franckowiak, personal communication, 2016). Unexpectedly, it does not have the same haplotype as KLBC4-130i-KK, which is a NIL with the Karl allele at the 6H GPC locus. Further investigation is needed to confirm or refine this result. Overall, more could be done to investigate the definition of marker haplotypes at the 6H GPC locus. Possibly, looking at the marker haplotypes in a more diverse set of lines such as the barley NAM populations, will allow more accurate haplotypes to be defined.

4. Though we identified a few QTL associated with NUE for relevant traits, additional variation in the trait may be due to small effect loci. To incorporate these small effect loci, genomic selection could be implemented. The data from this project could be utilized as calibration data to generate genomic predictions for NUE for the wider set of BarleyCAP lines.

In the second chapter of my thesis, our primary goal was to investigate the outcomes of using genomic selection to breed for improved winter hardiness in terms of the genetics and phenotype of the population. We saw that the first two cycles of selection resulted in near fixation of markers linked to major effect QTL for winter hardiness and in gains in two traits that were weighted highly in our selection index—winter survival and malt extract. Additionally, we observed that while phenotypic variance fluctuated, it did not change significantly with cycles of selection. While these results from two cycles of selection are promising, additional cycles of selection would allow us to confirm these trends. Additionally, the data collected for this project could be re-worked to look at a number of other questions. Accordingly, below is a list of potential projects that could stem from this work:

1. Data from further cycles of selection would allow us to answer a number of questions about whether the trends we observed continue: Does gain from selection continue for winter survival and malt extract? Do the other traits' responses to selection change or stay the same? Does the population become more genetically similar? For genotypic data questions, this would require us to somehow compare the different genotyping

platforms/markers used and/or re-genotype all the lines with the same set of markers. For phenotypic data, we would need to plant trials of lines from each cycle of selection.

2. A few studies of genomic selection in plants have looked at direct comparisons between genomic selection and phenotypic selection, and more information on this topic would be useful. Potentially, phenotypic selection starting from the C1-PS lines could be continued and compared with the results of genomic selection over a number of cycles. Further phenotypic selections could be made using the same index as used in the genomic selections or it could be based upon the breeders' selections based on field trial observations.
3. Although we found that GS holds promise for improving traits that are part of a selection index, researchers should continue to determine how to optimize prediction accuracy and how to minimize the resources needed to achieve high prediction accuracy. The data from this project could be used to answer questions about how, in hindsight, we could have optimized our genomic selection strategy. It would be interesting to analyze the optimization of the training population used for each cycle of selection including the addition of phenotypic data from selected lines to re-train the prediction model.
4. The weights for each trait in the selection indices were set based on the priority for each trait for our breeding goals and the correlations among the traits. The data collected from this study could be used to investigate how heavily each trait should be

weighted to achieve desired breeding outcomes, especially considering the desire to work winter barley into a double or relay cropping system with soybean.

5. Simulation research has suggested weighting marker alleles based on the inverse of their frequency to maintain genetic variation. However, this method has not been tested empirically. Future cycles of selection could implement this method to investigate the maintenance of rare alleles and whether this method improves sustained gain from selection.

6. Based on the sets of lines that were selected in each cycle (Supplemental Table S5), we could investigate whether lines were mostly selected out of particular families (i.e., genomic selection was really selecting for families not individual lines). Looking at the mean performance of each family and comparing families from which multiple lines were selected to those families where no lines were selected would also be interesting. Additionally, we could investigate whether certain families were predicted more accurately than others for each trait.

Bibliography

Agrama, H.A.S., A.G. Zakaria, F.B. Said, and M. Tuinstra. 1999. Identification of quantitative trait loci for nitrogen use efficiency in maize. Mol. Breed. 5:187-195.

Asoro, F.G., M.A. Newell, W.D. Beavis, M.P. Scott, and J. Jannink. 2011. Accuracy and training population design for genomic selection on quantitative traits in elite North American oats. The Plant Genome 4:132-144.

Asoro, F.G., M.A. Newell, W.D. Beavis, M.P. Scott, N.A. Tinker, and J. Jannink. 2013. Genomic, marker-assisted, and pedigree-BLUP selection methods for β-glucan concentration in elite oat. Crop Sci. 53:1894-1906.

Barrett, J.C., B. Fry, J. Maller, and M.J. Daly. 2005. Haploview: Analysis and visualization of LD and haplotype maps. Bioinformatics 21:263-265.

Beaulieu, J., T. Doerksen, S. Clément, J. MacKay, and J. Bousquet. 2014. Accuracy of genomic selection models in a large population of open-pollinated families in white spruce. Heredity 113:343-352.

Berger, G.L., S. Liu, M.D. Hall, W.S. Brooks, S. Chao, G.J. Muehlbauer, B. Baik, B. Steffenson, and C.A. Griffey. 2013. Marker-trait associations in Virginia Tech winter barley identified using genome-wide mapping. Theor. Appl. Genet. 126:693-710.

Bernardo, R. 2014. Genomewide selection of parental inbreds: Classes of loci and virtual biparental populations. Crop Sci. 54:2586-2595.

Bernardo, R., and J. Yu. 2007. Prospects for genomewide selection for quantitative traits in maize. Crop Sci. 47:1082-1090.

Bertholdsson, N. 1998. Selection methods for malting barley consistently low in protein concentration. Eur. J. Agron. 9:213-222.

Beyene, Y., K. Semagn, J. Crossa, S. Mugo, G.N. Atlin, A. Tarekegne, B. Meisel, P. Sehabiague, B.S. Vivek, and S. Oikeh. 2016. Improving maize grain yield under drought stress and non-stress environments in sub-Saharan Africa using marker-assisted recurrent selection. Crop Sci. 56:344-353.

Blake, V.C., C. Birkett, D.E. Matthews, D.L. Hane, P. Bradbury, and J. Jannink. 2016. The Triticeae Toolbox: Combining phenotype and genotype data to advance small-grains breeding. The Plant Genome 9:2.

Bradbury, P., T. Parker, M.T. Hamblin, and J. Jannink. 2011. Assessment of power and false discovery rate in genome-wide association studies using the BarleyCAP germplasm. Crop Sci. 51:52-59.

Bradbury, P.J., Z. Zhang, D.E. Kroon, T.M. Casstevens, Y. Ramdoss, and E.S. Buckler. 2007. TASSEL: Software for association mapping of complex traits in diverse samples. Bioinformatics 23:2633-2635.

Brevis, J.C., and J. Dubcovsky. 2010. Effects of the chromosome region including the Gpc-B1 locus on wheat grain and protein yield. Crop Sci. 50:93-104.

Broman, K.W., H. Wu, S. Sen, and G.A. Churchill. 2003. R/qtl: QTL mapping in experimental crosses. Bioinformatics 19:889-890.

Budde, A.D., C. Martens, and Staff. 2010. Mississippi valley regional spring barley Nursery—2009 preliminary quality report. (Technical Report), Available online at: http://www.ars.usda.gov/SP2UserFiles/Place/36551000/barleyreports/2009MVNfinal.pdf

Burger, W., D. Wesenberg, J. Carden, and P. Pawlisch. 1979. Protein content and composition of Karl and related barleys. Crop Sci. 19:235-238.

Cai, S., G. Yu, X. Chen, Y. Huang, X. Jiang, G. Zhang, and X. Jin. 2013. Grain protein content variation and its association analysis in barley. BMC Plant Biol. 13(35). doi:10.1186/1471-2229-13-35.

Canci, P.C., L.M. Nduulu, G.J. Muehlbauer, R. Dill-Macky, D.C. Rasmusson, and K.P. Smith. 2004. Validation of quantitative trait loci for fusarium head blight and kernel discoloration in barley. Molecular Breeding 14:91-104.

Canci, P.C., L.M. Nduulu, R. Dill-Macky, G.J. Muehlbauer, D.C. Rasmusson, and K.P. Smith. 2003. Genetic relationship between kernel discoloration and grain protein concentration in barley. Crop Sci. 43:1671-1679.

Carter, A.H., D.K. Santra, and K.K. Kidwell. 2012. Assessment of the effects of the *Gpc-B1* allele on senescence rate, grain protein concentration and mineral content in hard red

spring wheat (Triticum aestivum L.) from the Pacific Northwest Region of the USA. Plant Breed. 131:62-68.

Cavanagh, C.R., S. Chao, S. Wang, B.E. Huang, S. Stephen, S. Kiani, K. Forrest, C. Saintenac, G.L. Brown-Guedira, A. Akhunova, D. See, G. Bai, M. Pumphrey, L. Tomar, D. Wong, S. Kong, M. Reynolds, M.L. da Silva, H. Bockelman, L. Talbert, J.A. Anderson, S. Dreisigacker, S. Baenziger, A. Carter, V. Korzun, P.L. Morrell, J. Dubcovsky, M.K. Morell, M.E. Sorrells, M.J. Hayden, and E. Akhunov. 2013. Genome-wide comparative diversity uncovers multiple targets of selection for improvement in hexaploid wheat landraces and cultivars. Proc. Natl. Acad. Sci. USA 110:8057-8062.

Chen, A., L.V. Gusta, A. Brûlé-Babel, R. Leach, U. Baumann, G.B. Fincher, and N.C. Collins. 2009a. Varietal and chromosome 2H locus-specific frost tolerance in reproductive tissues of barley (*Hordeum vulgare* L.) detected using a frost simulation chamber. Theor. Appl. Genet. 119:685-694.

Chen, A., J. Reinheimer, A. Brûlé-Babel, U. Baumann, M. Pallotta, G.B. Fincher, and N.C. Collins. 2009b. Genes and traits associated with chromosome 2H and 5H regions controlling sensitivity of reproductive tissues to frost in barley. Theor. Appl. Genet. 118:1465-1476.

Cho, Y., W. Jiang, J. Chin, Z. Piao, Y. Cho, S.R. McCouch, and H. and Koh. 2007. Identification of QTLs associated with physiological nitrogen use efficiency in rice. Mol. Cells 23:72-79.

Clark, A. 2008. Managing cover crops profitably. DIANE Publishing.

Close, T.J., P.R. Bhat, S. Lonardi, Y. Wu, N. Rostoks, L. Ramsay, A. Druka, N. Stein, J.T. Svensson, S. Wanamaker, S. Bozdag, M.L. Roose, M.J. Moscou, S. Chao, R.K. Varshney, P. Szűcs, K. Sato, P.M. Hayes, D.E. Matthews, A. Kleinhofs, G.J. Muehlbauer, J. DeYoung, D.F. Marshall, K. Madishetty, R.D. Fenton, P. Condamine, A. Graner, and R. Waugh. 2009. Development and implementation of high-throughput SNP genotyping in barley. BMC Genomics 10(582). doi:10.1186/1471-2164-10-582.

Combs, E., and R. Bernardo. 2013. Accuracy of genomewide selection for different traits with constant population size, heritability, and number of markers. The Plant Genome 6:.

Condón, F., D.C. Rasmusson, E. Schiefelbein, G. Velasquez, and K.P. Smith. 2009. Effect of advanced cycle breeding on genetic gain and phenotypic diversity in barley breeding germplasm. Crop Sci. 49:1751-1761.

Crossa, J., L. Campos Gde, P. Perez, D. Gianola, J. Burgueno, J.L. Araus, D. Makumbi, R.P. Singh, S. Dreisigacker, J. Yan, V. Arief, M. Banziger, and H.J. Braun. 2010. Prediction of genetic values of quantitative traits in plant breeding using pedigree and molecular markers. Genetics 186:713-724.

Cuesta-Marcos, A., E. Igartua, P. Codesal, J.R. Russell, J.L. Molina-Cano, M. Moralejo, P. Szűcs, M.P. Gracia, J.M. Lasa, and A.M. Casas. 2008. Heading date QTL in a spring × winter barley cross evaluated in Mediterranean environments. Mol. Breed. 21:455-471.

Cuesta-Marcos, A., P. Szűcs, T.J. Close, T. Filichkin, G.J. Muehlbauer, K.P. Smith, and P.M. Hayes. 2010. Genome-wide SNPs and re-sequencing of growth habit and inflorescence genes in barley: Implications for association mapping in germplasm arrays varying in size and structure. BMC Genomics 11(707). doi:10.1186/1471-2164-11-707.

Daetwyler, H.D., B. Villanueva, P. Bijma, and J.A. Woolliams. 2007. Inbreeding in genome-wide selection. J. Anim. Breed. Genet. 124:369-376.

Dahleen, L., H. Agrama, R. Horsley, B. Steffenson, P. Schwarz, A. Mesfin, and J. Franckowiak. 2003. Identification of QTLs associated with fusarium head blight resistance in zhedar 2 barley. Theor. Appl. Genet. 108:95-104.

Danyluk, J., N.A. Kane, G. Breton, A.E. Limin, D.B. Fowler, and F. Sarhan. 2003. TaVRT-1, a putative transcription factor associated with vegetative to reproductive transition in cereals. Plant Physiol. 132:1849-1860.

de la Pena, R., K. Smith, F. Capettini, G. Muehlbauer, M. Gallo-Meagher, R. Dill-Macky, D. Somers, and D. Rasmusson. 1999. Quantitative trait loci associated with resistance to fusarium head blight and kernel discoloration in barley. Theor. Appl. Genet. 99:561-569.

Dekkers, J.C.M., and F. Hospital. 2002. The use of molecular genetics in the improvement of agricultural populations. Nat. Rev. Genet. 3:22-32.

Delogu, G., L. Cattivelli, N. Pecchioni, D. De Falcis, T. Maggiore, and A.M. Stanca. 1998. Uptake and agronomic efficiency of nitrogen in winter barley and winter wheat. Eur. J. Agron. 9:11-20.

Dhillon, T., S.P. Pearce, E.J. Stockinger, A. Distelfeld, C. Li, A.K. Knox, I. Vashegyi, A. Vagujfalvi, G. Galiba, and J. Dubcovsky. 2010. Regulation of freezing tolerance and flowering in temperate cereals: The VRN-1 connection. Plant Physiol. 153:1846-1858.

Distelfeld, A., A. Korol, J. Dubcovsky, C. Uauy, T. Blake, and T. Fahima. 2008. Colinearity between the barley grain protein content (GPC) QTL on chromosome arm 6HS and the wheat Gpc-B1 region. Mol. Breed. 22:25-38.

Distelfeld, A., I. Cakmak, Z. Peleg, L. Ozturk, A.M. Yazici, H. Budak, Y. Saranga, and T. Fahima. 2007. Multiple QTL-effects of wheat Gpc-B1 locus on grain protein and micronutrient concentrations. Physiol. Plant. 129:635-643.

Dubcovsky, J., C. Chen, and L. Yan. 2005. Molecular characterization of the allelic variation at the VRN-H2 vernalization locus in barley. Mol. Breed. 15:395-407.

Endelman, J.B. 2011. Ridge regression and other kernels for genomic selection with R package rrBLUP. Plant Gen. 4:250-255.

Faure, S., J. Higgins, A. Turner, and D.A. Laurie. 2007. The FLOWERING LOCUS T-like gene family in barley (*Hordeum vulgare*). Genetics 176:599-609.

Fernandez, G.C.J. 1992. Effective selection criteria for assessing stress tolerance. In: C.G. Kuo, editor, Proceedings of the International Symposium on "Adaptation of Vegetables and Other Food Crops in Temperature and Water Stress", Tainan, Taiwan. 13-16 Aug 1991. AVRDC, Shanhua, Taiwan. p. 257-270.

Fischbeck, G. 2002. Contribution of barley to agriculture: A brief overview. In: G.A. Slafer, J.L. Molina-Cano, R. Savin, J.L. Araus, and I. Romagosa, editors, Barley science: Recent advances from molecular biology to agronomy of yield and quality. The Haworth Press, Binghamton, NY. p. 1-14.

Fischer, R.A., and R. Maurer. 1978. Drought resistance in spring wheat cultivars. I. Grain yield responses. Aust. J. Agric. Res. 29:897-917.

Fisk, S.P., A. Cuesta-Marcos, L. Cistué, J. Russell, K.P. Smith, S. Baenziger, Z. Bedo, A. Corey, T. Filichkin, and I. Karsai. 2013. FR-H3: A new QTL to assist in the development of fall-sown barley with superior low temperature tolerance. Theor. Appl. Genet. 126:335-347.

Fowler, D.B., G. Breton, A.E. Limin, S. Mahfoozi, and F. Sarhan. 2001. Photoperiod and temperature interactions regulate low-temperature-induced gene expression in barley. Plant Physiol. 127:1676-1681.

Francia, E., F. Rizza, L. Cattivelli, A. Stanca, G. Galiba, B. Toth, P. Hayes, J. Skinner, and N. Pecchioni. 2004. Two loci on chromosome 5H determine low-temperature tolerance in a 'Nure'(winter) × 'Tremois'(spring) barley map. Theor. Appl. Genet. 108:670-680.

Fu, D., P. Szűcs, L. Yan, M. Helguera, J.S. Skinner, J. Von Zitzewitz, P.M. Hayes, and J. Dubcovsky. 2005. Large deletions within the first intron in VRN-1 are associated with spring growth habit in barley and wheat. Molecular Genetics and Genomics 273:54-65.

Gabriel, S.B., S.F. Schaffner, H. Nguyen, J.M. Moore, J. Roy, B. Blumenstiel, J. Higgins, M. DeFelice, A. Lochner, M. Faggart, S.N. Liu-Cordero, C. Rotimi, A. Adeyemo, R. Cooper, R. Ward, E.S. Lander, M.J. Daly, and D. Altshuler. 2002. The structure of haplotype blocks in the human genome. Science 296:2225-2229.

Galiba, G., A. Vágújfalvi, C. Li, A. Soltész, and J. Dubcovsky. 2009. Regulatory genes involved in the determination of frost tolerance in temperate cereals. Plant Science 176:12-19.

Gallais, A., and B. Hirel. 2003. An approach to the genetics of nitrogen use efficiency in maize.

Gallais, A., and M. Coque. 2005. Genetic variation and selection for nitrogen use efficiency in maize: A synthesis. Maydica 50:531-547.

Gao, X., J. Starmer, and E.R. Martin. 2008. A multiple testing correction method for genetic association studies using correlated single nucleotide polymorphisms. Genet. Epidemiol. 32:361.

Gao, X., L.C. Becker, D.M. Becker, J.D. Starmer, and M.A. Province. 2010. Avoiding the high Bonferroni penalty in genome- wide association studies. Genet. Epidemiol. 34:100-105.

Gastal, F., G. Lemaire, J. Durand, and G. Louarn. 2015. Quantifying crop responses to nitrogen and avenues to improve nitrogen-use efficiency. In: V.O. Sadras, and D.E.

Calderini, editors, Crop physiology: Applications for genetic improvement and agronomy. Elsevier Inc., Waltham, MA; San Diego, CA. p. 161-206.

Gianola, D., R.L. Fernando, and A. Stella. 2006. Genomic-assisted prediction of genetic value with semiparametric procedures. Genetics 173:1761-1776.

Goddard, M. 2009. Genomic selection: Prediction of accuracy and maximisation of long term response. Genetica 136:245-257.

Górny, A., and S. Garczyński. 2008. Nitrogen and phosphorus efficiency in wild and cultivated species of wheat. J. Plant Nutr. 31:263-279.

Górny, A.G. 2001. Variation in utilization efficiency and tolerance to reduced water and nitrogen supply among wild and cultivated barleys. Euphytica 117:59-66.

Górny, A.G., Z. Banaszak, B. Ługowska, and D. Ratajczak. 2011. Inheritance of the efficiency of nitrogen uptake and utilization in winter wheat (Triticum aestivum L.) under diverse nutrition levels. Euphytica 177:191-206.

Goudet, J. 2005. Hierfstat, a package for R to compute and test hierarchical F- statistics. Molecular Ecology Notes 5:184-186.

Grenier, C., T. Cao, Y. Ospina, C. Quintero, M.H. Châtel, J. Tohme, B. Courtois, and N. Ahmadi. 2015. Accuracy of genomic selection in a rice synthetic population developed for recurrent selection breeding. PloS One 10:e0136594.

Guo, Z., D.M. Tucker, C.J. Basten, H. Gandhi, E. Ersoz, B. Guo, Z. Xu, D. Wang, and G. Gay. 2014. The impact of population structure on genomic prediction in stratified populations. Theor. Appl. Genet. 127:749-762.

Hamblin, M.T., T.J. Close, P.R. Bhat, S. Chao, J.G. Kling, K.J. Abraham, T. Blake, W.S. Brooks, B. Cooper, and C.A. Griffey. 2010. Population structure and linkage disequilibrium in U.S. barley germplasm: Implications for association mapping. Crop Sci. 50:556-566.

Han, F., J. Clancy, B. Jones, D. Wesenberg, A. Kleinhofs, and S. Ullrich. 2004. Dissection of a malting quality QTL region on chromosome 1 (7H) of barley. Mol. Breed. 14:339-347.

Han, F., S. Ullrich, A. Kleinhofs, B. Jones, P. Hayes, and D. Wesenberg. 1997. Fine structure mapping of the barley chromosome-1 centromere region containing malting-quality QTLs. Theor. Appl. Genet. 95:903-910.

Harlan, J.R. 1968. On the origin of barley. In: G.A. Wiebe, editor, Barley: Origin, botany, culture, winter-hardiness, genetics, utilization, pests. Agriculture Handbook No. 338. U.S. Department of Agriculture, Washington, DC. p. 9-31.

Harvey, B.L., and B.G. Rossnagel. 1984. Harrington barley. Can. J. Plant Sci. 64:193-194.

Hayes, B., P. Bowman, A. Chamberlain, and M. Goddard. 2009. Invited review: Genomic selection in dairy cattle: Progress and challenges. J. Dairy Sci. 92:433-443.

Hayes, P.M., T. Blake, T.H.H. Chen, S. Tragoonrung, F. Chen, A. Pan, and B. Liu. 1993. Quantitative trait loci on barley (*Hordeum vulgare* L.) chromosome-7 associated with components of winterhardiness. Genome 36:66-71.

Hazel, L., and J.L. Lush. 1942. The efficiency of three methods of selection. J. Hered. 33:393-399.

Heffner, E.L., A.J. Lorenz, J. Jannink, and M.E. Sorrells. 2010. Plant breeding with genomic selection: Gain per unit time and cost. Crop Sci. 50:1681-1690.

Heffner, E.L., J. Jannink, and M.E. Sorrells. 2011. Genomic selection accuracy using multifamily prediction models in a wheat breeding program. The Plant Genome 4:65-75.

Heffner, E.L., M.E. Sorrells, and J. Jannink. 2009. Genomic selection for crop improvement. Crop Sci. 49:1-12.

Helback, H. 1959. Domestication of food plants in the Old World: Joint efforts by botanists and archeologists illuminate the obscure history of plant domestication. Science 130:365-372.

Heslot, N., H. Yang, M.E. Sorrells, and J. Jannink. 2012. Genomic selection in plant breeding: A comparison of models. Crop Sci. 52:146-160.

Hirel, B., P. Bertin, I. Quilleré, W. Bourdoncle, C. Attagnant, C. Dellay, A. Gouy, S. Cadiou, C. Retailliau, M. Falque, and A. Gallais. 2001. Towards a better understanding

of the genetic and physiological basis for nitrogen use efficiency in maize. Plant Physiol. 125:1258-1270.

Horsley, R., D. Schmierer, C. Maier, D. Kudrna, C. Urrea, B. Steffenson, P. Schwarz, J. Franckowiak, M. Green, and B. Zhang. 2006. Identification of QTLs associated with fusarium head blight resistance in barley accession CIho 4196. Crop Sci. 46:145-156.

Isidro, J., J. Jannink, D. Akdemir, J. Poland, N. Heslot, and M.E. Sorrells. 2015. Training set optimization under population structure in genomic selection. Theor. Appl. Genet. 128:145-158.

Jannink, J.L. 2010. Dynamics of long-term genomic selection. Genet. Sel. Evol. 42:35-9686-42-35.

Jannink, J.L., A.J. Lorenz, and H. Iwata. 2010. Genomic selection in plant breeding: From theory to practice. Brief Funct. Genomics 9:166-177.

Joppa, L.R., C. Du, G.E. Hart, and G.A. Hareland. 1997. Mapping gene(s) for grain protein in tetraploid wheat (Triticum turgidum L.) using a population of recombinant inbred chromosome lines. Crop Sci. 37:1586-1589.

Jukanti, A.K., and A.M. Fischer. 2008. A high- grain protein content locus on barley (*Hordeum vulgare*) chromosome 6 is associated with increased flag leaf proteolysis and nitrogen remobilization. Physiol. Plant. 132:426-439.

Jukanti, A.K., N.M. Heidlebaugh, D.L. Parrott, I.A. Fischer, K. McInnerney, and A.M. Fischer. 2008. Comparative transcriptome profiling of near- isogenic barley (*Hordeum vulgare*) lines differing in the allelic state of a major grain protein content locus identifies genes with possible roles in leaf senescence and nitrogen reallocation. New Phytol. 177:333-349.

Karsai, I., P. Szűcs, K. Mészáros, T. Filichkina, P. Hayes, J. Skinner, L. Láng, and Z. Bedő. 2005. The vrn-H2 locus is a major determinant of flowering time in a facultative × winter growth habit barley (*Hordeum vulgare* L.) mapping population. Theor. Appl. Genet. 110:1458-1466.

Kearsey, M., and A. Farquhar. 1998. QTL analysis in plants: Where are we now? Heredity 80:137-142.

Kikuchi, R., H. Kawahigashi, T. Ando, T. Tonooka, and H. Handa. 2009. Molecular and functional characterization of PEBP genes in barley reveal the diversification of their roles in flowering. Plant Physiol. 149:1341-1353.

Kimani, J., P. Tongoona, J. Derera. 2011. Genetic mechanisms controlling soil phosphorus and nitrogen tolerance as determined by leaf and seed content in the F2 and F3 rice populations. In: J. Tenywa, G. Taulya, G. Kawube, R. Kawuki, M. Namugwanya and L. Santos, editors, 10th African Crop Science Conference Proceedings, Maputo, Mozambique. 10-13 October 2011, African Crop Science Society, Maputo, Mozambique. p. 553-568.

Komatsuda, T., M. Pourkheirandish, C. He, P. Azhaguvel, H. Kanamori, D. Perovic, N. Stein, A. Graner, T. Wicker, A. Tagiri, U. Lundqvist, T. Fujimura, M. Matsuoka, T. Matsumoto, and M. Yano. 2007. Six-rowed barley originated from a mutation in a homeodomain-leucine zipper I-class homeobox gene. Proc. Natl. Acad. Sci. USA 104:1424-1429.

Konig, S., H. Simianer, and A. Willam. 2009. Economic evaluation of genomic breeding programs. J. Dairy Sci. 92:382-391.

Kutner, M.H., C.J. Nachtsheim, J. Neter, and W. Li. 2004. Applied linear statistical models, 4th ed. McGraw-Hill, Boston, MA.

Lacerenza, J.A., D.L. Parrott, and A.M. Fischer. 2010. A major grain protein content locus on barley (*Hordeum vulgare* L.) chromosome 6 influences flowering time and sequential leaf senescence. J. Exp. Bot. 61:3137-3149.

Laperche, A., F. Devienne-Barret, O. Maury, J. Le Gouis, and B. Ney. 2006. A simplified conceptual model of carbon/nitrogen functioning for QTL analysis of winter wheat adaptation to nitrogen deficiency Theor. Appl. Genet. 113:1131-1146.

Le Gouis, J., D. Béghin, E. Heumez, and P. Pluchard. 2000. Genetic differences for nitrogen uptake and nitrogen utilisation efficiencies in winter wheat. Eur. J. Agron. 12:163-173.

Le Gouis, J., O. Delebarre, D. Beghin, E. Heumez, and P. Pluchard. 1999. Nitrogen uptake and utilisation efficiency of two-row and six-row winter barley cultivars grown at two N levels. Eur. J. Agron. 10:73-79.

Levitt, J. 1980. Response of plants to environmental stresses. Academic Press, New York.

Lian, L., A. Jacobson, S. Zhong, and R. Bernardo. 2015. Prediction of genetic variance in biparental maize populations: Genomewide marker effects versus mean genetic variance in prior populations. Crop Sci. 55:1181-1188.

Limin, A., A. Corey, P. Hayes, and D.B. Fowler. 2007. Low-temperature acclimation of barley cultivars used as parents in mapping populations: Response to photoperiod, vernalization and phenological development. Planta 226:139-146.

Lin, C., G. Poushinsky, and P. Jui. 1983. Simulation study of three adjustment methods for the modified augmented design and comparison with the balanced lattice square design. J. Agric. Sci. 100:527-534.

Lin, C.S., and G. Poushinsky. 1985. A modified augmented design (type 2) for rectangular plots. Can. J. Plant Sci. 65:743-749.

Liu, Z., J. Tang, X. Wei, C. Wang, G. Tian, Y. Hu, and W. Chen. 2007. QTL mapping of ear traits under low and high nitrogen conditions in maize. Sci. Agric. Sin. 40:2409-2417.

Lorenz, A., K. Smith, and J. Jannink. 2012. Potential and optimization of genomic selection for fusarium head blight resistance in six-row barley. Crop Sci. 52:1609-1621.

Lorenz, A.J., and K.P. Smith. 2015. Adding genetically distant individuals to training populations reduces genomic prediction accuracy in barley. Crop Sci. 55:2657-2667.

Lorenz, A.J., S. Chao, F.G. Asoro, E.L. Heffner, T. Hayashi, H. Iwata, K.P. Smith, M.E. Sorrells, and J. Jannink. 2011. Genomic selection in plant breeding: Knowledge and prospects. Adv Agron 110:77-123.

Lorenzana, R.E., and R. Bernardo. 2009. Accuracy of genotypic value predictions for marker-based selection in biparental plant populations. Theor. Appl. Genet. 120:151-161.

Massman, J., B. Cooper, R. Horsley, S. Neate, R. Dill-Macky, S. Chao, Y. Dong, P. Schwarz, G. Muehlbauer, and K. Smith. 2011. Genome-wide association mapping of Fusarium head blight resistance in contemporary barley breeding germplasm. Mol. Breed. 27:439-454.

Massman, J.M., H.G. Jung, and R. Bernardo. 2013. Genomewide selection versus marker-assisted recurrent selection to improve grain yield and stover-quality traits for cellulosic ethanol in maize. Crop Sci. 53:58-66.

Mesfin, A., K. Smith, R. Dill-Macky, C. Evans, R. Waugh, C. Gustus, and G. Muehlbauer. 2003. Quantitative trait loci for fusarium head blight resistance in barley detected in a two-rowed by six-rowed population. Crop Sci. 43:307-318.

Meuwissen, T.H.E., B.J. Hayes, and M.E. Goddard. 2001. Prediction of total genetic value using genome-wide dense marker maps. Genetics 157:1819-1829.

Mickelson, S., D. See, F.D. Meyer, J.P. Garner, C.R. Foster, T.K. Blake, and A.M. Fischer. 2003. Mapping of QTL associated with nitrogen storage and remobilization in barley (*Hordeum vulgare* L.) leaves. J. Exp. Bot. 54:801-812.

Mohammadi, M., J.B. Endelman, S. Nair, S. Chao, S.S. Jones, G.J. Muehlbauer, S.E. Ullrich, B. Baik, M.L. Wise, and K.P. Smith. 2014. Association mapping of grain hardness, polyphenol oxidase, total phenolics, amylose content, and β-glucan in U.S. barley breeding germplasm. Mol. Breed. 34:1229-1243.

Mohammadi, M., T. Tiede, and K.P. Smith. 2015. PopVar: A genome-wide procedure for predicting genetic variance and correlated response in biparental breeding populations. Crop Sci. 55:2068-2077.

Mohammadi, M., T.K. Blake, A.D. Budde, S. Chao, P.M. Hayes, R.D. Horsley, D.E. Obert, S.E. Ullrich, and K.P. Smith. 2015. A genome-wide association study of malting quality across eight U.S. barley breeding programs. Theor. Appl. Genet. 128:705-721.

Moll, R.H., E.J. Kamprath, and W.A. Jackson. 1982. Analysis and interpretation of factors which contribute to efficiency of nitrogen utilization. Agron. J. 74:562-564.

Muñoz-Amatriaín, M., A. Cuesta-Marcos, J.B. Endelman, J. Comadran, J.M. Bonman, H.E. Bockelman, S. Chao, J. Russell, R. Waugh, and P.M. Hayes. 2014. The USDA Barley Core Collection: Genetic diversity, population structure, and potential for genome-wide association studies. PLoS One 9(4): e94688. doi:10.1371/journal.pone.0094688

Muñoz-Amatriaín, M., M.J. Moscou, P.R. Bhat, J.T. Svensson, J. Bartoš, P. Suchánková, H. Šimková, T.R. Endo, R.D. Fenton, S. Lonardi, A.M. Castillo, S. Chao, L. Cistué, A.

Cuesta-Marcos, K.L. Forrest, M.J. Hayden, P.M. Hayes, R.D. Horsley, K. Makoto, D. Moody, K. Sato, M.P. Vallés, B.B.H. Wulff, G.J. Muehlbauer, J. Doležel, and T.J. Close. 2011. An improved consensus linkage map of barley based on flow-sorted chromosomes and single nucleotide polymorphism markers. Plant Gen. 4:238-249.

Olmos, S., A. Distelfeld, O. Chicaiza, A.R. Schlatter, T. Fahima, V. Echenique, and J. Dubcovsky. 2003. Precise mapping of a locus affecting grain protein content in durum wheat. Theor. Appl. Genet. 107:1243-1251.

Pan, A., P. Hayes, F. Chen, T. Chen, T. Blake, S. Wright, I. Karsai, and Z. Bedö. 1994. Genetic analysis of the components of winterhardiness in barley (*Hordeum vulgare* L.). Theor. Appl. Genet. 89:900-910.

Paradis, E., J. Claude, and K. Strimmer. 2004. APE: Analyses of phylogenetics and evolution in R language. Bioinformatics 20:289-290.

Parrott, D.L., E.P. Downs, and A.M. Fischer. 2012. Control of barley (*Hordeum vulgare* L.) development and senescence by the interaction between a chromosome six grain protein content locus, day length, and vernalization. J. Exp. Bot. 63:1329-1339.

Pauli, D., G.J. Muehlbauer, K.P. Smith, B. Cooper, D. Hole, D.E. Obert, S.E. Ullrich, and T.K. Blake. 2014. Association mapping of agronomic QTLs in U.S. spring barley breeding germplasm. Plant Gen. 7(3). doi: 10.3835/plantgenome2013.11.0037

Poets, A.M., M. Mohammadi, K. Seth, H. Wang, T.J. Kono, Z. Fang, G.J. Muehlbauer, K.P. Smith, and P.L. Morrell. 2015. The effects of both recent and long-term selection and genetic drift are readily evident in North American barley breeding populations. G3 6(3):609-622. doi: 10.1534/g3.115.024349.

Pritchard, J.K., M. Stephens, and P. Donnelly. 2000. Inference of population structure using multilocus genotype data. Genetics 155:945-959.

R Core Team. 2015. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. Available at: https://www.R-project.org/. 2015.

Rameeh, V. 2012. Genetic parameters assessment of siliquae associated with stress indices in rapeseed cultivars. Annales Universitatis Mariae Curie Sklodowska Lublin-Polonia 17(4):35-44.

Rameeh, V. 2013. Combining ability of nitrogen deficiency stress indices for plant height in rapeseed varieties. J. Agric. Sci. (Belgrade) 58:19-30.

Rameeh, V. 2015. Nitrogen deficiency stress indices of seed yield in rapeseed (Brassica napus L.) genotypes. Cercet. Agron. in Moldova 48(1):89-96.

Rasmusson, D.C., and R.D. Wilcoxson. 1983. Registration of 'Robust' barley. Crop Sci. 23:1216.

Rasmusson, D.C., K.P. Smith, R. Dill-Macky, E.L. Schiefelbein, and J.V. Wiersma. 2001. Registration of 'Lacey' barley. Crop Sci. 41:1991.

Reinheimer, J.L., A.R. Barr, and J.K. Eglinton. 2004. QTL mapping of chromosomal regions conferring reproductive frost tolerance in barley (*Hordeum vulgare* L.). Theor. Appl. Genet. 109:1267-1274.

Riedelsheimer, C., J.B. Endelman, M. Stange, M.E. Sorrells, J.L. Jannink, and A.E. Melchinger. 2013. Genomic predictability of interconnected biparental maize populations. Genetics 194:493-503.

Rizza, F., D. Pagani, M. Gut, I. Prášil, C. Lago, A. Tondelli, L. Orru, E. Mazzucotelli, E. Francia, and F. Badeck. 2011. Diversity in the response to low temperature in representative barley genotypes cultivated in Europe. Crop Sci. 51:2759-2779.

Rosielle, A.A., and J. Hamblin. 1981. Theoretical aspects of selection for yield in stress and non-stress environments. Crop Sci. 21:943-946.

Rutkoski, J., J. Benson, Y. Jia, G. Brown-Guedira, J. Jannink, and M. Sorrells. 2012. Evaluation of genomic prediction methods for fusarium head blight resistance in wheat. The Plant Genome 5:51-61.

Rutkoski, J., R. Singh, J. Huerta-Espino, S. Bhavani, J. Poland, J. Jannink, and M. Sorrells. 2015. Efficient use of historical data for genomic selection: A case study of stem rust resistance in wheat. The Plant Genome 8:1.

Sallam, A., J. Endelman, J. Jannink, and K. Smith. 2015. Assessing genomic selection prediction accuracy in a dynamic barley breeding population. The Plant Genome 8:1.

Sasaki, A., M. Kiryu, T. Kato, and A. Kaminaga. 1992. Accumulation of dry matter and nitrogen in low protein barley [*Hordeum vulgare*] cv. Karl and its offsprings. Jpn. J. Breed. 42:853-862.

Schaeffer, L.R. 2006. Strategy for applying genome-wide selection in dairy cattle. J. Anim. Breed. Genet. 123:218-223.

Schum, A., and G. Jansen. 2014. In vitro method for early evaluation of nitrogen use efficiency associated traits in potato. J. Appl. Bot. Food Qual. 87:256-264.

Schwarz, P., and R. Horsley. 1995. Malt quality improvement in North American six-rowed barley cultivars since 1910. Journal of the American Society of Brewing Chemists 53:14-18.

See, D., V. Kanazin, K. Kephart, and T. Blake. 2002. Mapping genes controlling variation in barley grain protein concentration. Crop Sci. 42:680-685.

Sinebo, W., R. Gretzmacher, and A. Edelbauer. 2004. Genotypic variation for nitrogen use efficiency in Ethiopian barley. Field Crops Res. 85:43-60.

Skinner, J.S., J. von Zitzewitz, P. Szűcs, L. Marquez-Cedillo, T. Filichkin, K. Amundsen, E.J. Stockinger, M.F. Thomashow, T.H. Chen, and P.M. Hayes. 2005. Structural, functional, and phylogenetic characterization of a large CBF gene family in barley. Plant Mol. Biol. 59:533-551.

Skinner, J.S., P. Szűcs, J. von Zitzewitz, L. Marquez-Cedillo, T. Filichkin, E.J. Stockinger, M.F. Thomashow, T.H. Chen, and P.M. Hayes. 2006. Mapping of barley homologs to genes that regulate low temperature tolerance in *Arabidopsis*. Theor. Appl. Genet. 112:832-842.

Smith, K., A. Budde, R. Dill-Macky, D. Rasmusson, E. Schiefelbein, B. Steffenson, J. Wiersma, J. Wiersma, and B. Zhang. 2013. Registration of 'Quest' spring malting barley with improved resistance to fusarium head blight. Journal of Plant Registrations 7:125-129.

Steffenson, B. 2003. Fusarium head blight of barley: Impact, epidemics, management, and strategies for identifying and utilizing genetic resistance. p. 241-295. In K. Leonard, and W. Bushnell (eds.) Fusarium head blight of wheat and barley. APS Press, St. Paul, MN.

Szűcs, P., J.S. Skinner, I. Karsai, A. Cuesta-Marcos, K.G. Haggard, A.E. Corey, T.H. Chen, and P.M. Hayes. 2007. Validation of the VRN-H2/VRN-H1 epistatic model in barley reveals that intron length variation in VRN-H1 may account for a continuum of vernalization sensitivity. Mol. Genet. Genomics 277:249-261.

Technow, F. 2012. R package for moving grid adjustment in plant breeding field trials. Available at: http://artax.karlin.mff.cuni.cz/r-help/library/mvngGrAd/html/00Index.html. 2015.

Tiede, T., L. Kumar, M. Mohammadi, and K.P. Smith. 2015. Predicting genetic variance in bi-parental breeding populations is more accurate when explicitly modeling the segregation of informative genomewide markers. Mol. Breed. 35:1-13.

Tilman, D., K.G. Cassman, P.A. Matson, R. Naylor, and S. Polasky. 2002. Agricultural sustainability and intensive production practices. Nature 418:671-677.

Tong, H., L. Chen, W. Li, H. Mei, Y. Xing, X. Yu, X. Xu, S. Zhang, and L. Luo. 2011. Identification and characterization of quantitative trait loci for grain yield and its components under different nitrogen fertilization levels in rice (Oryza sativa L.). Mol Breed. 28:495-509.

Toomajian, C., T.T. Hu, M.J. Aranzana, C. Lister, C. Tang, H. Zheng, K. Zhao, P. Calabrese, C. Dean, and M. Nordborg. 2006. A nonparametric test reveals selection for rapid flowering in the Arabidopsis genome. PLoS Biol. 4(5): e137. doi:10.1371/journal.pbio.0040137

Trevaskis, B., D.J. Bagnall, M.H. Ellis, W.J. Peacock, and E.S. Dennis. 2003. MADS box genes control vernalization-induced flowering in cereals. Proc. Natl. Acad. Sci. U. S. A. 100:13099-13104.

Turner, A., J. Beales, S. Faure, R.P. Dunford, and D.A. Laurie. 2005. The pseudo-response regulator ppd-H1 provides adaptation to photoperiod in barley. Science 310:1031-1034.

Uauy, C., A. Distelfeld, T. Fahima, A. Blechl, and J. Dubcovsky. 2006b. A NAC gene regulating senescence improves grain protein, zinc, and iron content in wheat. Science 314:1298-1301.

Uauy, C., J.C. Brevis, and J. Dubcovsky. 2006a. The high grain protein content gene Gpc-B1 accelerates senescence and has pleiotropic effects on protein content in wheat. J. Exp. Bot. 57:2785-2794.

von Zitzewitz, J., A. Cuesta-Marcos, F. Condon, A.J. Castro, S. Chao, A. Corey, T. Filichkin, S.P. Fisk, L. Gutierrez, K. Haggard, I. Karsai, G.J. Muehlbauer, K.P. Smith, O. Veisz, and P.M. Hayes. 2011. The genetics of winterhardiness in barley: Perspectives from genome- wide association mapping. The Plant Genome 4:76-91.

von Zitzewitz, J., P. Szűcs, J. Dubcovsky, L. Yan, E. Francia, N. Pecchioni, A. Casas, T.H.H. Chen, P.M. Hayes, and J.S. Skinner. 2005. Molecular and structural characterization of barley vernalization genes. Plant Mol Biol 59:449-467.

Wang, H., K.P. Smith, E. Combs, T. Blake, R.D. Horsley, and G.J. Muehlbauer. 2012. Effect of population size and unbalanced data sets on QTL detection using genome-wide association mapping in barley breeding germplasm. Theor. Appl. Genet. 124:111-124.

Waugh, R., J. Jannink, G.J. Muehlbauer, and L. Ramsay. 2009. The emergence of whole genome association scans in barley. Curr. Opin. Plant Biol. 12:218-222.

Wei, D., K. Cui, G. Ye, J. Pan, J. Xiang, J. Huang, and L. Nie. 2012. QTL mapping for nitrogen-use efficiency and nitrogen-deficiency tolerance traits in rice. Plant Soil 359:281-295.

Wei, D., K. Cui, J. Pan, G. Ye, J. Xiang, L. Nie, and J. Huang. 2011. Genetic dissection of grain nitrogen use efficiency and grain yield and their relationship in rice. Field Crops Res. 124:340-346.

Weir, B.S., and C.C. Cockerham. 1984. Estimating F-statistics for the analysis of population structure. Evolution1358-1370.

Wesenberg, D., R. Hayes, N. Standridge, W. Burger, E. Goplin, and F. Petr. 1976. Registration of Karl barley. Crop Sci. 16:737.

Yan, L., A. Loukoianov, A. Blechl, G. Tranquilli, W. Ramakrishna, P. SanMiguel, J.L. Bennetzen, V. Echenique, and J. Dubcovsky. 2004. The wheat VRN2 gene is a flowering repressor down-regulated by vernalization. Science 303:1640-1644.

Yan, L., A. Loukoianov, G. Tranquilli, M. Helguera, T. Fahima, and J. Dubcovsky. 2003. Positional cloning of the wheat vernalization gene VRN1. Proc. Natl. Acad. Sci. U. S. A. 100:6263-6268.

Yan, L., D. Fu, C. Li, A. Blechl, G. Tranquilli, M. Bonafede, A. Sanchez, M. Valarik, S. Yasuda, and J. Dubcovsky. 2006. The wheat and barley vernalization gene VRN3 is an orthologue of FT. Proc. Natl. Acad. Sci. U. S. A. 103:19581-19586.

Yu, J., G. Pressoir, W.H. Briggs, I. Vroh Bi, M. Yamasaki, J.F. Doebley, M.D. McMullen, B.S. Gaut, D.M. Nielsen, J.B. Holland, S. Kresovich, and E.S. Buckler. 2006. A unified mixed-model method for association mapping that accounts for multiple levels of relatedness. Nat. Genet. 38:203-208.

Zhou, H., and B. Steffenson. 2013b. Genome-wide association mapping reveals genetic architecture of durable spot blotch resistance in US barley breeding germplasm. Mol. Breed. 32:139-154.

Zhou, H., and B.J. Steffenson. 2013a. Association mapping of Septoria speckled leaf blotch resistance in U.S. barley breeding germplasm. Phytopathology 103:600-609.

Zhou, H., B. Steffenson, G. Muehlbauer, R. Wanyera, P. Njau, and S. Ndeda. 2014. Association mapping of stem rust race TTKSK resistance in US barley breeding germplasm. Theor. Appl. Genet. 127:1293-1304.

Zhou, H., G. Muehlbauer, and B. Steffenson. 2012. Population structure and linkage disequilibrium in elite barley breeding germplasm from the United States. J. Zhejiang Univ., Sci., B 13:438-451.

Zhu, C.G., M. Buckler, and S.Y. Edward. 2008. Status and prospects of association mapping in plants. Plant Gen. 1(1):5-20. doi: 10.3835/plantgenome2008.02.0089.

Zohary, D., M. Hopf, and E. Weiss. 2012. Domestication of plants in the Old World: The origin and spread of domesticated plants in Southwest Asia, Europe, and the Mediterranean Basin. Oxford University Press Inc., New York.

Appendix

From Chapter 1

Supplemental Table S 1. Locations, years, field designs, field plot details, planting and harvest dates, and near infrared spectroscopy (NIRS) device details for phenotypic evaluation of the AM panels.

	Location-Year (Latitude/Longitude) Irrigated?	Field design	Plot size (m^2)	Harvested area (m^2)	Seeding rate (plants/m^2)	Planting date	Harvest date	NIRS device
2-row barley AM panel	Aberdeen, ID-2012 (42.943 / -112.839) Irrigated	Type II MAD†	6.5	4.8	200	4/11/2012	8/15/2012 (Norm N) 8/19/12 (Low N)	FOSS DS2500
	Aberdeen, ID-2013 (42.943 / -112.839) Irrigated	Type II MAD	6.5	4.8	200	4/3/2013	8/7/2013 (Norm N) 8/8/2013 (Low N)	
	Bozeman, MT-2012 (45.675 / -111.127) Not irrigated	Type II MAD	1.8	1.8	200	5/11/2012	8/30/2012 (Low N) 9/1/2012 (Norm N)	Infratec Grain Analyzer (Foss, Hillerod, Denmark)
	Bozeman, MT-2013 (45.675 / -111.127) Not irrigated	Type II MAD	1.8	1.8	200	5/8/13 (Low N) 5/9/2013 (Norm N)	9/6/2013 (Low N) 9/7/2013 (Norm N)	
6-row barley AM panel	Crookston, MN-2011 (47.824 / 96.616) Not irrigated	ABD	1.9	1.5	300	5/11/2011	8/9/2011	Perten DA 7250 NIR analyzer
	Crookston, MN-2012 (47.824 / 96.616) Not irrigated	Type II MAD	1.9	1.5	300	4/24/2012	7/30/2012	
	Prosper, ND-2012 (46.964 / 97.020) Not irrigated	Type II MAD	3.72	3.72	247	5/12/12	8/27/12	Foss Infratec 1241 Grain Analyzer
	Prosper, ND-2013 (46.964 / 97.020) Not irrigated	Type II MAD	3.72	3.72	247	5/17/13	8/27/13	

† *Type II MAD*: Type II Modified Augmented Design; *ABD*: Augmented Block Design

Supplemental Table S 2. QTL identified for each trait in each AM panel under each nitrogen treatment or for the geometric mean index. Alternating white and gray shading indicates the delineation of QTL regions.

Two-row AM Panel							
Nitrogen/Index	Trait	Marker	Chrom	Pos	MAF	–log*P* value	Marker effect
Low N	Heading date	11_10259	1H	40.40	0.07	3.69	1.27
		12_30298	1H	73.13	0.06	3.86	0.91
		12_30930	5H	132.32	0.44	4.21	0.15
		12_10218	7H	32.13	0.28	3.82	0.73
	Plant height	12_30894	7H	31.35	0.19	4.57	2.17
		12_30895	7H	31.35	0.20	4.57	2.26
	Grain yield	12_20201	7H	2.13	0.06	4.50	45.20
	Grain protein	11_20475	1H	93.48	0.05	6.23	6.98
		12_10811	6H	49.67	0.22	5.70	4.16
		12_20201	7H	2.13	0.06	4.30	8.46
		11_10069	7H	83.42	0.08	4.18	5.21
	Plump grain	12_10859	2H	93.26	0.06	3.70	4.09
		12_31367	3H	106.00	0.06	4.84	5.68
		11_11445	7H	85.28	0.12	6.98	4.04
		11_20880	7H	85.28	0.11	6.74	4.01
		12_30998	7H	85.28	0.12	7.15	4.04
		11_20230	7H	88.06	0.50	4.43	0.05
		12_30199	7H	88.06	0.43	4.88	0.24
	Test weight	11_10442	7H	85.28	0.49	4.22	1.89
		11_10531	7H	85.28	0.48	4.35	1.96
		11_11445	7H	85.28	0.12	5.84	10.87
		11_20880	7H	85.28	0.11	4.57	10.72
		12_30998	7H	85.28	0.12	6.00	10.87
		12_30199	7H	88.06	0.43	5.47	3.35
		11_10303	7H	89.78	0.34	5.77	4.55
Normal N	Heading date	11_10259	1H	40.40	0.07	3.75	1.31
		12_30108	2H	72.99	0.23	4.83	1.69
		12_30724	2H	72.99	0.24	4.41	1.73
		12_11278	2H	73.89	0.24	3.98	1.73

		12_31252	2H	74.55	0.23	4.88	1.68
		11_21094	2H	75.30	0.25	4.34	1.70
		12_10218	7H	32.13	0.28	4.08	0.79
	Plant height	12_30894	7H	31.35	0.19	4.44	2.26
		12_30895	7H	31.35	0.20	3.99	2.24
		12_10218	7H	32.13	0.28	3.98	1.44
	Grain yield	12_10777	2H	20.45	0.09	4.06	331.30
		12_20201	7H	2.13	0.06	5.43	551.92
	Grain protein	11_20475	1H	93.48	0.05	3.90	5.62
		11_11341	5H	108.28	0.05	4.44	4.93
		12_30619	5H	108.28	0.05	4.46	4.89
		11_11097	6H	49.67	0.36	4.50	3.95
		12_10199	6H	49.67	0.21	4.44	6.57
		12_10575	6H	49.67	0.21	4.44	6.57
		12_10811	6H	49.67	0.22	9.65	6.89
		12_30658	6H	52.19	0.36	4.64	4.00
		11_10069	7H	83.42	0.08	4.56	4.96
	Plump grain	11_20444	3H	68.51	0.05	4.87	8.42
		12_31367	3H	106.00	0.06	6.40	8.32
		11_11445	7H	85.28	0.12	5.38	5.04
		11_20880	7H	85.28	0.11	4.99	5.00
		12_30998	7H	85.28	0.12	5.53	5.04
		11_20230	7H	88.06	0.50	4.48	0.34
		12_30199	7H	88.06	0.43	4.18	0.07
	Test weight	11_10442	7H	85.28	0.49	3.75	1.24
		11_11445	7H	85.28	0.12	4.83	10.03
		12_30998	7H	85.28	0.12	4.90	10.03
		12_30199	7H	88.06	0.43	7.83	3.36
		11_10303	7H	89.78	0.34	5.92	4.48
Geometric mean	Heading date	11_10259	1H	40.40	0.07	3.82	2.28
		12_30108	2H	72.99	0.23	4.46	2.77
		12_30724	2H	72.99	0.24	3.95	2.72
		12_31252	2H	74.55	0.23	4.45	2.74
		11_21094	2H	75.30	0.25	3.81	2.67
		12_10218	7H	32.13	0.28	4.39	1.64

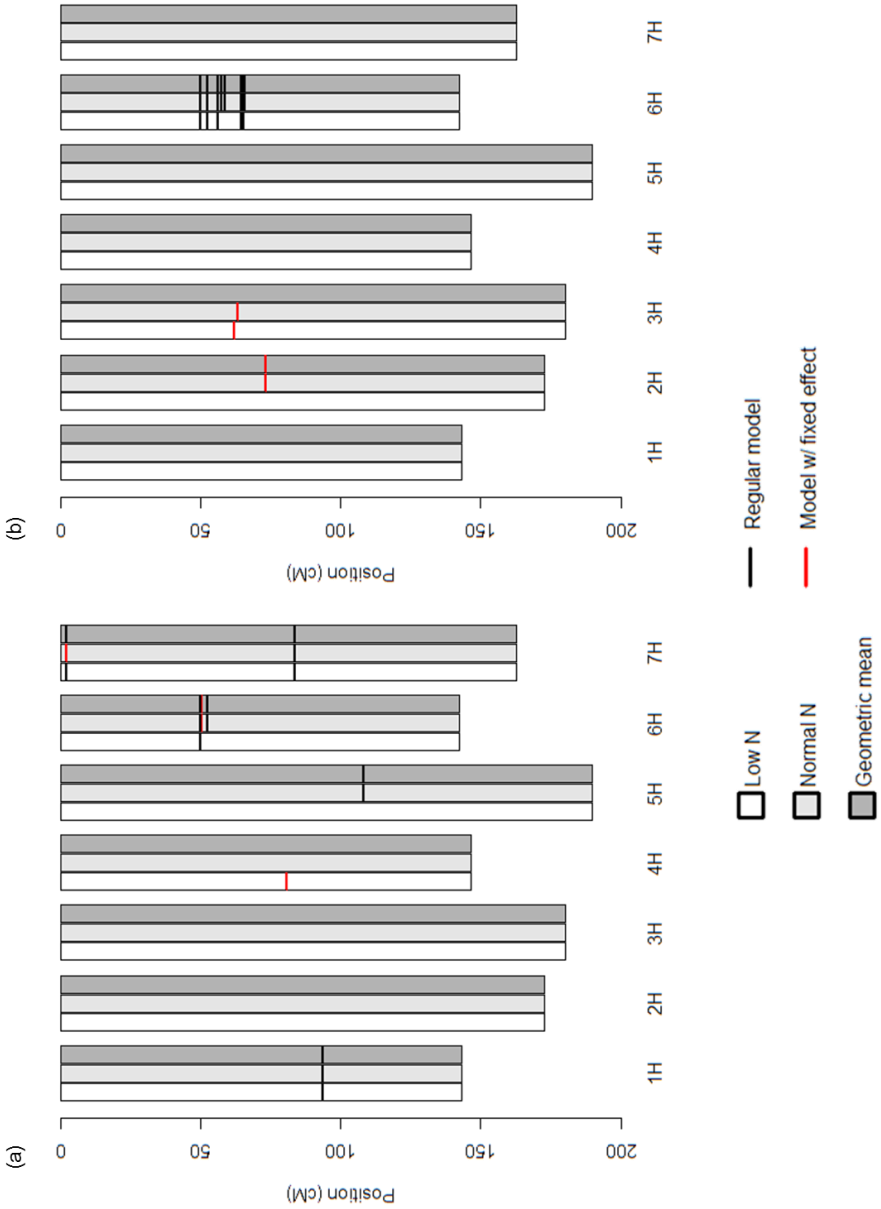
Plant height	12_30894	7H	31.35	0.19	5.03	2.21
	12_30895	7H	31.35	0.20	4.71	2.25
Grain yield	12_20201	7H	2.13	0.06	5.51	515.56
Grain protein	11_20475	1H	93.48	0.05	5.71	6.32
	11_11341	5H	108.28	0.05	3.74	5.17
	12_30619	5H	108.28	0.05	3.73	5.12
	11_11097	6H	49.67	0.36	4.38	3.06
	12_10199	6H	49.67	0.21	4.09	5.30
	12_10575	6H	49.67	0.21	4.09	5.30
	12_10811	6H	49.67	0.22	8.15	5.44
	12_30658	6H	52.19	0.36	4.44	3.09
	12_20201	7H	2.13	0.06	3.79	8.68
	11_10069	7H	83.42	0.08	4.72	5.22
Plump grain	12_10859	2H	93.26	0.06	3.76	4.12
	11_20444	3H	68.51	0.05	4.13	7.14
	12_31367	3H	106.00	0.06	5.61	7.03
	11_11445	7H	85.28	0.12	6.07	4.60
	11_20880	7H	85.28	0.11	5.64	4.57
	12_30998	7H	85.28	0.12	6.22	4.60
	11_20230	7H	88.06	0.50	4.67	0.11
	12_30199	7H	88.06	0.43	4.81	0.12
Test weight	11_10442	7H	85.28	0.49	4.28	1.39
	11_10531	7H	85.28	0.48	4.26	1.43
	11_11445	7H	85.28	0.12	5.51	9.78
	11_20880	7H	85.28	0.11	3.72	9.60
	12_30998	7H	85.28	0.12	5.59	9.78
	12_30199	7H	88.06	0.43	6.76	3.18
	11_10303	7H	89.78	0.34	6.24	4.27

Six-row AM Panel							
Nitrogen/Index	Trait	Marker	Chrom	Pos	MAF	–log*P* value	Marker effect
Low N	Heading date	11_10796	2H	63.55	0.05	5.36	1.82
		11_11133	2H	63.55	0.05	5.17	1.71
		11_10070	2H	66.20	0.05	5.17	1.71
		11_11046	2H	66.20	0.05	5.17	1.71
		11_10012	2H	67.08	0.05	5.10	1.70
		11_10624	2H	67.08	0.05	5.72	1.70
		11_20039	2H	67.63	0.06	5.17	1.64
		11_20438	2H	69.05	0.06	4.06	1.60
		11_10191	2H	72.99	0.05	5.10	1.70
		11_10685	2H	72.99	0.05	5.17	1.71
		11_20532	2H	72.99	0.05	5.10	1.70
		11_21399	2H	72.99	0.05	5.17	1.71
		12_30265	2H	72.99	0.05	5.17	1.71
		12_30275	2H	72.99	0.05	5.39	1.71
		12_30323	2H	72.99	0.05	4.62	1.71
		12_30680	3H	61.94	0.19	4.75	0.38
		11_21109	3H	63.25	0.18	6.48	0.39
	Plant height	12_31236	5H	103.01	0.14	4.77	1.63
	Grain yield	11_20230	7H	88.06	0.12	3.75	154.48
	Spikes per meter	11_21001	5H	63.93	0.20	3.70	3.83
		11_20249	7H	44.12	0.15	3.80	5.35
	Kernels per spike	11_21312	1H	45.20	0.20	3.66	1.56
		12_30927	3H	127.26	0.18	3.90	1.19
		11_10918	3H	132.62	0.15	3.98	1.17
		11_21405	3H	132.62	0.15	3.98	1.17
	Test weight	11_21032	6H	11.68	0.17	4.35	11.08
	Plump grain	11_10686	1H	77.92	0.08	4.78	4.78
		12_10670	4H	94.07	0.06	3.85	4.12
		11_21224	6H	86.96	0.13	4.42	3.95
	Kernel weight	12_30782	6H	53.54	0.18	4.18	0.05
	Grain protein	12_10199	6H	49.67	0.10	9.47	11.70
		12_10575	6H	49.67	0.10	9.47	11.70
		12_10811	6H	49.67	0.10	10.06	11.65

		12_30658	6H	52.19	0.37	3.63	2.81
		12_11353	6H	56.06	0.12	9.74	10.57
		12_30032	6H	56.06	0.10	9.47	11.70
		12_31003	6H	64.65	0.11	5.69	10.86
		11_21339	6H	65.29	0.18	3.72	7.45
Normal N	Heading date	11_11133	2H	63.55	0.05	4.33	1.42
		11_10070	2H	66.20	0.05	4.33	1.42
		11_11046	2H	66.20	0.05	4.33	1.42
		11_10012	2H	67.08	0.05	4.24	1.41
		11_10624	2H	67.08	0.05	4.74	1.41
		11_20039	2H	67.63	0.06	5.26	1.39
		11_10191	2H	72.99	0.05	4.24	1.41
		11_10685	2H	72.99	0.05	4.33	1.42
		11_20532	2H	72.99	0.05	4.24	1.41
		11_21399	2H	72.99	0.05	4.33	1.42
		12_30265	2H	72.99	0.05	4.33	1.42
		12_30275	2H	72.99	0.05	4.50	1.42
		12_30680	3H	61.94	0.19	5.61	0.34
		11_21109	3H	63.25	0.18	7.27	0.33
		11_20670	4H	90.11	0.19	4.41	0.39
	Plant height	12_31236	5H	103.01	0.14	4.06	1.55
		11_11341	5H	108.28	0.06	4.18	2.86
		12_30619	5H	108.28	0.05	4.05	2.93
	Grain yield	11_21250	2H	159.62	0.38	4.24	137.64
		12_10487	2H	159.62	0.42	3.62	136.51
		11_10120	6H	6.54	0.36	3.76	107.70
		11_10964	6H	65.29	0.07	4.14	130.85
	Spikes per area	11_21480	5H	78.19	0.48	4.28	3.33
		11_20327	5H	93.22	0.22	3.87	2.92
	Kernels per spike	11_10796	2H	63.55	0.05	4.49	3.45
		12_31252	2H	74.55	0.05	3.62	3.09
		12_10218	7H	32.13	0.32	4.60	1.38
	Test weight	12_11353	6H	56.06	0.12	4.05	15.85
	Plump grain	11_10686	1H	77.92	0.08	4.00	4.19
	Kernel weight	11_10686	1H	77.92	0.08	4.19	0.06
		11_20894	5H	1.26	0.18	3.62	0.04
	Grain	11_11097	6H	49.67	0.37	5.21	3.09

	protein						
		12_10199	6H	49.67	0.10	9.34	11.55
		12_10575	6H	49.67	0.10	9.34	11.55
		12_10811	6H	49.67	0.10	9.80	11.58
		12_30658	6H	52.19	0.37	5.34	3.17
		12_11353	6H	56.06	0.12	11.90	10.52
		12_30032	6H	56.06	0.10	9.34	11.55
		11_21473	6H	57.18	0.24	3.64	4.46
		12_31007	6H	58.48	0.11	6.97	4.57
		12_31003	6H	64.65	0.11	4.59	10.65
		11_20266	6H	65.29	0.18	3.62	7.23
		11_21339	6H	65.29	0.18	3.72	7.24
		11_10635	6H	65.83	0.18	3.88	7.15
		12_30346	6H	65.83	0.18	3.88	7.15
Geometric mean	Heading date	11_10796	2H	63.55	0.05	4.01	1.63
		11_11133	2H	63.55	0.05	4.67	1.56
		11_10070	2H	66.20	0.05	4.67	1.56
		11_11046	2H	66.20	0.05	4.67	1.56
		11_10012	2H	67.08	0.05	4.60	1.55
		11_10624	2H	67.08	0.05	5.22	1.55
		11_20039	2H	67.63	0.06	5.20	1.51
		11_10191	2H	72.99	0.05	4.60	1.55
		11_10685	2H	72.99	0.05	4.67	1.56
		11_20532	2H	72.99	0.05	4.60	1.55
		11_21399	2H	72.99	0.05	4.67	1.56
		12_30265	2H	72.99	0.05	4.67	1.56
		12_30275	2H	72.99	0.05	4.88	1.56
		12_30323	2H	72.99	0.05	3.88	1.56
		12_30680	3H	61.94	0.19	5.79	0.36
		11_21109	3H	63.25	0.18	8.02	0.35
		11_20670	4H	90.11	0.19	4.31	0.37
		11_10861	7H	134.10	0.08	3.79	0.31
	Plant height	11_20422	4H	28.00	0.18	3.80	1.92
		11_21070	4H	28.00	0.18	3.86	1.94
		12_31236	5H	103.01	0.14	4.66	1.58
		11_11341	5H	108.28	0.06	4.39	2.71
		12_30619	5H	108.28	0.05	3.84	2.70
	Grain yield	11_10964	6H	65.29	0.07	4.39	97.56
	Kernels per	11_10796	2H	63.55	0.05	3.96	3.12

spike						
Test weight	11_21032	6H	11.68	0.17	3.92	10.93
Plump grain	11_10686	1H	77.92	0.08	4.50	4.50
	11_21224	6H	86.96	0.13	3.95	4.27
Kernel weight	12_30782	6H	53.54	0.18	3.79	0.05
Grain protein	11_11097	6H	49.67	0.37	4.83	2.89
	12_10199	6H	49.67	0.10	9.79	11.58
	12_10575	6H	49.67	0.10	9.79	11.58
	12_10811	6H	49.67	0.10	10.26	11.57
	11_10461	6H	52.19	0.29	3.70	3.89
	12_30658	6H	52.19	0.37	5.07	2.97
	12_11353	6H	56.06	0.12	11.23	10.49
	12_30032	6H	56.06	0.10	9.79	11.58
	11_21473	6H	57.18	0.24	3.95	4.47
	12_31007	6H	58.48	0.11	4.30	3.55
	12_31003	6H	64.65	0.11	4.95	10.71
	11_21339	6H	65.29	0.18	3.68	7.30
	11_10635	6H	65.83	0.18	3.62	7.17
	12_30346	6H	65.83	0.18	3.62	7.17



Supplemental Figure S1. Significant marker-trait associations for grain protein concentration for the low and normal nitrogen treatments and the geometric mean stress index in the two-row panel (a) and the six-row panel (b). Black lines indicate associations identified under the regular association mapping model, and red lines indicate associations identified when the 6H GPC QTL haplotype was modeled as a fixed effect. In the two-row panel, several associations on chromosome 6H were identified under both models.

From Chapter 2

Supplemental Table S1. SNP markers in custom Veracode SNP assay, their chromosome and genetic positions based on the map generated by Muñoz-Amatriaín (2011).

Marker	Chromosome	Position (cM)	Marker	Chrom	Position (cM)
11_10460	1H	2.44	11_20226	5H	1.22
11_20502	1H	2.44	11_21202	5H	7.24
11_21226	1H	10.35	11_11381	5H	7.93
11_10332	1H	19.61	11_20533	5H	8.88
11_10775	1H	21.35	11_20010	5H	11.32
11_20371	1H	21.97	11_10695	5H	19.11
11_10873	1H	26.05	11_20873	5H	21.24
11_10186	1H	28.42	11_21426	5H	21.24
11_10744	1H	31.24	11_11048	5H	27.8
11_10760	1H	36.02	11_20386	5H	28.56
11_10764	1H	43.62	11_10621	5H	35.35
11_10275	1H	44.69	11_10260	5H	42.07
11_10597	1H	45.01	11_21253	5H	42.07
11_10438	1H	50	11_10058	5H	43.92
11_10470	1H	50	11_21011	5H	43.92
11_21000	1H	50	11_21260	5H	43.92
11_10324	1H	51.86	11_20239	5H	44.2
11_10552	1H	55.57	11_21508	5H	44.99
11_20095	1H	56.7	11_20713	5H	47.3
11_21431	1H	62.83	11_10641	5H	50.88
11_10516	1H	64.44	11_20367	5H	55.83
11_10002	1H	64.93	11_21309	5H	55.83
11_20956	1H	64.93	11_21133	5H	59.03
11_20290	1H	69.73	11_20736	5H	60.99
11_10006	1H	72.86	11_21445	5H	64.65
11_10686	1H	72.86	11_21480	5H	66.78
11_21126	1H	72.86	11_11355	5H	68.58

11_20657	1H	75.65	11_10578	5H	72.22
11_21192	1H	83.15	11_20097	5H	76.34
11_20550	1H	83.85	11_20850	5H	77.32
11_20792	1H	88.25	11_20327	5H	84.62
11_20149	1H	94.48	11_11350	5H	84.96
11_20125	1H	97.23	11_20134	5H	87.71
11_10357	1H	99.45	11_20795	5H	87.71
11_20909	1H	104.1	12_30850	5H	87.71
11_20625	1H	108.4	12_30854	5H	87.71
11_20844	1H	109.53	12_31236	5H	90.22
11_21392	1H	114.3	11_10477	5H	95.65
11_10729	1H	116.83	11_11200	5H	99.58
11_20959	1H	122.29	11_10094	5H	108.79
11_11528	1H	126.6	11_20629	5H	109.14
11_21068	1H	128.92	11_20127	5H	111.21
11_21140	1H	128.92	11_11456	5H	114.19
11_10644	1H	130.02	11_11024	5H	116.93
11_10782	1H	137.75	11_11375	5H	116.93
11_20603	1H	142.16	11_10521	5H	125.23
11_20772	1H	142.74	11_10783	5H	126.39
11_10326	2H	7.29	11_11080	5H	126.39
11_11059	2H	11.86	12_30883	5H	126.43
11_21377	2H	13.19	11_10095	5H	127.52
11_20563	2H	13.39	11_10819	5H	132
11_20107	2H	24.16	11_10292	5H	132.47
11_10943	2H	25.53	11_10104	5H	134.12
11_10180	2H	31.94	11_11441	5H	135.42
12_30872	2H	38.6	11_20388	5H	137.38
11_21015	2H	39.69	11_11497	5H	147.7
11_10216	2H	40.73	11_20545	5H	149.41
11_20864	2H	44.93	11_11216	5H	161.41
11_21304	2H	47.35	11_20686	5H	161.41
11_10525	2H	52.96	11_10869	5H	163.16

11_10648	2H	53.26	11_21141	5H	166.26
11_10837	2H	53.26	11_21138	5H	169.97
11_10919	2H	53.26	11_10405	5H	171.16
11_11061	2H	62.38	11_20189	5H	172.03
11_11505	2H	63.62	11_10310	5H	177.5
11_11054	2H	64.55	11_21052	5H	177.5
11_10638	2H	66.11	11_21162	5H	177.53
11_20387	2H	66.11	11_11364	5H	179.67
11_11015	2H	66.82	11_21521	6H	2.86
11_11384	2H	69	11_11406	6H	4.41
11_20160	2H	69	11_10120	6H	4.71
11_10436	2H	69.55	11_21032	6H	11.35
11_20438	2H	69.55	11_11479	6H	14.26
11_21110	2H	69.88	11_20415	6H	15.16
11_21258	2H	75.18	11_10165	6H	17.58
11_21205	2H	76.3	11_10023	6H	20.36
11_20960	2H	78.02	11_10064	6H	20.36
11_10818	2H	81.26	11_10868	6H	27.19
11_20699	2H	81.26	11_10676	6H	34.46
11_20781	2H	88.04	11_10799	6H	38.12
11_10213	2H	90.99	11_10129	6H	50.54
11_21351	2H	93.83	11_20052	6H	50.54
11_10214	2H	99.04	11_10494	6H	50.61
11_21175	2H	101.98	11_21281	6H	51.94
11_11307	2H	102.28	11_10013	6H	54.14
11_20923	2H	106.9	11_20675	6H	55.9
11_20498	2H	107.47	11_20720	6H	58.34
11_11094	2H	114.3	11_20600	6H	58.91
11_10128	2H	124.5	11_21124	6H	58.91
11_10731	2H	125.76	11_21509	6H	61.46
11_11236	2H	125.76	11_20266	6H	65.08
11_10429	2H	126.63	11_20058	6H	65.38
11_10707	2H	129.47	11_20714	6H	73.83

11_21315	2H	138.54	11_20636	6H	74.18
11_21440	2H	142.03	11_20744	6H	76.14
11_21406	2H	143.07	11_20682	6H	77.7
11_21125	2H	145.2	11_21224	6H	79.74
11_11227	2H	149.13	11_11458	6H	80.31
11_20590	2H	155.66	11_10331	6H	81.11
11_11262	2H	157.42	11_11147	6H	85.23
11_10315	2H	159.5	11_20654	6H	85.23
11_10072	2H	171.55	11_10202	6H	92.8
11_10770	2H	175.48	11_11294	6H	97.15
11_10085	2H	177.38	11_20972	6H	99.15
11_10101	2H	179.41	11_10139	6H	102.03
11_20858	3H	0	11_20531	6H	102.03
11_20797	3H	5.39	11_20379	6H	105.23
11_20159	3H	5.91	11_20036	6H	110.59
11_20252	3H	6.46	11_10239	6H	114.27
11_20976	3H	11.94	11_10107	6H	122.64
11_10112	3H	13.88	11_10645	6H	122.99
11_20742	3H	24.63	11_21455	6H	122.99
11_10565	3H	25.27	11_20868	6H	129.12
11_10559	3H	28.78	11_11111	6H	129.22
11_20552	3H	28.78	11_21112	6H	129.32
11_20607	3H	38.19	11_10682	7H	1.08
11_10026	3H	40.34	11_20710	7H	2.47
11_10825	3H	45.39	11_20245	7H	9.82
11_20193	3H	48.25	11_20014	7H	15.72
11_20647	3H	50.66	11_10025	7H	16.78
11_11002	3H	51.95	11_20722	7H	19.22
11_10601	3H	54.92	11_20495	7H	22.12
11_21093	3H	55.36	11_10920	7H	31.83
11_21189	3H	55.57	11_20162	7H	32.81
11_11086	3H	58.31	11_20758	7H	33.9
11_11502	3H	58.31	11_20126	7H	38.31

11_20970	3H	58.31	12_30895	7H	38.31
11_21109	3H	58.31	11_10576	7H	46.89
11_21402	3H	58.31	11_21528	7H	49.96
11_20995	3H	59.56	11_21491	7H	53
11_20704	3H	64.07	11_20249	7H	56.37
11_21305	3H	65.16	11_10772	7H	56.83
11_20877	3H	66.84	11_20466	7H	58.39
11_20566	3H	67.53	11_11014	7H	62.19
11_20115	3H	71.74	11_10346	7H	63.19
11_21163	3H	71.84	11_10721	7H	65.25
11_10628	3H	76.76	11_10050	7H	66.61
11_21505	3H	79.13	11_11098	7H	71.76
11_10253	3H	82.19	11_20060	7H	72.84
11_20626	3H	91.33	11_10431	7H	73.16
11_10184	3H	91.62	11_10299	7H	74.21
11_21381	3H	92.18	11_10983	7H	74.84
11_21495	3H	94.03	11_10534	7H	78.07
11_20009	3H	97.5	11_10700	7H	78.07
11_21513	3H	97.95	11_10069	7H	81.07
11_20023	3H	99.46	11_11445	7H	82.16
11_10753	3H	100.56	11_10303	7H	84.09
11_20944	3H	109.12	11_20083	7H	84.09
11_10867	3H	113.42	11_11343	7H	89.32
11_20650	3H	113.42	11_21448	7H	92
11_10842	3H	118.71	11_10301	7H	98.14
11_20527	3H	123.16	11_20103	7H	101.99
11_11127	3H	125.23	11_10169	7H	104.63
11_20085	3H	126.41	11_20092	7H	110.4
11_21427	3H	129.62	11_20570	7H	113.8
11_21266	3H	137.08	11_20247	7H	117.1
11_21272	3H	137.48	11_11243	7H	125.55
11_20155	3H	144.57	11_21229	7H	133.84
11_11436	3H	145.65	11_10182	7H	133.92

11_21008	3H	151.17	11_21209	7H	135.99
11_10702	3H	151.23	11_10861	7H	138.76
11_20605	3H	152.29	11_10078	7H	142.91
11_11516	3H	159.55	11_10454	7H	146.08
11_10343	3H	164.42	11_20139	7H	148.45
11_20145	4H	1.17	11_11440	7H	150.36
11_21056	4H	3.91	11_21223	7H	150.36
11_11345	4H	5.84	11_10130	7H	156.54
11_10319	4H	9.14	11_20962	7H	156.69
11_10738	4H	20.65	11_10999	7H	160.25
11_21359	4H	21.74	11_20504	7H	162.38
11_20557	4H	22.43	11_20365	7H	167.58
11_10221	4H	24.23			
11_10574	4H	24.23			
11_20302	4H	31.14			
11_21389	4H	37.05			
11_21122	4H	38.79			
11_20012	4H	46.19			
11_20114	4H	46.87			
11_20180	4H	46.87			
11_11180	4H	50.7			
11_20939	4H	52.67			
11_10480	4H	53.87			
11_21073	4H	53.87			
11_10379	4H	54.44			
11_20412	4H	54.95			
11_21191	4H	55.64			
11_21254	4H	55.64			
11_10914	4H	55.85			
11_20062	4H	57.44			
11_10052	4H	58.82			
11_20740	4H	64.45			
11_10309	4H	67.91			

11_10247	4H	70.33
11_20197	4H	76.31
11_20765	4H	81.96
11_10588	4H	83.34
11_20384	4H	87.9
11_10785	4H	90.97
11_21243	4H	95.23
11_20119	4H	98.65
11_20515	4H	99.08
11_10510	4H	100.38
11_20974	4H	105.14
11_11299	4H	112.79
11_10712	4H	113.07
11_20701	4H	114.98
11_11066	4H	117.13
11_10697	4H	117.33
11_21210	4H	120.53
11_20224	4H	121.74
12_30889	4H	122.96
11_20668	4H	127.12
11_10387	4H	128.59

Supplemental Table S2. SNP markers for winter hardiness traits, which were used in the 384 SNP assay.

BOPA marker	Chrom; Pos	Gene	Description
12_30872	2H; 26.6	Ppd-H1	SNP-Causal polymorphism
12_30889	4H; 119.1	VRN-H2	INDEL-Polymorphism based on insertion/deletion of cluster of 3 genes
12_30883	5H; 135.7	VRNH1/ FR-H1	INDEL-Polymorphism based on insertion/deletion of region on the first
11_11080	5H; 137.2	VRNH1/ FR-H1	SNP-Significant for LTT in a AM paper about Oregon CAPIV lines (unpublished)
12_30854	5H; 108.2	FR-H2	SNP-Highly significant for LTT (von Zitzewitz et al. 2011); located in HvCBF9
12_31236	5H; 110.3	FR-H2	SNP-Highly significant for LTT (von Zitzewitz et al. 2011)
11_20126	7H; 37.5	VRN-H3	SNP-Highly significant in a AM paper about Oregon CAPIV lines (unpublished)

Supplemental Table S3. Phenotypic trials for the parents and selected sets (C1-R, C1-GS, C1-PS, C2-R, C2-GS).

	Trials	
Trait	Location	Season planted
Winter survival (percent of plot survived)	Mead, NE	Fall 2013
	Lamberton, MN	Fall 2013
	St. Paul, MN	Fall 2013
Grain yield ($kg\ ha^{-1}$)	Corvallis, OR	Fall 2013
	St. Paul, MN	Spring 2014
	Corvallis, OR	Fall 2014
	Crookston, MN	Spring 2015
Heading date (Julian days)	St. Paul, MN	Fall 2013
	St. Paul, MN	Spring 2014
	St. Paul, MN (FHB trial)	Spring 2014
	Corvallis, OR	Fall 2014
	St. Paul, MN (FHB trial)	Spring 2015
	Crookston, MN	Spring 2015
Plant height (cm)	Corvallis, OR	Fall 2013
	St. Paul, MN	Fall 2013
	St. Paul, MN	Spring 2014
	Corvallis, OR	Fall 2014
	Crookston, MN	Spring 2015
FHB severity (percent diseased kernels)	Crookston, MN (FHB trial)	Spring 2014
	St. Paul, MN (FHB trial)	Spring 2014
	St. Paul, MN (FHB trial)	Spring 2015
Malt quality traits†	Corvallis, OR	Fall 2013
	St. Paul, MN	Spring 2014
	Corvallis, OR	Fall 2014
	Crookston, MN	Spring 2015

Footnotes † Malt quality traits evaluated were malt extract (percent), grain plumpness (%), kernel weight (mg), grain protein concentration ($g\ kg^{-1}$), wort protein (%), soluble over total protein ratio (%), alpha-amylase (20°DU), beta-glucan (ppm), diastatic power (°ASBC), and free amino nitrogen (ppm).

Supplemental Table S4. Phenotypic trait data summary for the base population, C1-R ("C0"), C1-GS ("C1"), and C2-GS ("C2").

Trait Index (using C1 weights)					
	Min	Mean	Med	Max	Var
C0	455.3	481.7	479.8	528.0	365.8
C1	455.3	501.9	505.9	536.3	440.3
C2	451.9	488.9	491.1	511.3	183.3

Winter survival (% plot survival)					
	Min	Mean	Med	Max	Var
C0	7.1	11.6	9.6	30.4	28.1
C1	6.9	13.2	12.1	31.3	21.6
C2	7.9	14.8	12.8	33.0	33.5

Grain yield (kg ha^{-1})					
	Min	Mean	Med	Max	Var
C0	4358	4762	4711	5250	38892
C1	4503	4939	4899	5310	39270
C2	4387	4820	4813	5175	24402

Heading date (Julian days)					
	Min	Mean	Med	Max	Var
C0	152.2	159.0	159.4	164.0	6.9
C1	157.1	160.1	160.2	164.0	2.3
C2	156.1	160.0	159.4	165.7	5.6

Kernel weight (mg)					
	Min	Mean	Med	Max	Var
C0	29.8	33.6	33.8	39.0	4.4
C1	31.7	34.0	33.9	36.6	1.1
C2	30.8	33.6	33.4	37.5	2.4

FHB severity (% kernels diseased)					
	Min	Mean	Med	Max	Var
C0	31.4	40.8	40.7	54.0	30.4
C1	31.4	41.5	42.2	53.5	31.2
C2	32.7	41.2	40.4	52.7	18.9

S/T (%)					
	Min	Mean	Med	Max	Var
C0	33.5	39.7	40.7	43.3	7.2
C1	34.4	40.1	40.0	44.9	5.4
C2	38.3	41.4	41.2	46.2	4.8

Beta-glucan (ppm)					
	Min	Mean	Med	Max	Var
C0	186.4	348.8	350.1	570.0	10109.4
C1	178.7	318.9	306.1	505.1	6471.4
C2	171.6	311.4	311.7	448.8	5075.5

FAN (ppm)					
	Min	Mean	Med	Max	Var
C0	177.0	208.7	208.4	239.4	367.3
C1	108.4	204.6	206.0	250.3	782.1
C2	197.1	225.2	224.4	265.6	361.7

Trait Index (using C2 weights)					
	Min	Mean	Med	Max	Var
C0	13.1	16.3	15.2	26.7	9.6
C1	13.8	17.0	16.4	26.9	6.8
C2	14.2	17.3	16.6	26.5	6.9

Malt extract (percent)					
	Min	Mean	Med	Max	Var
C0	75.7	78.1	78.0	80.3	1.3
C1	76.5	78.4	78.5	80.3	0.9
C2	77.0	78.7	78.7	80.4	0.6

Plant height (cm)					
	Min	Mean	Med	Max	Var
C0	79.7	89.5	89.8	98.2	16.6
C1	85.5	92.1	92.4	100.4	13.3
C2	77.7	91.3	91.1	99.8	16.4

Grain plumpness (%)					
	Min	Mean	Med	Max	Var
C0	73.50	84.32	85.67	90.10	15.66
C1	76.70	85.00	85.59	91.42	12.89
C2	74.44	84.42	85.60	89.18	14.27

Grain protein concentration (g kg^{-1})					
	Min	Mean	Med	Max	Var
C0	11.5	12.1	12.1	12.8	12.1
C1	11.1	11.9	11.9	12.7	14.0
C2	11.6	12.0	12.1	12.6	6.9

Wort protein (%)					
	Min	Mean	Med	Max	Var
C0	4.0	4.6	4.7	5.2	0.1
C1	3.7	4.5	4.5	5.2	0.1
C2	4.4	4.8	4.8	5.4	0.1

Alpha-amylase (20°DU)					
	Min	Mean	Med	Max	Var
C0	53.0	64.4	65.3	76.7	37.5
C1	51.8	62.7	62.1	73.4	45.1
C2	53.7	66.2	65.3	81.1	41.5

Diastatic Power (°ASBC)					
	Min	Mean	Med	Max	Var
C0	123.5	151.3	150.6	193.0	352.7
C1	107.1	142.6	142.8	171.8	223.1
C2	124.1	154.6	158.7	186.3	334.5

Supplemental Table S5. All lines used a parents and developed for cycle 1 (C1) and cycle 2 (C2) with their cycle, family, pedigree, and membership in the selected sets indicated. Under GS (genomic selection sets) and PS (phenotypic selection set), "50/100" indicates lines that were included in the 50 lines tested in field trials for this study while "100" indicates lines that were selected as being in the top 100 but were not tested in field trials. Under RS (random selection sets), "50" indicates the lines chosen at random and tested in the field trials for this study. Under MQ (malt quality), "25" indicates that the line was one of the 25 from each selected set that was tested for malt quality traits.

Cycle-Family	Name	Pedigree	GS	PS	RS	MQ
Parents	DH01-05	NB03437/OR71				
Parents	DH01-113	NB03437/OR71				
Parents	DH01-39	NB03437/OR71				
Parents	DH01-84	NB03437/OR72	No progeny in C1			
Parents	LACEY	M78 / M79				
Parents	M115	MN94-111/MN94-33				
Parents	M135	FEG97-44/M118				
Parents	MW09_4077-001	TAMBAR 501 / FEG188-02	No progeny in C1			
Parents	MW09_4076-001	TAMBAR 501 / M115				
Parents	MW09_4078-001	NB99845 / M115				
Parents	MW09_4079-001	NB99845 / Quest				
Parents	MW09_4080-001	88AB536/RASMUSSON				
Parents	MW09_4083-001	OR72 / Quest				
Parents	MW09_5084-001	OR72 / FEG183-28				
Parents		OR72/M109	No progeny in C1			
Parents		OR72/M115	No progeny in C1			
Parents	MW09_5085-001	OR76 / M115				
Parents	OR83	Stab47/Excel//Stab47				
Parents	QUEST	FEG18-20/M110				
Parents	RASMUSSON	LACEY/M95				
Parents	TCFW6-295	NB99845 / M115	No progeny in C1			
Parents	TCFW6-297	88ab536 / Rasmusson				
Parents	WGS_06OR-07	Strider/88Ab536				
Parents	WGS_06OR-37	Stab 47/Kab 51				
Parents	WGS_06OR-40	Stab 47/Kab 51				
Parents	WGS_06OR-41	Strider/88Ab 536,F1//88Ab 536				
Parents	WGS_06OR-48	Stab 113/Kab 50				
Parents	WGS_06OR-51	Stab47/Excel,F1//Stab47				
Parents	WGS_06OR-76	Kab51/Legacy,F1//Kab51				
Parents	WGS_06OR-79	Kab51/Excel,F1//Kab51				
Parents	WGS_06OR-83	Stab113/Excel,F1//Kab51				
Parents	WGS_06OR-87	Stab47/Excel,F1//Stab47				
Parents	WGS_06OR-95	Complex - composite cross				

Parents	WGS_07OR-06	Bu 27/Stab 47(F1)/3/Stab 113/Stab 47- 49-4	
Parents	WGS_07OR-09	Bu 27/Stab 47(F1)/3/Stab 113/Stab 47- 49-4	
Parents	WGS_07OR-52	NB92711/P-954	
Parents	WGS_07OR-55	Stab113/kab50//Kab37-1 Stab113/Kab 50//Jari2 Stab113/Kab50//Kab65-3	
Parents	WGS_07OR-58	Stab113/kab50//Kab37-1 Stab113/Kab 50//Jari2 Stab113/Kab50//Kab65-3	
Parents	WGS_07OR-59	Stab113/kab50//Kab37-1 Stab113/Kab 50//Jari2 Stab113/Kab50//Kab65-3	
Parents	WGS_07OR-63	Stab113/kab50//Kab37-1 Stab113/Kab 50//Jari2 Stab113/Kab50//Kab65-3	
Parents	WGS_08OR-30	StabBC 42-4-2/Stab 7-1	
Parents	WGS_08OR-39	StabBC 42-4-2/3/K51/L//K51	
Parents	WGS_08OR-40	StabBC 42-4-2/3/K51/L//K51	
Parents	WGS_08OR-69	S113/L//S113/3/Kab 47	
Parents	WGS_08OR-77	K51/E//S113/3/Stab 7/Stab 113-8	
Parents	WGS_08OR-79	S113/L//S113/3/Stab 7/Kab 43-1	
Parents	WGS_08OR-82	Kab 47/B98-9339	
C1-1	MW11S3001-001	NB99845 / M115 // M115	
C1-1	MW11S3001-002	NB99845 / M115 // M115	
C1-1	MW11S3001-003	NB99845 / M115 // M115	
C1-1	MW11S3001-004	NB99845 / M115 // M115	
C1-1	MW11S3001-005	NB99845 / M115 // M115	
C1-1	MW11S3001-006	NB99845 / M115 // M115	
C1-1	MW11S3001-007	NB99845 / M115 // M115	
C1-1	MW11S3001-008	NB99845 / M115 // M115	
C1-1	MW11S3001-009	NB99845 / M115 // M115	
C1-1	MW11S3001-010	NB99845 / M115 // M115	
C1-1	MW11S3001-011	NB99845 / M115 // M115	
C1-1	MW11S3001-012	NB99845 / M115 // M115	
C1-1	MW11S3001-013	NB99845 / M115 // M115	
C1-1	MW11S3001-014	NB99845 / M115 // M115	
C1-1	MW11S3001-015	NB99845 / M115 // M115	
C1-1	MW11S3001-016	NB99845 / M115 // M115	
C1-2	MW11S3004-001	TAMBAR 501 / FEG188-02 // Quest	
C1-2	MW11S3004-002	TAMBAR 501 / FEG188-02 // Quest	
C1-2	MW11S3004-003	TAMBAR 501 / FEG188-02 // Quest	
C1-2	MW11S3004-004	TAMBAR 501 / FEG188-02 // Quest	50
C1-2	MW11S3004-005	TAMBAR 501 / FEG188-02 // Quest	50
C1-2	MW11S3004-006	TAMBAR 501 / FEG188-02 // Quest	
C1-2	MW11S3004-007	TAMBAR 501 / FEG188-02 // Quest	
C1-2	MW11S3004-008	TAMBAR 501 / FEG188-02 // Quest	
C1-2	MW11S3004-009	TAMBAR 501 / FEG188-02 // Quest	
C1-2	MW11S3004-010	TAMBAR 501 / FEG188-02 // Quest	
C1-2	MW11S3004-011	TAMBAR 501 / FEG188-02 // Quest	
C1-2	MW11S3004-012	TAMBAR 501 / FEG188-02 // Quest	
C1-2	MW11S3004-013	TAMBAR 501 / FEG188-02 // Quest	
C1-2	MW11S3004-014	TAMBAR 501 / FEG188-02 // Quest	
C1-2	MW11S3004-015	TAMBAR 501 / FEG188-02 // Quest	

C1-2	MW11S3004-016	TAMBAR 501 / FEG188-02 // Quest		
C1-3	MW11S3005-001	TAMBAR 501 / FEG188-02 // M135		
C1-3	MW11S3005-002	TAMBAR 501 / FEG188-02 // M135		
C1-3	MW11S3005-003	TAMBAR 501 / FEG188-02 // M135		
C1-3	MW11S3005-004	TAMBAR 501 / FEG188-02 // M135		
C1-3	MW11S3005-005	TAMBAR 501 / FEG188-02 // M135		
C1-3	MW11S3005-006	TAMBAR 501 / FEG188-02 // M135		
C1-3	MW11S3005-007	TAMBAR 501 / FEG188-02 // M135		
C1-3	MW11S3005-008	TAMBAR 501 / FEG188-02 // M135		
C1-3	MW11S3005-009	TAMBAR 501 / FEG188-02 // M135		
C1-3	MW11S3005-010	TAMBAR 501 / FEG188-02 // M135		
C1-3	MW11S3005-011	TAMBAR 501 / FEG188-02 // M135		
C1-3	MW11S3005-012	TAMBAR 501 / FEG188-02 // M135		
C1-3	MW11S3005-013	TAMBAR 501 / FEG188-02 // M135		
C1-3	MW11S3005-014	TAMBAR 501 / FEG188-02 // M135		
C1-3	MW11S3005-015	TAMBAR 501 / FEG188-02 // M135		
C1-3	MW11S3005-016	TAMBAR 501 / FEG188-02 // M135		
C1-4	MW11S3006-001	NB99845 / Quest // Quest		
C1-4	MW11S3006-002	NB99845 / Quest // Quest		
C1-4	MW11S3006-003	NB99845 / Quest // Quest		
C1-4	MW11S3006-004	NB99845 / Quest // Quest		
C1-4	MW11S3006-005	NB99845 / Quest // Quest		
C1-4	MW11S3006-006	NB99845 / Quest // Quest		
C1-4	MW11S3006-007	NB99845 / Quest // Quest		
C1-4	MW11S3006-008	NB99845 / Quest // Quest		
C1-4	MW11S3006-009	NB99845 / Quest // Quest		
C1-4	MW11S3006-010	NB99845 / Quest // Quest		
C1-4	MW11S3006-011	NB99845 / Quest // Quest		
C1-4	MW11S3006-012	NB99845 / Quest // Quest		
C1-4	MW11S3006-013	NB99845 / Quest // Quest		
C1-4	MW11S3006-014	NB99845 / Quest // Quest	50	25
C1-4	MW11S3006-015	NB99845 / Quest // Quest		
C1-4	MW11S3006-016	NB99845 / Quest // Quest		
C1-5	MW11S3007-001	NB99845 / Quest // F4HR 44-3		
C1-5	MW11S3007-002	NB99845 / Quest // F4HR 44-3		
C1-5	MW11S3007-003	NB99845 / Quest // F4HR 44-3		
C1-5	MW11S3007-004	NB99845 / Quest // F4HR 44-3		
C1-5	MW11S3007-005	NB99845 / Quest // F4HR 44-3		
C1-5	MW11S3007-006	NB99845 / Quest // F4HR 44-3		
C1-5	MW11S3007-007	NB99845 / Quest // F4HR 44-3		
C1-5	MW11S3007-008	NB99845 / Quest // F4HR 44-3		
C1-5	MW11S3007-009	NB99845 / Quest // F4HR 44-3	50	25
C1-5	MW11S3007-010	NB99845 / Quest // F4HR 44-3		
C1-5	MW11S3007-011	NB99845 / Quest // F4HR 44-3		
C1-5	MW11S3007-012	NB99845 / Quest // F4HR 44-3		

C1-5	MW11S3007-013	NB99845 / Quest // F4HR 44-3				
C1-5	MW11S3007-014	NB99845 / Quest // F4HR 44-3				
C1-5	MW11S3007-015	NB99845 / Quest // F4HR 44-3				
C1-5	MW11S3007-016	NB99845 / Quest // F4HR 44-3				
C1-6	MW11S3008-001	NB99845 / Quest // M135				
C1-6	MW11S3008-002	NB99845 / Quest // M135				
C1-6	MW11S3008-003	NB99845 / Quest // M135				
C1-6	MW11S3008-004	NB99845 / Quest // M135				
C1-6	MW11S3008-005	NB99845 / Quest // M135				
C1-6	MW11S3008-006	NB99845 / Quest // M135		100		
C1-6	MW11S3008-007	NB99845 / Quest // M135				
C1-6	MW11S3008-008	NB99845 / Quest // M135				
C1-6	MW11S3008-009	NB99845 / Quest // M135				
C1-6	MW11S3008-010	NB99845 / Quest // M135				
C1-6	MW11S3008-011	NB99845 / Quest // M135			50	
C1-6	MW11S3008-012	NB99845 / Quest // M135				
C1-6	MW11S3008-013	NB99845 / Quest // M135				
C1-6	MW11S3008-014	NB99845 / Quest // M135				
C1-6	MW11S3008-015	NB99845 / Quest // M135				
C1-6	MW11S3008-016	NB99845 / Quest // M135		100		
C1-7	MW11S3009-001	NB99845 / Quest // Misc seg 3-A				
C1-7	MW11S3009-002	NB99845 / Quest // Misc seg 3-A				
C1-7	MW11S3009-003	NB99845 / Quest // Misc seg 3-A	100			
C1-7	MW11S3009-004	NB99845 / Quest // Misc seg 3-A				
C1-7	MW11S3009-005	NB99845 / Quest // Misc seg 3-A				
C1-7	MW11S3009-006	NB99845 / Quest // Misc seg 3-A	50/100	50/100		
C1-7	MW11S3009-007	NB99845 / Quest // Misc seg 3-A				
C1-7	MW11S3009-008	NB99845 / Quest // Misc seg 3-A			50	25
C1-7	MW11S3009-009	NB99845 / Quest // Misc seg 3-A		50/100		25
C1-7	MW11S3009-010	NB99845 / Quest // Misc seg 3-A		50/100		
C1-7	MW11S3009-011	NB99845 / Quest // Misc seg 3-A	50/100			25
C1-7	MW11S3009-012	NB99845 / Quest // Misc seg 3-A				
C1-7	MW11S3009-013	NB99845 / Quest // Misc seg 3-A	50/100	50/100		25
C1-7	MW11S3009-014	NB99845 / Quest // Misc seg 3-A				
C1-7	MW11S3009-015	NB99845 / Quest // Misc seg 3-A	50/100	50/100	50	
C1-7	MW11S3009-016	NB99845 / Quest // Misc seg 3-A	50/100	50/100		25
C1-8	MW11S3010-001	NB99845 / Quest // Quest				
C1-8	MW11S3010-002	NB99845 / Quest // Quest				
C1-8	MW11S3010-003	NB99845 / Quest // Quest				
C1-8	MW11S3010-004	NB99845 / Quest // Quest				
C1-8	MW11S3010-005	NB99845 / Quest // Quest			50	25
C1-8	MW11S3010-006	NB99845 / Quest // Quest				
C1-8	MW11S3010-007	NB99845 / Quest // Quest				
C1-8	MW11S3010-008	NB99845 / Quest // Quest				
C1-8	MW11S3010-009	NB99845 / Quest // Quest			50	25

C1-8	MW11S3010-010	NB99845 / Quest // Quest				
C1-8	MW11S3010-011	NB99845 / Quest // Quest				
C1-8	MW11S3010-012	NB99845 / Quest // Quest				
C1-8	MW11S3010-013	NB99845 / Quest // Quest				
C1-8	MW11S3010-014	NB99845 / Quest // Quest			50	25
C1-8	MW11S3010-015	NB99845 / Quest // Quest				
C1-8	MW11S3010-016	NB99845 / Quest // Quest				
C1-9	MW11S3011-001	OR72 / Rasmusson // M115				
C1-9	MW11S3011-002	OR72 / Rasmusson // M115				
C1-9	MW11S3011-003	OR72 / Rasmusson // M115				
C1-9	MW11S3011-004	OR72 / Rasmusson // M115				
C1-9	MW11S3011-005	OR72 / Rasmusson // M115				
C1-9	MW11S3011-006	OR72 / Rasmusson // M115				
C1-9	MW11S3011-007	OR72 / Rasmusson // M115				
C1-9	MW11S3011-008	OR72 / Rasmusson // M115				
C1-9	MW11S3011-009	OR72 / Rasmusson // M115				
C1-9	MW11S3011-010	OR72 / Rasmusson // M115				
C1-9	MW11S3011-011	OR72 / Rasmusson // M115				
C1-9	MW11S3011-012	OR72 / Rasmusson // M115				
C1-9	MW11S3011-013	OR72 / Rasmusson // M115				
C1-9	MW11S3011-014	OR72 / Rasmusson // M115				
C1-9	MW11S3011-015	OR72 / Rasmusson // M115				
C1-9	MW11S3011-016	OR72 / Rasmusson // M115				
C1-10	MW11S3016-001	OR72 / FEG183-28 // S47/E//S47-37		100		
C1-10	MW11S3016-002	OR72 / FEG183-28 // S47/E//S47-37	100			
C1-10	MW11S3016-003	OR72 / FEG183-28 // S47/E//S47-37	50/100	50/100		
C1-10	MW11S3016-004	OR72 / FEG183-28 // S47/E//S47-37		100		
C1-10	MW11S3016-005	OR72 / FEG183-28 // S47/E//S47-37				
C1-10	MW11S3016-006	OR72 / FEG183-28 // S47/E//S47-37				
C1-10	MW11S3016-007	OR72 / FEG183-28 // S47/E//S47-37				
C1-10	MW11S3016-008	OR72 / FEG183-28 // S47/E//S47-37		100		
C1-10	MW11S3016-009	OR72 / FEG183-28 // S47/E//S47-37				
C1-10	MW11S3016-010	OR72 / FEG183-28 // S47/E//S47-37				
C1-10	MW11S3016-011	OR72 / FEG183-28 // S47/E//S47-37	50/100		50	25
C1-10	MW11S3016-012	OR72 / FEG183-28 // S47/E//S47-37				
C1-10	MW11S3016-013	OR72 / FEG183-28 // S47/E//S47-37				
C1-10	MW11S3016-014	OR72 / FEG183-28 // S47/E//S47-37	50/100	50/100		25
C1-10	MW11S3016-015	OR72 / FEG183-28 // S47/E//S47-37		50/100		25
C1-10	MW11S3016-016	OR72 / FEG183-28 // S47/E//S47-37				
C1-11	MW11S3019-001	OR72 / FEG183-28 // Stab 47/Kab 51-9				
C1-11	MW11S3019-002	OR72 / FEG183-28 // Stab 47/Kab 51-9				
C1-11	MW11S3019-003	OR72 / FEG183-28 // Stab 47/Kab 51-9				
C1-11	MW11S3019-004	OR72 / FEG183-28 // Stab 47/Kab 51-9	50/100			25
C1-11	MW11S3019-005	OR72 / FEG183-28 // Stab 47/Kab 51-9		100		

C1-11	MW11S3019-006	OR72 / FEG183-28 // Stab 47/Kab 51-9				
C1-11	MW11S3019-007	OR72 / FEG183-28 // Stab 47/Kab 51-9	50/100		50	25
C1-11	MW11S3019-008	OR72 / FEG183-28 // Stab 47/Kab 51-9	50/100			25
C1-11	MW11S3019-009	OR72 / FEG183-28 // Stab 47/Kab 51-9	100			
C1-11	MW11S3019-010	OR72 / FEG183-28 // Stab 47/Kab 51-9				
C1-11	MW11S3019-011	OR72 / FEG183-28 // Stab 47/Kab 51-9	50/100	50/100		25
C1-11	MW11S3019-012	OR72 / FEG183-28 // Stab 47/Kab 51-9				
C1-11	MW11S3019-013	OR72 / FEG183-28 // Stab 47/Kab 51-9	50/100			
C1-11	MW11S3019-014	OR72 / FEG183-28 // Stab 47/Kab 51-9	50/100		50	25
C1-11	MW11S3019-015	OR72 / FEG183-28 // Stab 47/Kab 51-9				
C1-11	MW11S3019-016	OR72 / FEG183-28 // Stab 47/Kab 51-9				
C1-12	MW11S3020-001	OR72 / FEG183-28 // Stab 113/Kab 50-26	100			
C1-12	MW11S3020-002	OR72 / FEG183-28 // Stab 113/Kab 50-26	50/100			25
C1-12	MW11S3020-003	OR72 / FEG183-28 // Stab 113/Kab 50-26	100			
C1-12	MW11S3020-004	OR72 / FEG183-28 // Stab 113/Kab 50-26				
C1-12	MW11S3020-005	OR72 / FEG183-28 // Stab 113/Kab 50-26				
C1-12	MW11S3020-006	OR72 / FEG183-28 // Stab 113/Kab 50-26				
C1-12	MW11S3020-007	OR72 / FEG183-28 // Stab 113/Kab 50-26				
C1-12	MW11S3020-008	OR72 / FEG183-28 // Stab 113/Kab 50-26				
C1-12	MW11S3020-009	OR72 / FEG183-28 // Stab 113/Kab 50-26			50	
C1-12	MW11S3020-010	OR72 / FEG183-28 // Stab 113/Kab 50-26	100			
C1-12	MW11S3020-011	OR72 / FEG183-28 // Stab 113/Kab 50-26				
C1-12	MW11S3020-012	OR72 / FEG183-28 // Stab 113/Kab 50-26	100	100		
C1-12	MW11S3020-013	OR72 / FEG183-28 // Stab 113/Kab 50-26				
C1-12	MW11S3020-014	OR72 / FEG183-28 // Stab 113/Kab 50-26				
C1-12	MW11S3020-015	OR72 / FEG183-28 // Stab 113/Kab 50-26			50	
C1-12	MW11S3020-016	OR72 / FEG183-28 // Stab 113/Kab 50-26				
C1-13	MW11S3023-001	OR76 / M115 // StabBC 50-7-2				
C1-13	MW11S3023-002	OR76 / M115 // StabBC 50-7-2				
C1-13	MW11S3023-003	OR76 / M115 // StabBC 50-7-2				
C1-13	MW11S3023-004	OR76 / M115 // StabBC 50-7-2				
C1-13	MW11S3023-005	OR76 / M115 // StabBC 50-7-2			50	
C1-13	MW11S3023-006	OR76 / M115 // StabBC 50-7-2				
C1-13	MW11S3023-007	OR76 / M115 // StabBC 50-7-2				
C1-13	MW11S3023-008	OR76 / M115 // StabBC 50-7-2				
C1-13	MW11S3023-009	OR76 / M115 // StabBC 50-7-2				
C1-13	MW11S3023-010	OR76 / M115 // StabBC 50-7-2				
C1-13	MW11S3023-011	OR76 / M115 // StabBC 50-7-2				
C1-13	MW11S3023-012	OR76 / M115 // StabBC 50-7-2				
C1-13	MW11S3023-013	OR76 / M115 // StabBC 50-7-2				
C1-13	MW11S3023-014	OR76 / M115 // StabBC 50-7-2				
C1-13	MW11S3023-015	OR76 / M115 // StabBC 50-7-2				
C1-13	MW11S3023-016	OR76 / M115 // StabBC 50-7-2				
C1-14	MW11S3024-001	OR76 / M115 // K51/L//K51-10		100		
C1-14	MW11S3024-002	OR76 / M115 // K51/L//K51-10				

C1-14	MW11S3024-003	OR76 / M115 // K51/L//K51-10				
C1-14	MW11S3024-004	OR76 / M115 // K51/L//K51-10		100	50	25
C1-14	MW11S3024-005	OR76 / M115 // K51/L//K51-10		100		
C1-14	MW11S3024-006	OR76 / M115 // K51/L//K51-10		100		
C1-14	MW11S3024-007	OR76 / M115 // K51/L//K51-10				
C1-14	MW11S3024-008	OR76 / M115 // K51/L//K51-10				
C1-14	MW11S3024-009	OR76 / M115 // K51/L//K51-10				
C1-14	MW11S3024-010	OR76 / M115 // K51/L//K51-10				
C1-14	MW11S3024-011	OR76 / M115 // K51/L//K51-10		100		
C1-14	MW11S3024-012	OR76 / M115 // K51/L//K51-10	100	100		
C1-14	MW11S3024-013	OR76 / M115 // K51/L//K51-10				
C1-14	MW11S3024-014	OR76 / M115 // K51/L//K51-10				
C1-14	MW11S3024-015	OR76 / M115 // K51/L//K51-10		100	50	
C1-14	MW11S3024-016	OR76 / M115 // K51/L//K51-10		100		
C1-15	MW11S3025-001	Stab 113 // OR76 / M115	50/100	50/100		25
C1-15	MW11S3025-002	Stab 113 // OR76 / M115		100		
C1-15	MW11S3025-003	Stab 113 // OR76 / M115				
C1-15	MW11S3025-004	Stab 113 // OR76 / M115				
C1-15	MW11S3025-005	Stab 113 // OR76 / M115				
C1-15	MW11S3025-006	Stab 113 // OR76 / M115				
C1-15	MW11S3025-007	Stab 113 // OR76 / M115	100			
C1-15	MW11S3025-008	Stab 113 // OR76 / M115	100			
C1-15	MW11S3025-009	Stab 113 // OR76 / M115	50/100			25
C1-15	MW11S3025-010	Stab 113 // OR76 / M115		100		
C1-15	MW11S3025-011	Stab 113 // OR76 / M115				
C1-15	MW11S3025-012	Stab 113 // OR76 / M115	100			
C1-15	MW11S3025-013	Stab 113 // OR76 / M115				
C1-15	MW11S3025-014	Stab 113 // OR76 / M115				
C1-15	MW11S3025-015	Stab 113 // OR76 / M115	50/100	50/100		25
C1-15	MW11S3025-016	Stab 113 // OR76 / M115				
C1-16	MW11S3026-001	Stab 47/Kab 51-27 // OR76 / M115				
C1-16	MW11S3026-002	Stab 47/Kab 51-27 // OR76 / M115				
C1-16	MW11S3026-003	Stab 47/Kab 51-27 // OR76 / M115				
C1-16	MW11S3026-004	Stab 47/Kab 51-27 // OR76 / M115				
C1-16	MW11S3026-005	Stab 47/Kab 51-27 // OR76 / M115				
C1-16	MW11S3026-006	Stab 47/Kab 51-27 // OR76 / M115				
C1-16	MW11S3026-007	Stab 47/Kab 51-27 // OR76 / M115	50/100			
C1-16	MW11S3026-008	Stab 47/Kab 51-27 // OR76 / M115				
C1-16	MW11S3026-009	Stab 47/Kab 51-27 // OR76 / M115				
C1-16	MW11S3026-010	Stab 47/Kab 51-27 // OR76 / M115				
C1-16	MW11S3026-011	Stab 47/Kab 51-27 // OR76 / M115				
C1-16	MW11S3026-012	Stab 47/Kab 51-27 // OR76 / M115	50/100			25
C1-16	MW11S3026-013	Stab 47/Kab 51-27 // OR76 / M115		50/100		25
C1-16	MW11S3026-014	Stab 47/Kab 51-27 // OR76 / M115	50/100			
C1-16	MW11S3026-015	Stab 47/Kab 51-27 // OR76 / M115				

C1-16	MW11S3026-016	Stab 47/Kab 51-27 // OR76 / M115		100	50	25
C1-17	MW11S3028-001	Stab 47/Kab 51-27 // OR72 / FEG183-28				
C1-17	MW11S3028-002	Stab 47/Kab 51-27 // OR72 / FEG183-28				
C1-17	MW11S3028-003	Stab 47/Kab 51-27 // OR72 / FEG183-28				
C1-17	MW11S3028-004	Stab 47/Kab 51-27 // OR72 / FEG183-28				
C1-17	MW11S3028-005	Stab 47/Kab 51-27 // OR72 / FEG183-28				
C1-17	MW11S3028-006	Stab 47/Kab 51-27 // OR72 / FEG183-28				
C1-17	MW11S3028-007	Stab 47/Kab 51-27 // OR72 / FEG183-28				
C1-17	MW11S3028-008	Stab 47/Kab 51-27 // OR72 / FEG183-28				
C1-17	MW11S3028-009	Stab 47/Kab 51-27 // OR72 / FEG183-28				
C1-17	MW11S3028-010	Stab 47/Kab 51-27 // OR72 / FEG183-28		50/100		
C1-17	MW11S3028-011	Stab 47/Kab 51-27 // OR72 / FEG183-28				
C1-17	MW11S3028-012	Stab 47/Kab 51-27 // OR72 / FEG183-28				
C1-17	MW11S3028-013	Stab 47/Kab 51-27 // OR72 / FEG183-28				
C1-17	MW11S3028-014	Stab 47/Kab 51-27 // OR72 / FEG183-28				
C1-17	MW11S3028-015	Stab 47/Kab 51-27 // OR72 / FEG183-28				
C1-17	MW11S3028-016	Stab 47/Kab 51-27 // OR72 / FEG183-28				
C1-18	MW11S3029-001	Stab 113/Kab 50-26 // OR72 / FEG183-28				
C1-18	MW11S3029-002	Stab 113/Kab 50-26 // OR72 / FEG183-28	100			
C1-18	MW11S3029-003	Stab 113/Kab 50-26 // OR72 / FEG183-28	50/100			25
C1-18	MW11S3029-004	Stab 113/Kab 50-26 // OR72 / FEG183-28				
C1-18	MW11S3029-005	Stab 113/Kab 50-26 // OR72 / FEG183-28				
C1-18	MW11S3029-006	Stab 113/Kab 50-26 // OR72 / FEG183-28		100		
C1-18	MW11S3029-007	Stab 113/Kab 50-26 // OR72 / FEG183-28		100		
C1-18	MW11S3029-008	Stab 113/Kab 50-26 // OR72 / FEG183-28				
C1-18	MW11S3029-009	Stab 113/Kab 50-26 // OR72 / FEG183-28				
C1-18	MW11S3029-010	Stab 113/Kab 50-26 // OR72 / FEG183-28		100		
C1-18	MW11S3029-011	Stab 113/Kab 50-26 // OR72 / FEG183-28		50/100		25
C1-18	MW11S3029-012	Stab 113/Kab 50-26 // OR72 / FEG183-28	50/100			
C1-18	MW11S3029-013	Stab 113/Kab 50-26 // OR72 / FEG183-28	50/100			
C1-18	MW11S3029-014	Stab 113/Kab 50-26 // OR72 / FEG183-28				
C1-18	MW11S3029-015	Stab 113/Kab 50-26 // OR72 / FEG183-28				
C1-18	MW11S3029-016	Stab 113/Kab 50-26 // OR72 / FEG183-28	50/100			25
C1-19	MW11S3030-001	K51/L//K51-10 // OR72 / FEG183-28				
C1-19	MW11S3030-002	K51/L//K51-10 // OR72 / FEG183-28		100		
C1-19	MW11S3030-003	K51/L//K51-10 // OR72 / FEG183-28		100		
C1-19	MW11S3030-004	K51/L//K51-10 // OR72 / FEG183-28		100		
C1-19	MW11S3030-005	K51/L//K51-10 // OR72 / FEG183-28		100		
C1-19	MW11S3030-006	K51/L//K51-10 // OR72 / FEG183-28		100		
C1-19	MW11S3030-007	K51/L//K51-10 // OR72 / FEG183-28				
C1-19	MW11S3030-008	K51/L//K51-10 // OR72 / FEG183-28		50/100		
C1-19	MW11S3030-009	K51/L//K51-10 // OR72 / FEG183-28		100		
C1-19	MW11S3030-010	K51/L//K51-10 // OR72 / FEG183-28	50/100			
C1-19	MW11S3030-011	K51/L//K51-10 // OR72 / FEG183-28				
C1-19	MW11S3030-012	K51/L//K51-10 // OR72 / FEG183-28	50/100	50/100		25

C1-19	MW11S3030-013	K51/L//K51-10 // OR72 / FEG183-28		100		
C1-19	MW11S3030-014	K51/L//K51-10 // OR72 / FEG183-28		50/100		25
C1-19	MW11S3030-015	K51/L//K51-10 // OR72 / FEG183-28		50/100		25
C1-19	MW11S3030-016	K51/L//K51-10 // OR72 / FEG183-28		100		
C1-20	MW11S3031-001	K51/E//K51-16 // 88ab536 / Rasmusson				
C1-20	MW11S3031-002	K51/E//K51-16 // 88ab536 / Rasmusson			50	25
C1-20	MW11S3031-003	K51/E//K51-16 // 88ab536 / Rasmusson				
C1-20	MW11S3031-004	K51/E//K51-16 // 88ab536 / Rasmusson				
C1-20	MW11S3031-005	K51/E//K51-16 // 88ab536 / Rasmusson				
C1-20	MW11S3031-006	K51/E//K51-16 // 88ab536 / Rasmusson				
C1-20	MW11S3031-007	K51/E//K51-16 // 88ab536 / Rasmusson				
C1-20	MW11S3031-008	K51/E//K51-16 // 88ab536 / Rasmusson				
C1-20	MW11S3031-009	K51/E//K51-16 // 88ab536 / Rasmusson			50	
C1-20	MW11S3031-010	K51/E//K51-16 // 88ab536 / Rasmusson				
C1-20	MW11S3031-011	K51/E//K51-16 // 88ab536 / Rasmusson				
C1-20	MW11S3031-012	K51/E//K51-16 // 88ab536 / Rasmusson			50	
C1-20	MW11S3031-013	K51/E//K51-16 // 88ab536 / Rasmusson				
C1-20	MW11S3031-014	K51/E//K51-16 // 88ab536 / Rasmusson				
C1-20	MW11S3031-015	K51/E//K51-16 // 88ab536 / Rasmusson				
C1-20	MW11S3031-016	K51/E//K51-16 // 88ab536 / Rasmusson				
C1-21	MW11S3032-001	S113/E//K51-15 // 88ab536 / Rasmusson				
C1-21	MW11S3032-002	S113/E//K51-15 // 88ab536 / Rasmusson				
C1-21	MW11S3032-003	S113/E//K51-15 // 88ab536 / Rasmusson				
C1-21	MW11S3032-004	S113/E//K51-15 // 88ab536 / Rasmusson				
C1-21	MW11S3032-005	S113/E//K51-15 // 88ab536 / Rasmusson				
C1-21	MW11S3032-006	S113/E//K51-15 // 88ab536 / Rasmusson				
C1-21	MW11S3032-007	S113/E//K51-15 // 88ab536 / Rasmusson				
C1-21	MW11S3032-008	S113/E//K51-15 // 88ab536 / Rasmusson				
C1-21	MW11S3032-009	S113/E//K51-15 // 88ab536 / Rasmusson				
C1-21	MW11S3032-010	S113/E//K51-15 // 88ab536 / Rasmusson				
C1-21	MW11S3032-011	S113/E//K51-15 // 88ab536 / Rasmusson				
C1-21	MW11S3032-012	S113/E//K51-15 // 88ab536 / Rasmusson				
C1-21	MW11S3032-013	S113/E//K51-15 // 88ab536 / Rasmusson				
C1-21	MW11S3032-014	S113/E//K51-15 // 88ab536 / Rasmusson				
C1-21	MW11S3032-015	S113/E//K51-15 // 88ab536 / Rasmusson				
C1-21	MW11S3032-016	S113/E//K51-15 // 88ab536 / Rasmusson				
C1-22	MW11S3033-001	S47/E//S47-40 // OR72 / FEG183-28		100		
C1-22	MW11S3033-002	S47/E//S47-40 // OR72 / FEG183-28	50/100	50/100	50	25
C1-22	MW11S3033-003	S47/E//S47-40 // OR72 / FEG183-28				
C1-22	MW11S3033-004	S47/E//S47-40 // OR72 / FEG183-28		50/100		
C1-22	MW11S3033-005	S47/E//S47-40 // OR72 / FEG183-28			50	25
C1-22	MW11S3033-006	S47/E//S47-40 // OR72 / FEG183-28		100		
C1-22	MW11S3033-007	S47/E//S47-40 // OR72 / FEG183-28		100		
C1-22	MW11S3033-008	S47/E//S47-40 // OR72 / FEG183-28		100		
C1-22	MW11S3033-009	S47/E//S47-40 // OR72 / FEG183-28		50/100		

C1-22	MW11S3033-010	S47/E//S47-40 // OR72 / FEG183-28	50/100	50/100		25
C1-22	MW11S3033-011	S47/E//S47-40 // OR72 / FEG183-28		50/100		25
C1-22	MW11S3033-012	S47/E//S47-40 // OR72 / FEG183-28				
C1-22	MW11S3033-013	S47/E//S47-40 // OR72 / FEG183-28		50/100		
C1-22	MW11S3033-014	S47/E//S47-40 // OR72 / FEG183-28			50	
C1-22	MW11S3033-015	S47/E//S47-40 // OR72 / FEG183-28		100		
C1-22	MW11S3033-016	S47/E//S47-40 // OR72 / FEG183-28	100	100		
C1-23	MW11S3034-001	Misc seg 3-D // 88ab536 / Rasmusson				
C1-23	MW11S3034-002	Misc seg 3-D // 88ab536 / Rasmusson				
C1-23	MW11S3034-003	Misc seg 3-D // 88ab536 / Rasmusson	100			
C1-23	MW11S3034-004	Misc seg 3-D // 88ab536 / Rasmusson				
C1-23	MW11S3034-005	Misc seg 3-D // 88ab536 / Rasmusson	100	100		
C1-23	MW11S3034-006	Misc seg 3-D // 88ab536 / Rasmusson		50/100		25
C1-23	MW11S3034-007	Misc seg 3-D // 88ab536 / Rasmusson				
C1-23	MW11S3034-008	Misc seg 3-D // 88ab536 / Rasmusson		50/100		
C1-23	MW11S3034-009	Misc seg 3-D // 88ab536 / Rasmusson				
C1-23	MW11S3034-010	Misc seg 3-D // 88ab536 / Rasmusson		50/100		
C1-23	MW11S3034-011	Misc seg 3-D // 88ab536 / Rasmusson		50/100		25
C1-23	MW11S3034-012	Misc seg 3-D // 88ab536 / Rasmusson				
C1-23	MW11S3034-013	Misc seg 3-D // 88ab536 / Rasmusson				
C1-23	MW11S3034-014	Misc seg 3-D // 88ab536 / Rasmusson				
C1-23	MW11S3034-015	Misc seg 3-D // 88ab536 / Rasmusson				
C1-23	MW11S3034-016	Misc seg 3-D // 88ab536 / Rasmusson				
C1-24	MW11S3035-001	Misc seg 3-E // OR72 / FEG183-28	50/100			
C1-24	MW11S3035-002	Misc seg 3-E // OR72 / FEG183-28				
C1-24	MW11S3035-003	Misc seg 3-E // OR72 / FEG183-28				
C1-24	MW11S3035-004	Misc seg 3-E // OR72 / FEG183-28				
C1-24	MW11S3035-005	Misc seg 3-E // OR72 / FEG183-28				
C1-24	MW11S3035-006	Misc seg 3-E // OR72 / FEG183-28	100			
C1-24	MW11S3035-007	Misc seg 3-E // OR72 / FEG183-28				
C1-24	MW11S3035-008	Misc seg 3-E // OR72 / FEG183-28	50/100			25
C1-24	MW11S3035-009	Misc seg 3-E // OR72 / FEG183-28				
C1-24	MW11S3035-010	Misc seg 3-E // OR72 / FEG183-28	100	100		
C1-24	MW11S3035-011	Misc seg 3-E // OR72 / FEG183-28				
C1-24	MW11S3035-012	Misc seg 3-E // OR72 / FEG183-28	100			
C1-24	MW11S3035-013	Misc seg 3-E // OR72 / FEG183-28	100			
C1-24	MW11S3035-014	Misc seg 3-E // OR72 / FEG183-28				
C1-24	MW11S3035-015	Misc seg 3-E // OR72 / FEG183-28	50/100			25
C1-24	MW11S3035-016	Misc seg 3-E // OR72 / FEG183-28		50/100		25
C1-25	MW11S3036-001	F4HR 35-12 // OR76 / M115				
C1-25	MW11S3036-002	F4HR 35-12 // OR76 / M115				
C1-25	MW11S3036-003	F4HR 35-12 // OR76 / M115		50/100		
C1-25	MW11S3036-004	F4HR 35-12 // OR76 / M115	50/100			
C1-25	MW11S3036-005	F4HR 35-12 // OR76 / M115				
C1-25	MW11S3036-006	F4HR 35-12 // OR76 / M115	50/100			25

C1-25	MW11S3036-007	F4HR 35-12 // OR76 / M115	50/100	50/100		25
C1-25	MW11S3036-008	F4HR 35-12 // OR76 / M115				
C1-25	MW11S3036-009	F4HR 35-12 // OR76 / M115				
C1-25	MW11S3036-010	F4HR 35-12 // OR76 / M115	100			
C1-25	MW11S3036-011	F4HR 35-12 // OR76 / M115				
C1-25	MW11S3036-012	F4HR 35-12 // OR76 / M115				
C1-25	MW11S3036-013	F4HR 35-12 // OR76 / M115	50/100	50/100		25
C1-25	MW11S3036-014	F4HR 35-12 // OR76 / M115				
C1-25	MW11S3036-015	F4HR 35-12 // OR76 / M115				
C1-25	MW11S3036-016	F4HR 35-12 // OR76 / M115	100			
C1-26	MW11S3037-001	F4HR 44-1 // NB99845 / Quest		100		
C1-26	MW11S3037-002	F4HR 44-1 // NB99845 / Quest		100	50	25
C1-26	MW11S3037-003	F4HR 44-1 // NB99845 / Quest		50/100		25
C1-26	MW11S3037-004	F4HR 44-1 // NB99845 / Quest		50/100		
C1-26	MW11S3037-005	F4HR 44-1 // NB99845 / Quest		50/100		
C1-26	MW11S3037-006	F4HR 44-1 // NB99845 / Quest				
C1-26	MW11S3037-007	F4HR 44-1 // NB99845 / Quest		50/100		25
C1-26	MW11S3037-008	F4HR 44-1 // NB99845 / Quest				
C1-26	MW11S3037-009	F4HR 44-1 // NB99845 / Quest				
C1-26	MW11S3037-010	F4HR 44-1 // NB99845 / Quest		50/100		25
C1-26	MW11S3037-011	F4HR 44-1 // NB99845 / Quest		50/100		
C1-26	MW11S3037-012	F4HR 44-1 // NB99845 / Quest				
C1-26	MW11S3037-013	F4HR 44-1 // NB99845 / Quest				
C1-26	MW11S3037-014	F4HR 44-1 // NB99845 / Quest		50/100		25
C1-26	MW11S3037-015	F4HR 44-1 // NB99845 / Quest		100		
C1-26	MW11S3037-016	F4HR 44-1 // NB99845 / Quest				
C1-27	MW11S3038-001	F4HR 70-1 // OR72 / FEG183-28				
C1-27	MW11S3038-002	F4HR 70-1 // OR72 / FEG183-28	100			
C1-27	MW11S3038-003	F4HR 70-1 // OR72 / FEG183-28	100			
C1-27	MW11S3038-004	F4HR 70-1 // OR72 / FEG183-28				
C1-27	MW11S3038-005	F4HR 70-1 // OR72 / FEG183-28	50/100			
C1-27	MW11S3038-006	F4HR 70-1 // OR72 / FEG183-28				
C1-27	MW11S3038-007	F4HR 70-1 // OR72 / FEG183-28				
C1-27	MW11S3038-008	F4HR 70-1 // OR72 / FEG183-28	100			
C1-27	MW11S3038-009	F4HR 70-1 // OR72 / FEG183-28	50/100			25
C1-27	MW11S3038-010	F4HR 70-1 // OR72 / FEG183-28	50/100			
C1-27	MW11S3038-011	F4HR 70-1 // OR72 / FEG183-28	50/100			25
C1-27	MW11S3038-012	F4HR 70-1 // OR72 / FEG183-28	100			
C1-27	MW11S3038-013	F4HR 70-1 // OR72 / FEG183-28	50/100			25
C1-27	MW11S3038-014	F4HR 70-1 // OR72 / FEG183-28				
C1-27	MW11S3038-015	F4HR 70-1 // OR72 / FEG183-28			50	
C1-27	MW11S3038-016	F4HR 70-1 // OR72 / FEG183-28	50/100			
C1-28	MW11S3039-001	F4HR 86-3 // OR72 / FEG183-28				
C1-28	MW11S3039-002	F4HR 86-3 // OR72 / FEG183-28	50/100			25
C1-28	MW11S3039-003	F4HR 86-3 // OR72 / FEG183-28				

C1-28	MW11S3039-004	F4HR 86-3 // OR72 / FEG183-28			50	
C1-28	MW11S3039-005	F4HR 86-3 // OR72 / FEG183-28	100			
C1-28	MW11S3039-006	F4HR 86-3 // OR72 / FEG183-28				
C1-28	MW11S3039-007	F4HR 86-3 // OR72 / FEG183-28		100		
C1-28	MW11S3039-008	F4HR 86-3 // OR72 / FEG183-28				
C1-28	MW11S3039-009	F4HR 86-3 // OR72 / FEG183-28				
C1-28	MW11S3039-010	F4HR 86-3 // OR72 / FEG183-28				
C1-28	MW11S3039-011	F4HR 86-3 // OR72 / FEG183-28	50/100			25
C1-28	MW11S3039-012	F4HR 86-3 // OR72 / FEG183-28	100			
C1-28	MW11S3039-013	F4HR 86-3 // OR72 / FEG183-28	50/100	50/100		
C1-28	MW11S3039-014	F4HR 86-3 // OR72 / FEG183-28				
C1-28	MW11S3039-015	F4HR 86-3 // OR72 / FEG183-28	50/100			25
C1-28	MW11S3039-016	F4HR 86-3 // OR72 / FEG183-28	50/100			
C1-29	MW11S3041-001	NB03437 / M115				
C1-29	MW11S3041-002	NB03437 / M115			50	
C1-29	MW11S3041-003	NB03437 / M115				
C1-29	MW11S3041-004	NB03437 / M115				
C1-29	MW11S3041-005	NB03437 / M115				
C1-29	MW11S3041-006	NB03437 / M115				
C1-29	MW11S3041-007	NB03437 / M115				
C1-29	MW11S3041-008	NB03437 / M115				
C1-29	MW11S3041-009	NB03437 / M115				
C1-29	MW11S3041-010	NB03437 / M115				
C1-29	MW11S3041-011	NB03437 / M115			50	
C1-29	MW11S3041-012	NB03437 / M115				
C1-29	MW11S3041-013	NB03437 / M115				
C1-29	MW11S3041-014	NB03437 / M115				
C1-29	MW11S3041-015	NB03437 / M115				
C1-29	MW11S3041-016	NB03437 / M115				
C1-30	MW11S3042-001	Misc seg 4-C / M115				
C1-30	MW11S3042-002	Misc seg 4-C / M115				
C1-30	MW11S3042-003	Misc seg 4-C / M115				
C1-30	MW11S3042-004	Misc seg 4-C / M115				
C1-30	MW11S3042-005	Misc seg 4-C / M115				
C1-30	MW11S3042-006	Misc seg 4-C / M115			50	25
C1-30	MW11S3042-007	Misc seg 4-C / M115				
C1-30	MW11S3042-008	Misc seg 4-C / M115				
C1-30	MW11S3042-009	Misc seg 4-C / M115				
C1-30	MW11S3042-010	Misc seg 4-C / M115				
C1-30	MW11S3042-011	Misc seg 4-C / M115				
C1-30	MW11S3042-012	Misc seg 4-C / M115				
C1-30	MW11S3042-013	Misc seg 4-C / M115				
C1-30	MW11S3042-014	Misc seg 4-C / M115				
C1-30	MW11S3042-015	Misc seg 4-C / M115				
C1-30	MW11S3042-016	Misc seg 4-C / M115				

C1-31	MW11S3045-001	Rasmusson / NB03437			
C1-31	MW11S3045-002	Rasmusson / NB03437			
C1-31	MW11S3045-003	Rasmusson / NB03437			
C1-31	MW11S3045-004	Rasmusson / NB03437			
C1-31	MW11S3045-005	Rasmusson / NB03437			
C1-31	MW11S3045-006	Rasmusson / NB03437			
C1-31	MW11S3045-007	Rasmusson / NB03437			
C1-31	MW11S3045-008	Rasmusson / NB03437			
C1-31	MW11S3045-009	Rasmusson / NB03437			
C1-31	MW11S3045-010	Rasmusson / NB03437			
C1-31	MW11S3045-011	Rasmusson / NB03437			
C1-31	MW11S3045-012	Rasmusson / NB03437			
C1-31	MW11S3045-013	Rasmusson / NB03437			
C1-31	MW11S3045-014	Rasmusson / NB03437			
C1-31	MW11S3045-015	Rasmusson / NB03437			
C1-31	MW11S3045-016	Rasmusson / NB03437			
C1-32	MW11S3046-001	Lacey / F5-5			
C1-32	MW11S3046-002	Lacey / F5-5			
C1-32	MW11S3046-003	Lacey / F5-5			
C1-32	MW11S3046-004	Lacey / F5-5			
C1-32	MW11S3046-005	Lacey / F5-5			
C1-32	MW11S3046-006	Lacey / F5-5			
C1-32	MW11S3046-007	Lacey / F5-5			
C1-32	MW11S3046-008	Lacey / F5-5			50
C1-32	MW11S3046-009	Lacey / F5-5			
C1-32	MW11S3046-010	Lacey / F5-5			
C1-32	MW11S3046-011	Lacey / F5-5			
C1-32	MW11S3046-012	Lacey / F5-5			
C1-32	MW11S3046-013	Lacey / F5-5			
C1-32	MW11S3046-014	Lacey / F5-5			
C1-32	MW11S3046-015	Lacey / F5-5			
C1-32	MW11S3046-016	Lacey / F5-5	100		
C1-33	MW11S3047-001	Lacey / F5-8			
C1-33	MW11S3047-002	Lacey / F5-8			
C1-33	MW11S3047-003	Lacey / F5-8			
C1-33	MW11S3047-004	Lacey / F5-8			
C1-33	MW11S3047-005	Lacey / F5-8			
C1-33	MW11S3047-006	Lacey / F5-8		10	
C1-33	MW11S3047-007	Lacey / F5-8			
C1-33	MW11S3047-008	Lacey / F5-8			
C1-33	MW11S3047-009	Lacey / F5-8			
C1-33	MW11S3047-010	Lacey / F5-8			
C1-33	MW11S3047-011	Lacey / F5-8			
C1-33	MW11S3047-012	Lacey / F5-8			
C1-33	MW11S3047-013	Lacey / F5-8			

C1-33	MW11S3047-014	Lacey / F5-8			
C1-33	MW11S3047-015	Lacey / F5-8			
C1-33	MW11S3047-016	Lacey / F5-8	100		
C1-34	MW11S3048-001	Quest / Dicktoo			
C1-34	MW11S3048-002	Quest / Dicktoo			
C1-34	MW11S3048-003	Quest / Dicktoo			
C1-34	MW11S3048-004	Quest / Dicktoo			
C1-34	MW11S3048-005	Quest / Dicktoo		50	
C1-34	MW11S3048-006	Quest / Dicktoo			
C1-34	MW11S3048-007	Quest / Dicktoo			
C1-34	MW11S3048-008	Quest / Dicktoo			
C1-34	MW11S3048-009	Quest / Dicktoo			
C1-34	MW11S3048-010	Quest / Dicktoo			
C1-34	MW11S3048-011	Quest / Dicktoo			
C1-34	MW11S3048-012	Quest / Dicktoo			
C1-34	MW11S3048-013	Quest / Dicktoo			
C1-34	MW11S3048-014	Quest / Dicktoo			
C1-34	MW11S3048-015	Quest / Dicktoo			
C1-34	MW11S3048-016	Quest / Dicktoo			
C1-35	MW11S3049-001	M135 / F5-5			
C1-35	MW11S3049-002	M135 / F5-5	100		
C1-35	MW11S3049-003	M135 / F5-5			
C1-35	MW11S3049-004	M135 / F5-5			
C1-35	MW11S3049-005	M135 / F5-5			
C1-35	MW11S3049-006	M135 / F5-5			
C1-35	MW11S3049-007	M135 / F5-5			
C1-35	MW11S3049-008	M135 / F5-5			
C1-35	MW11S3049-009	M135 / F5-5	100		
C1-35	MW11S3049-010	M135 / F5-5	50/100		25
C1-35	MW11S3049-011	M135 / F5-5			
C1-35	MW11S3049-012	M135 / F5-5			
C1-35	MW11S3049-013	M135 / F5-5			
C1-35	MW11S3049-014	M135 / F5-5		50	25
C1-35	MW11S3049-015	M135 / F5-5			
C1-35	MW11S3049-016	M135 / F5-5			
C1-36	MW11S3050-001	F4HR 83-1 / Lacey			
C1-36	MW11S3050-002	F4HR 83-1 / Lacey			
C1-36	MW11S3050-003	F4HR 83-1 / Lacey			
C1-36	MW11S3050-004	F4HR 83-1 / Lacey			
C1-36	MW11S3050-005	F4HR 83-1 / Lacey			
C1-36	MW11S3050-006	F4HR 83-1 / Lacey			
C1-36	MW11S3050-007	F4HR 83-1 / Lacey			
C1-36	MW11S3050-008	F4HR 83-1 / Lacey			
C1-36	MW11S3050-009	F4HR 83-1 / Lacey			
C1-36	MW11S3050-010	F4HR 83-1 / Lacey			

C1-36	MW11S3050-011	F4HR 83-1 / Lacey			
C1-36	MW11S3050-012	F4HR 83-1 / Lacey			
C1-36	MW11S3050-013	F4HR 83-1 / Lacey			
C1-36	MW11S3050-014	F4HR 83-1 / Lacey			
C1-36	MW11S3050-015	F4HR 83-1 / Lacey		50	25
C1-36	MW11S3050-016	F4HR 83-1 / Lacey			
C1-37	MW11S3051-001	F4HR 95-1 / M135			
C1-37	MW11S3051-002	F4HR 95-1 / M135			
C1-37	MW11S3051-003	F4HR 95-1 / M135			
C1-37	MW11S3051-004	F4HR 95-1 / M135			
C1-37	MW11S3051-005	F4HR 95-1 / M135		50	
C1-37	MW11S3051-006	F4HR 95-1 / M135			
C1-37	MW11S3051-007	F4HR 95-1 / M135			
C1-37	MW11S3051-008	F4HR 95-1 / M135			
C1-37	MW11S3051-009	F4HR 95-1 / M135			
C1-37	MW11S3051-010	F4HR 95-1 / M135			
C1-37	MW11S3051-011	F4HR 95-1 / M135			
C1-37	MW11S3051-012	F4HR 95-1 / M135			
C1-37	MW11S3051-013	F4HR 95-1 / M135			
C1-37	MW11S3051-014	F4HR 95-1 / M135			
C1-37	MW11S3051-015	F4HR 95-1 / M135			
C1-37	MW11S3051-016	F4HR 95-1 / M135			
C1-38	MW11S3052-001	OR83 / Rasmusson		50	
C1-38	MW11S3052-002	OR83 / Rasmusson			
C1-38	MW11S3052-003	OR83 / Rasmusson			
C1-38	MW11S3052-004	OR83 / Rasmusson			
C1-38	MW11S3052-005	OR83 / Rasmusson			
C1-38	MW11S3052-006	OR83 / Rasmusson			
C1-38	MW11S3052-007	OR83 / Rasmusson			
C1-38	MW11S3052-008	OR83 / Rasmusson			
C1-38	MW11S3052-009	OR83 / Rasmusson			
C1-38	MW11S3052-010	OR83 / Rasmusson			
C1-38	MW11S3052-011	OR83 / Rasmusson			
C1-38	MW11S3052-012	OR83 / Rasmusson			
C1-38	MW11S3052-013	OR83 / Rasmusson			
C1-38	MW11S3052-014	OR83 / Rasmusson			
C1-38	MW11S3052-015	OR83 / Rasmusson			
C1-38	MW11S3052-016	OR83 / Rasmusson			
C1-39	MW11S3053-001	OR83 / Quest			
C1-39	MW11S3053-002	OR83 / Quest			
C1-39	MW11S3053-003	OR83 / Quest			
C1-39	MW11S3053-004	OR83 / Quest			
C1-39	MW11S3053-005	OR83 / Quest	100		
C1-39	MW11S3053-006	OR83 / Quest			
C1-39	MW11S3053-007	OR83 / Quest			

C1-39	MW11S3053-008	OR83 / Quest			
C1-39	MW11S3053-009	OR83 / Quest			
C1-39	MW11S3053-010	OR83 / Quest		50	25
C1-39	MW11S3053-011	OR83 / Quest			
C1-39	MW11S3053-012	OR83 / Quest			
C1-39	MW11S3053-013	OR83 / Quest			
C1-39	MW11S3053-014	OR83 / Quest			
C1-39	MW11S3053-015	OR83 / Quest			
C1-39	MW11S3053-016	OR83 / Quest			
C1-40	MW11S3054-001	M115 / OR83			
C1-40	MW11S3054-002	M115 / OR83			
C1-40	MW11S3054-003	M115 / OR83			
C1-40	MW11S3054-004	M115 / OR83			
C1-40	MW11S3054-005	M115 / OR83			
C1-40	MW11S3054-006	M115 / OR83			
C1-40	MW11S3054-007	M115 / OR83			
C1-40	MW11S3054-008	M115 / OR83			
C1-40	MW11S3054-009	M115 / OR83			
C1-40	MW11S3054-010	M115 / OR83			
C1-40	MW11S3054-011	M115 / OR83			
C1-40	MW11S3054-012	M115 / OR83			
C1-40	MW11S3054-013	M115 / OR83			
C1-40	MW11S3054-014	M115 / OR83			
C1-40	MW11S3054-015	M115 / OR83			
C1-40	MW11S3054-016	M115 / OR83			
C1-41	MW11S3055-001	M115 / DH01-39			
C1-41	MW11S3055-002	M115 / DH01-39			
C1-41	MW11S3055-003	M115 / DH01-39			
C1-41	MW11S3055-004	M115 / DH01-39			
C1-41	MW11S3055-005	M115 / DH01-39			
C1-41	MW11S3055-006	M115 / DH01-39			
C1-41	MW11S3055-007	M115 / DH01-39			
C1-41	MW11S3055-008	M115 / DH01-39			
C1-41	MW11S3055-009	M115 / DH01-39			
C1-41	MW11S3055-010	M115 / DH01-39		50	
C1-41	MW11S3055-011	M115 / DH01-39			
C1-41	MW11S3055-012	M115 / DH01-39			
C1-41	MW11S3055-013	M115 / DH01-39			
C1-41	MW11S3055-014	M115 / DH01-39			
C1-41	MW11S3055-015	M115 / DH01-39			
C1-41	MW11S3055-016	M115 / DH01-39	100		
C1-42	MW11S3056-001	Quest / DH01-05			
C1-42	MW11S3056-002	Quest / DH01-05		50	
C1-42	MW11S3056-003	Quest / DH01-05			
C1-42	MW11S3056-004	Quest / DH01-05			

C1-42	MW11S3056-005	Quest / DH01-05			50	25
C1-42	MW11S3056-006	Quest / DH01-05				
C1-42	MW11S3056-007	Quest / DH01-05				
C1-42	MW11S3056-008	Quest / DH01-05				
C1-42	MW11S3056-009	Quest / DH01-05				
C1-42	MW11S3056-010	Quest / DH01-05				
C1-42	MW11S3056-011	Quest / DH01-05				
C1-42	MW11S3056-012	Quest / DH01-05				
C1-42	MW11S3056-013	Quest / DH01-05				
C1-42	MW11S3056-014	Quest / DH01-05				
C1-42	MW11S3056-015	Quest / DH01-05				
C1-42	MW11S3056-016	Quest / DH01-05			50	25
C1-43	MW11S3057-001	Quest / DH01-113				
C1-43	MW11S3057-002	Quest / DH01-113				
C1-43	MW11S3057-003	Quest / DH01-113				
C1-43	MW11S3057-004	Quest / DH01-113				
C1-43	MW11S3057-005	Quest / DH01-113				
C1-43	MW11S3057-006	Quest / DH01-113				
C1-43	MW11S3057-007	Quest / DH01-113				
C1-43	MW11S3057-008	Quest / DH01-113				
C1-43	MW11S3057-009	Quest / DH01-113				
C1-43	MW11S3057-010	Quest / DH01-113				
C1-43	MW11S3057-011	Quest / DH01-113				
C1-43	MW11S3057-012	Quest / DH01-113		100	50	25
C1-43	MW11S3057-013	Quest / DH01-113				
C1-43	MW11S3057-014	Quest / DH01-113				
C1-43	MW11S3057-015	Quest / DH01-113				
C1-43	MW11S3057-016	Quest / DH01-113				
C1-44	MW11S3060-001	S47/E//S47-37 // DH01-05	100			
C1-44	MW11S3060-002	S47/E//S47-37 // DH01-05	100	100		
C1-44	MW11S3060-003	S47/E//S47-37 // DH01-05				
C1-44	MW11S3060-004	S47/E//S47-37 // DH01-05	100	100		
C1-44	MW11S3060-005	S47/E//S47-37 // DH01-05		50/100		
C1-44	MW11S3060-006	S47/E//S47-37 // DH01-05				
C1-44	MW11S3060-007	S47/E//S47-37 // DH01-05		100		
C1-44	MW11S3060-008	S47/E//S47-37 // DH01-05		100	50	
C1-44	MW11S3060-009	S47/E//S47-37 // DH01-05		50/100		25
C1-44	MW11S3060-010	S47/E//S47-37 // DH01-05	50/100	50/100		25
C1-44	MW11S3060-011	S47/E//S47-37 // DH01-05		50/100		
C1-44	MW11S3060-012	S47/E//S47-37 // DH01-05				
C1-44	MW11S3060-013	S47/E//S47-37 // DH01-05				
C1-44	MW11S3060-014	S47/E//S47-37 // DH01-05	50/100	50/100		
C1-44	MW11S3060-015	S47/E//S47-37 // DH01-05		100	50	25
C1-44	MW11S3060-016	S47/E//S47-37 // DH01-05		100		
C1-45	MW11S3061-001	DH01-05 / M115				

C1-45	MW11S3061-002	DH01-05 / M115			
C1-45	MW11S3061-003	DH01-05 / M115			
C1-45	MW11S3061-004	DH01-05 / M115			
C1-45	MW11S3061-005	DH01-05 / M115			
C1-45	MW11S3061-006	DH01-05 / M115			
C1-45	MW11S3061-007	DH01-05 / M115			
C1-45	MW11S3061-008	DH01-05 / M115			
C1-45	MW11S3061-009	DH01-05 / M115		50	25
C1-45	MW11S3061-010	DH01-05 / M115			
C1-45	MW11S3061-011	DH01-05 / M115			
C1-45	MW11S3061-012	DH01-05 / M115			
C1-45	MW11S3061-013	DH01-05 / M115			
C1-45	MW11S3061-014	DH01-05 / M115			
C1-45	MW11S3061-015	DH01-05 / M115			
C1-45	MW11S3061-016	DH01-05 / M115			
C1-46	MW11S3062-001	DH01-05 / Rasmusson			
C1-46	MW11S3062-002	DH01-05 / Rasmusson			
C1-46	MW11S3062-003	DH01-05 / Rasmusson			
C1-46	MW11S3062-004	DH01-05 / Rasmusson			
C1-46	MW11S3062-005	DH01-05 / Rasmusson			
C1-46	MW11S3062-006	DH01-05 / Rasmusson			
C1-46	MW11S3062-007	DH01-05 / Rasmusson	100		
C1-46	MW11S3062-008	DH01-05 / Rasmusson		50	25
C1-46	MW11S3062-009	DH01-05 / Rasmusson		50	25
C1-46	MW11S3062-010	DH01-05 / Rasmusson			
C1-46	MW11S3062-011	DH01-05 / Rasmusson			
C1-46	MW11S3062-012	DH01-05 / Rasmusson			
C1-46	MW11S3062-013	DH01-05 / Rasmusson			
C1-46	MW11S3062-014	DH01-05 / Rasmusson			
C1-46	MW11S3062-015	DH01-05 / Rasmusson			
C1-46	MW11S3062-016	DH01-05 / Rasmusson		50	25
C1-47	MW11S3063-001	DH01-39 / Lacey			
C1-47	MW11S3063-002	DH01-39 / Lacey			
C1-47	MW11S3063-003	DH01-39 / Lacey			
C1-47	MW11S3063-004	DH01-39 / Lacey			
C1-47	MW11S3063-005	DH01-39 / Lacey			
C1-47	MW11S3063-006	DH01-39 / Lacey		50	
C1-47	MW11S3063-007	DH01-39 / Lacey			
C1-47	MW11S3063-008	DH01-39 / Lacey			
C1-47	MW11S3063-009	DH01-39 / Lacey			
C1-47	MW11S3063-010	DH01-39 / Lacey			
C1-47	MW11S3063-011	DH01-39 / Lacey			
C1-47	MW11S3063-012	DH01-39 / Lacey			
C1-47	MW11S3063-013	DH01-39 / Lacey			
C1-47	MW11S3063-014	DH01-39 / Lacey			

C1-47	MW11S3063-015	DH01-39 / Lacey
C1-47	MW11S3063-016	DH01-39 / Lacey
C1-48	MW11S3064-001	DH01-113 / Rasmusson
C1-48	MW11S3064-002	DH01-113 / Rasmusson
C1-48	MW11S3064-003	DH01-113 / Rasmusson
C1-48	MW11S3064-004	DH01-113 / Rasmusson
C1-48	MW11S3064-005	DH01-113 / Rasmusson
C1-48	MW11S3064-006	DH01-113 / Rasmusson
C1-48	MW11S3064-007	DH01-113 / Rasmusson
C1-48	MW11S3064-008	DH01-113 / Rasmusson
C1-48	MW11S3064-009	DH01-113 / Rasmusson
C1-48	MW11S3064-010	DH01-113 / Rasmusson
C1-48	MW11S3064-011	DH01-113 / Rasmusson
C1-48	MW11S3064-012	DH01-113 / Rasmusson
C1-48	MW11S3064-013	DH01-113 / Rasmusson
C1-48	MW11S3064-014	DH01-113 / Rasmusson
C1-48	MW11S3064-015	DH01-113 / Rasmusson
C1-48	MW11S3064-016	DH01-113 / Rasmusson
C2-1	MW12_2002-001	MW11S4009-006/MW11S4026-007
C2-1	MW12_2002-002	MW11S4009-006/MW11S4026-007
C2-1	MW12_2002-003	MW11S4009-006/MW11S4026-007
C2-1	MW12_2002-004	MW11S4009-006/MW11S4026-007
C2-1	MW12_2002-005	MW11S4009-006/MW11S4026-007
C2-1	MW12_2002-006	MW11S4009-006/MW11S4026-007
C2-1	MW12_2002-007	MW11S4009-006/MW11S4026-007
C2-1	MW12_2002-008	MW11S4009-006/MW11S4026-007
C2-1	MW12_2002-009	MW11S4009-006/MW11S4026-007
C2-1	MW12_2002-010	MW11S4009-006/MW11S4026-007
C2-1	MW12_2002-011	MW11S4009-006/MW11S4026-007
C2-1	MW12_2002-012	MW11S4009-006/MW11S4026-007
C2-2	MW12_2003-001	MW11S4009-006/MW11S4019-007
C2-2	MW12_2003-002	MW11S4009-006/MW11S4019-007
C2-2	MW12_2003-003	MW11S4009-006/MW11S4019-007
C2-2	MW12_2003-004	MW11S4009-006/MW11S4019-007
C2-2	MW12_2003-005	MW11S4009-006/MW11S4019-007
C2-2	MW12_2003-006	MW11S4009-006/MW11S4019-007
C2-2	MW12_2003-007	MW11S4009-006/MW11S4019-007
C2-2	MW12_2003-008	MW11S4009-006/MW11S4019-007
C2-2	MW12_2003-009	MW11S4009-006/MW11S4019-007
C2-2	MW12_2003-010	MW11S4009-006/MW11S4019-007
C2-2	MW12_2003-011	MW11S4009-006/MW11S4019-007
C2-2	MW12_2003-012	MW11S4009-006/MW11S4019-007
C2-3	MW12_2004-001	MW11S4009-011/MW11S4020-003
C2-3	MW12_2004-002	MW11S4009-011/MW11S4020-003

C2-3	MW12_2004-003	MW11S4009-011/MW11S4020-003		
C2-3	MW12_2004-004	MW11S4009-011/MW11S4020-003		
C2-3	MW12_2004-005	MW11S4009-011/MW11S4020-003		
C2-3	MW12_2004-006	MW11S4009-011/MW11S4020-003		
C2-3	MW12_2004-007	MW11S4009-011/MW11S4020-003		
C2-3	MW12_2004-008	MW11S4009-011/MW11S4020-003		
C2-3	MW12_2004-009	MW11S4009-011/MW11S4020-003		
C2-3	MW12_2004-010	MW11S4009-011/MW11S4020-003		
C2-3	MW12_2004-011	MW11S4009-011/MW11S4020-003		
C2-3	MW12_2004-012	MW11S4009-011/MW11S4020-003		
C2-4	MW12_2005-001	MW11S4009-015/MW11S4036-004		
C2-4	MW12_2005-002	MW11S4009-015/MW11S4036-004		
C2-4	MW12_2005-003	MW11S4009-015/MW11S4036-004		
C2-4	MW12_2005-004	MW11S4009-015/MW11S4036-004		
C2-4	MW12_2005-005	MW11S4009-015/MW11S4036-004		
C2-4	MW12_2005-006	MW11S4009-015/MW11S4036-004		
C2-4	MW12_2005-007	MW11S4009-015/MW11S4036-004		
C2-4	MW12_2005-008	MW11S4009-015/MW11S4036-004		
C2-4	MW12_2005-009	MW11S4009-015/MW11S4036-004		
C2-4	MW12_2005-010	MW11S4009-015/MW11S4036-004		
C2-4	MW12_2005-011	MW11S4009-015/MW11S4036-004		
C2-4	MW12_2005-012	MW11S4009-015/MW11S4036-004		
C2-5	MW12_2006-001	MW11S4009-016/MW11S4016-011		
C2-5	MW12_2006-002	MW11S4009-016/MW11S4016-011		
C2-5	MW12_2006-003	MW11S4009-016/MW11S4016-011		
C2-5	MW12_2006-004	MW11S4009-016/MW11S4016-011		
C2-5	MW12_2006-005	MW11S4009-016/MW11S4016-011		
C2-5	MW12_2006-006	MW11S4009-016/MW11S4016-011		
C2-5	MW12_2006-007	MW11S4009-016/MW11S4016-011	50/100	25
C2-5	MW12_2006-008	MW11S4009-016/MW11S4016-011		
C2-5	MW12_2006-009	MW11S4009-016/MW11S4016-011		
C2-5	MW12_2006-010	MW11S4009-016/MW11S4016-011		
C2-5	MW12_2006-011	MW11S4009-016/MW11S4016-011		
C2-5	MW12_2006-012	MW11S4009-016/MW11S4016-011		
C2-6	MW12_2007-001	MW11S4016-002/MW11S4024-012	50/100	
C2-6	MW12_2007-002	MW11S4016-002/MW11S4024-012	50/100	25
C2-6	MW12_2007-003	MW11S4016-002/MW11S4024-012	100	
C2-6	MW12_2007-004	MW11S4016-002/MW11S4024-012	50/100	
C2-6	MW12_2007-005	MW11S4016-002/MW11S4024-012	100	
C2-6	MW12_2007-006	MW11S4016-002/MW11S4024-012	100	
C2-6	MW12_2007-007	MW11S4016-002/MW11S4024-012	50/100	
C2-6	MW12_2007-008	MW11S4016-002/MW11S4024-012	50/100	25
C2-6	MW12_2007-009	MW11S4016-002/MW11S4024-012	100	
C2-6	MW12_2007-010	MW11S4016-002/MW11S4024-012	100	
C2-6	MW12_2007-011	MW11S4016-002/MW11S4024-012	100	

C2-6	MW12_2007-012	MW11S4016-002/MW11S4024-012	100		
C2-7	MW12_2011-001	MW11S4016-014/MW11S4025-012			
C2-7	MW12_2011-002	MW11S4016-014/MW11S4025-012			
C2-7	MW12_2011-003	MW11S4016-014/MW11S4025-012			
C2-7	MW12_2011-004	MW11S4016-014/MW11S4025-012	50/100		25
C2-7	MW12_2011-005	MW11S4016-014/MW11S4025-012	100		
C2-7	MW12_2011-006	MW11S4016-014/MW11S4025-012	50/100		25
C2-7	MW12_2011-007	MW11S4016-014/MW11S4025-012			
C2-7	MW12_2011-008	MW11S4016-014/MW11S4025-012			
C2-7	MW12_2011-009	MW11S4016-014/MW11S4025-012		50	
C2-7	MW12_2011-010	MW11S4016-014/MW11S4025-012			
C2-7	MW12_2011-011	MW11S4016-014/MW11S4025-012			
C2-7	MW12_2011-012	MW11S4016-014/MW11S4025-012	100	50	25
C2-8	MW12_2012-001	MW11S4019-004/MW11S4029-016			
C2-8	MW12_2012-002	MW11S4019-004/MW11S4029-016			
C2-8	MW12_2012-003	MW11S4019-004/MW11S4029-016			
C2-8	MW12_2012-004	MW11S4019-004/MW11S4029-016			
C2-8	MW12_2012-005	MW11S4019-004/MW11S4029-016			
C2-8	MW12_2012-006	MW11S4019-004/MW11S4029-016			
C2-8	MW12_2012-007	MW11S4019-004/MW11S4029-016			
C2-8	MW12_2012-008	MW11S4019-004/MW11S4029-016			
C2-8	MW12_2012-009	MW11S4019-004/MW11S4029-016			
C2-8	MW12_2012-010	MW11S4019-004/MW11S4029-016			
C2-8	MW12_2012-011	MW11S4019-004/MW11S4029-016			
C2-8	MW12_2012-012	MW11S4019-004/MW11S4029-016			
C2-9	MW12_2014-001	MW11S4019-008/MW11S4035-006			
C2-9	MW12_2014-002	MW11S4019-008/MW11S4035-006	50/100		25
C2-9	MW12_2014-003	MW11S4019-008/MW11S4035-006	50/100	50	25
C2-9	MW12_2014-004	MW11S4019-008/MW11S4035-006			
C2-9	MW12_2014-005	MW11S4019-008/MW11S4035-006			
C2-9	MW12_2014-006	MW11S4019-008/MW11S4035-006			
C2-9	MW12_2014-007	MW11S4019-008/MW11S4035-006			
C2-9	MW12_2014-008	MW11S4019-008/MW11S4035-006	100		
C2-9	MW12_2014-009	MW11S4019-008/MW11S4035-006	100		
C2-9	MW12_2014-010	MW11S4019-008/MW11S4035-006			
C2-9	MW12_2014-011	MW11S4019-008/MW11S4035-006	50/100		25
C2-9	MW12_2014-012	MW11S4019-008/MW11S4035-006			
C2-10	MW12_2015-001	MW11S4019-009/MW11S4020-010			
C2-10	MW12_2015-002	MW11S4019-009/MW11S4020-010			
C2-10	MW12_2015-003	MW11S4019-009/MW11S4020-010			
C2-10	MW12_2015-004	MW11S4019-009/MW11S4020-010			
C2-10	MW12_2015-005	MW11S4019-009/MW11S4020-010			
C2-10	MW12_2015-006	MW11S4019-009/MW11S4020-010			
C2-10	MW12_2015-007	MW11S4019-009/MW11S4020-010			

C2-10	MW12_2015-008	MW11S4019-009/MW11S4020-010		
C2-10	MW12_2015-009	MW11S4019-009/MW11S4020-010		
C2-10	MW12_2015-010	MW11S4019-009/MW11S4020-010		
C2-10	MW12_2015-011	MW11S4019-009/MW11S4020-010		
C2-10	MW12_2015-012	MW11S4019-009/MW11S4020-010		
C2-11	MW12_2016-001	MW11S4019-011/MW11S4036-004		
C2-11	MW12_2016-002	MW11S4019-011/MW11S4036-004	100	
C2-11	MW12_2016-003	MW11S4019-011/MW11S4036-004		
C2-11	MW12_2016-004	MW11S4019-011/MW11S4036-004	50/100	25
C2-11	MW12_2016-005	MW11S4019-011/MW11S4036-004		
C2-11	MW12_2016-006	MW11S4019-011/MW11S4036-004	50/100	25
C2-11	MW12_2016-007	MW11S4019-011/MW11S4036-004		
C2-11	MW12_2016-008	MW11S4019-011/MW11S4036-004		
C2-11	MW12_2016-009	MW11S4019-011/MW11S4036-004		
C2-11	MW12_2016-010	MW11S4019-011/MW11S4036-004		
C2-11	MW12_2016-011	MW11S4019-011/MW11S4036-004		
C2-11	MW12_2016-012	MW11S4019-011/MW11S4036-004		
C2-12	MW12_2017-001	MW11S4019-013/MW11S4039-011		
C2-12	MW12_2017-002	MW11S4019-013/MW11S4039-011		
C2-12	MW12_2017-003	MW11S4019-013/MW11S4039-011		
C2-12	MW12_2017-004	MW11S4019-013/MW11S4039-011		
C2-12	MW12_2017-005	MW11S4019-013/MW11S4039-011		
C2-12	MW12_2017-006	MW11S4019-013/MW11S4039-011		
C2-12	MW12_2017-007	MW11S4019-013/MW11S4039-011		
C2-12	MW12_2017-008	MW11S4019-013/MW11S4039-011		
C2-12	MW12_2017-009	MW11S4019-013/MW11S4039-011		
C2-12	MW12_2017-010	MW11S4019-013/MW11S4039-011		
C2-12	MW12_2017-011	MW11S4019-013/MW11S4039-011	50/100	
C2-12	MW12_2017-012	MW11S4019-013/MW11S4039-011		
C2-13	MW12_2021-001	MW11S4020-002/MW11S4039-002		
C2-13	MW12_2021-002	MW11S4020-002/MW11S4039-002		
C2-13	MW12_2021-003	MW11S4020-002/MW11S4039-002		
C2-13	MW12_2021-004	MW11S4020-002/MW11S4039-002		
C2-13	MW12_2021-005	MW11S4020-002/MW11S4039-002		
C2-13	MW12_2021-006	MW11S4020-002/MW11S4039-002		
C2-13	MW12_2021-007	MW11S4020-002/MW11S4039-002		
C2-13	MW12_2021-008	MW11S4020-002/MW11S4039-002		
C2-13	MW12_2021-009	MW11S4020-002/MW11S4039-002		
C2-13	MW12_2021-010	MW11S4020-002/MW11S4039-002		
C2-13	MW12_2021-011	MW11S4020-002/MW11S4039-002		
C2-13	MW12_2021-012	MW11S4020-002/MW11S4039-002		
C2-14	MW12_2022-001	MW11S4020-002/MW11S4025-001		
C2-14	MW12_2022-002	MW11S4020-002/MW11S4025-001		
C2-14	MW12_2022-003	MW11S4020-002/MW11S4025-001		

C2-14	MW12_2022-004	MW11S4020-002/MW11S4025-001			
C2-14	MW12_2022-005	MW11S4020-002/MW11S4025-001		50	25
C2-14	MW12_2022-006	MW11S4020-002/MW11S4025-001			
C2-14	MW12_2022-007	MW11S4020-002/MW11S4025-001		50	25
C2-14	MW12_2022-008	MW11S4020-002/MW11S4025-001			
C2-14	MW12_2022-009	MW11S4020-002/MW11S4025-001			
C2-14	MW12_2022-010	MW11S4020-002/MW11S4025-001			
C2-14	MW12_2022-011	MW11S4020-002/MW11S4025-001			
C2-14	MW12_2022-012	MW11S4020-002/MW11S4025-001			
C2-15	MW12_2024-001	MW11S4020-012/MW11S4026-012			
C2-15	MW12_2024-002	MW11S4020-012/MW11S4026-012			
C2-15	MW12_2024-003	MW11S4020-012/MW11S4026-012			
C2-15	MW12_2024-004	MW11S4020-012/MW11S4026-012			
C2-15	MW12_2024-005	MW11S4020-012/MW11S4026-012		50	25
C2-15	MW12_2024-006	MW11S4020-012/MW11S4026-012			
C2-15	MW12_2024-007	MW11S4020-012/MW11S4026-012			
C2-15	MW12_2024-008	MW11S4020-012/MW11S4026-012			
C2-15	MW12_2024-009	MW11S4020-012/MW11S4026-012			
C2-15	MW12_2024-010	MW11S4020-012/MW11S4026-012			
C2-15	MW12_2024-011	MW11S4020-012/MW11S4026-012			
C2-15	MW12_2024-012	MW11S4020-012/MW11S4026-012			
C2-16	MW12_2025-001	MW11S4024-012/MW11S4039-005			
C2-16	MW12_2025-002	MW11S4024-012/MW11S4039-005			
C2-16	MW12_2025-003	MW11S4024-012/MW11S4039-005	100		
C2-16	MW12_2025-004	MW11S4024-012/MW11S4039-005	100		
C2-16	MW12_2025-005	MW11S4024-012/MW11S4039-005	100		
C2-16	MW12_2025-006	MW11S4024-012/MW11S4039-005			
C2-16	MW12_2025-007	MW11S4024-012/MW11S4039-005			
C2-16	MW12_2025-008	MW11S4024-012/MW11S4039-005			
C2-16	MW12_2025-009	MW11S4024-012/MW11S4039-005			
C2-16	MW12_2025-010	MW11S4024-012/MW11S4039-005			
C2-16	MW12_2025-011	MW11S4024-012/MW11S4039-005			
C2-16	MW12_2025-012	MW11S4024-012/MW11S4039-005	50/100		
C2-17	MW12_2026-001	MW11S4025-001/MW11S4039-015			
C2-17	MW12_2026-002	MW11S4025-001/MW11S4039-015			
C2-17	MW12_2026-003	MW11S4025-001/MW11S4039-015			
C2-17	MW12_2026-004	MW11S4025-001/MW11S4039-015			
C2-17	MW12_2026-005	MW11S4025-001/MW11S4039-015			
C2-17	MW12_2026-006	MW11S4025-001/MW11S4039-015			
C2-17	MW12_2026-007	MW11S4025-001/MW11S4039-015	100		
C2-17	MW12_2026-008	MW11S4025-001/MW11S4039-015			
C2-17	MW12_2026-009	MW11S4025-001/MW11S4039-015			
C2-17	MW12_2026-010	MW11S4025-001/MW11S4039-015			
C2-17	MW12_2026-011	MW11S4025-001/MW11S4039-015			

C2-17	MW12_2026-012	MW11S4025-001/MW11S4039-015			
C2-18	MW12_2028-001	MW11S4025-007/MW11S4033-002	50/100	50	
C2-18	MW12_2028-002	MW11S4025-007/MW11S4033-002	100		
C2-18	MW12_2028-003	MW11S4025-007/MW11S4033-002			
C2-18	MW12_2028-004	MW11S4025-007/MW11S4033-002	100		
C2-18	MW12_2028-005	MW11S4025-007/MW11S4033-002	100		
C2-18	MW12_2028-006	MW11S4025-007/MW11S4033-002			
C2-18	MW12_2028-007	MW11S4025-007/MW11S4033-002	50/100		
C2-18	MW12_2028-008	MW11S4025-007/MW11S4033-002	100		
C2-18	MW12_2028-009	MW11S4025-007/MW11S4033-002	50/100		25
C2-18	MW12_2028-010	MW11S4025-007/MW11S4033-002	50/100		
C2-18	MW12_2028-011	MW11S4025-007/MW11S4033-002			
C2-18	MW12_2028-012	MW11S4025-007/MW11S4033-002	100		
C2-19	MW12_2030-001	MW11S4025-007/MW11S4034-003	100		
C2-19	MW12_2030-002	MW11S4025-007/MW11S4034-003			
C2-19	MW12_2030-003	MW11S4025-007/MW11S4034-003			
C2-19	MW12_2030-004	MW11S4025-007/MW11S4034-003		50	25
C2-19	MW12_2030-005	MW11S4025-007/MW11S4034-003			
C2-19	MW12_2030-006	MW11S4025-007/MW11S4034-003			
C2-19	MW12_2030-007	MW11S4025-007/MW11S4034-003			
C2-19	MW12_2030-008	MW11S4025-007/MW11S4034-003			
C2-19	MW12_2030-009	MW11S4025-007/MW11S4034-003			
C2-19	MW12_2030-010	MW11S4025-007/MW11S4034-003			
C2-19	MW12_2030-011	MW11S4025-007/MW11S4034-003			
C2-19	MW12_2030-012	MW11S4025-007/MW11S4034-003			
C2-20	MW12_2032-001	MW11S4025-008/MW11S4046-016			
C2-20	MW12_2032-002	MW11S4025-008/MW11S4046-016			
C2-20	MW12_2032-003	MW11S4025-008/MW11S4046-016			
C2-20	MW12_2032-004	MW11S4025-008/MW11S4046-016			
C2-20	MW12_2032-005	MW11S4025-008/MW11S4046-016			
C2-20	MW12_2032-006	MW11S4025-008/MW11S4046-016	100		
C2-20	MW12_2032-007	MW11S4025-008/MW11S4046-016			
C2-20	MW12_2032-008	MW11S4025-008/MW11S4046-016			
C2-20	MW12_2032-009	MW11S4025-008/MW11S4046-016			
C2-20	MW12_2032-010	MW11S4025-008/MW11S4046-016			
C2-20	MW12_2032-011	MW11S4025-008/MW11S4046-016			
C2-20	MW12_2032-012	MW11S4025-008/MW11S4046-016			
C2-21	MW12_2033-001	MW11S4025-009/MW11S4029-012			
C2-21	MW12_2033-002	MW11S4025-009/MW11S4029-012			
C2-21	MW12_2033-003	MW11S4025-009/MW11S4029-012			
C2-21	MW12_2033-004	MW11S4025-009/MW11S4029-012			
C2-21	MW12_2033-005	MW11S4025-009/MW11S4029-012		50	25
C2-21	MW12_2033-006	MW11S4025-009/MW11S4029-012			
C2-21	MW12_2033-007	MW11S4025-009/MW11S4029-012			

C2-21	MW12_2033-008	MW11S4025-009/MW11S4029-012		
C2-21	MW12_2033-009	MW11S4025-009/MW11S4029-012		
C2-21	MW12_2033-010	MW11S4025-009/MW11S4029-012		
C2-21	MW12_2033-011	MW11S4025-009/MW11S4029-012		
C2-21	MW12_2033-012	MW11S4025-009/MW11S4029-012		
C2-22	MW12_2035-001	MW11S4026-012/MW11S4060-002		
C2-22	MW12_2035-002	MW11S4026-012/MW11S4060-002		
C2-22	MW12_2035-003	MW11S4026-012/MW11S4060-002		
C2-22	MW12_2035-004	MW11S4026-012/MW11S4060-002		
C2-22	MW12_2035-005	MW11S4026-012/MW11S4060-002		
C2-22	MW12_2035-006	MW11S4026-012/MW11S4060-002		
C2-22	MW12_2035-007	MW11S4026-012/MW11S4060-002		
C2-22	MW12_2035-008	MW11S4026-012/MW11S4060-002		
C2-22	MW12_2035-009	MW11S4026-012/MW11S4060-002		
C2-22	MW12_2035-010	MW11S4026-012/MW11S4060-002		
C2-22	MW12_2035-011	MW11S4026-012/MW11S4060-002		
C2-22	MW12_2035-012	MW11S4026-012/MW11S4060-002		
C2-23	MW12_2038-001	MW11S4029-003/MW11S4038-005		
C2-23	MW12_2038-002	MW11S4029-003/MW11S4038-005		
C2-23	MW12_2038-003	MW11S4029-003/MW11S4038-005		
C2-23	MW12_2038-004	MW11S4029-003/MW11S4038-005		
C2-23	MW12_2038-005	MW11S4029-003/MW11S4038-005		
C2-23	MW12_2038-006	MW11S4029-003/MW11S4038-005		
C2-23	MW12_2038-007	MW11S4029-003/MW11S4038-005		50
C2-23	MW12_2038-008	MW11S4029-003/MW11S4038-005		
C2-23	MW12_2038-009	MW11S4029-003/MW11S4038-005	100	
C2-23	MW12_2038-010	MW11S4029-003/MW11S4038-005		
C2-23	MW12_2038-011	MW11S4029-003/MW11S4038-005	50/100	
C2-23	MW12_2038-012	MW11S4029-003/MW11S4038-005		50
C2-24	MW12_2039-001	MW11S4029-012/MW11S4039-012		
C2-24	MW12_2039-002	MW11S4029-012/MW11S4039-012		
C2-24	MW12_2039-003	MW11S4029-012/MW11S4039-012		
C2-24	MW12_2039-004	MW11S4029-012/MW11S4039-012		
C2-24	MW12_2039-005	MW11S4029-012/MW11S4039-012		
C2-24	MW12_2039-006	MW11S4029-012/MW11S4039-012		
C2-24	MW12_2039-007	MW11S4029-012/MW11S4039-012		
C2-24	MW12_2039-008	MW11S4029-012/MW11S4039-012		50
C2-24	MW12_2039-009	MW11S4029-012/MW11S4039-012		
C2-24	MW12_2039-010	MW11S4029-012/MW11S4039-012		
C2-24	MW12_2039-011	MW11S4029-012/MW11S4039-012		
C2-24	MW12_2039-012	MW11S4029-012/MW11S4039-012		
C2-25	MW12_2040-001	MW11S4029-013/MW11S4036-010		50
C2-25	MW12_2040-002	MW11S4029-013/MW11S4036-010		
C2-25	MW12_2040-003	MW11S4029-013/MW11S4036-010		

C2-25	MW12_2040-004	MW11S4029-013/MW11S4036-010			
C2-25	MW12_2040-005	MW11S4029-013/MW11S4036-010			
C2-25	MW12_2040-006	MW11S4029-013/MW11S4036-010			
C2-25	MW12_2040-007	MW11S4029-013/MW11S4036-010			
C2-25	MW12_2040-008	MW11S4029-013/MW11S4036-010			
C2-25	MW12_2040-009	MW11S4029-013/MW11S4036-010			
C2-25	MW12_2040-010	MW11S4029-013/MW11S4036-010			
C2-25	MW12_2040-011	MW11S4029-013/MW11S4036-010			
C2-25	MW12_2040-012	MW11S4029-013/MW11S4036-010			
C2-26	MW12_2042-001	MW11S4030-010/MW11S4016-003			
C2-26	MW12_2042-002	MW11S4030-010/MW11S4016-003	50/100		
C2-26	MW12_2042-003	MW11S4030-010/MW11S4016-003			
C2-26	MW12_2042-004	MW11S4030-010/MW11S4016-003			
C2-26	MW12_2042-005	MW11S4030-010/MW11S4016-003	50/100	50	
C2-26	MW12_2042-006	MW11S4030-010/MW11S4016-003			
C2-26	MW12_2042-007	MW11S4030-010/MW11S4016-003	50/100		25
C2-26	MW12_2042-008	MW11S4030-010/MW11S4016-003	100		
C2-26	MW12_2042-009	MW11S4030-010/MW11S4016-003	50/100		25
C2-26	MW12_2042-010	MW11S4030-010/MW11S4016-003	50/100		25
C2-26	MW12_2042-011	MW11S4030-010/MW11S4016-003	50/100		
C2-26	MW12_2042-012	MW11S4030-010/MW11S4016-003	50/100		25
C2-27	MW12_2043-001	MW11S4030-012/MW11S4019-014		50	
C2-27	MW12_2043-002	MW11S4030-012/MW11S4019-014			
C2-27	MW12_2043-003	MW11S4030-012/MW11S4019-014			
C2-27	MW12_2043-004	MW11S4030-012/MW11S4019-014			
C2-27	MW12_2043-005	MW11S4030-012/MW11S4019-014			
C2-27	MW12_2043-006	MW11S4030-012/MW11S4019-014			
C2-27	MW12_2043-007	MW11S4030-012/MW11S4019-014			
C2-27	MW12_2043-008	MW11S4030-012/MW11S4019-014		50	
C2-27	MW12_2043-009	MW11S4030-012/MW11S4019-014			
C2-27	MW12_2043-010	MW11S4030-012/MW11S4019-014			
C2-27	MW12_2043-011	MW11S4030-012/MW11S4019-014			
C2-27	MW12_2043-012	MW11S4030-012/MW11S4019-014			
C2-28	MW12_2045-001	MW11S4033-002/MW11S4038-002			
C2-28	MW12_2045-002	MW11S4033-002/MW11S4038-002			
C2-28	MW12_2045-003	MW11S4033-002/MW11S4038-002			
C2-28	MW12_2045-004	MW11S4033-002/MW11S4038-002			
C2-28	MW12_2045-005	MW11S4033-002/MW11S4038-002		50	
C2-28	MW12_2045-006	MW11S4033-002/MW11S4038-002			
C2-28	MW12_2045-007	MW11S4033-002/MW11S4038-002			
C2-28	MW12_2045-008	MW11S4033-002/MW11S4038-002			
C2-28	MW12_2045-009	MW11S4033-002/MW11S4038-002		50	25
C2-28	MW12_2045-010	MW11S4033-002/MW11S4038-002			
C2-28	MW12_2045-011	MW11S4033-002/MW11S4038-002			

C2-28	MW12_2045-012	MW11S4033-002/MW11S4038-002			
C2-29	MW12_2046-001	MW11S4033-002/MW11S4020-001			
C2-29	MW12_2046-002	MW11S4033-002/MW11S4020-001	50/100		
C2-29	MW12_2046-003	MW11S4033-002/MW11S4020-001	50/100		25
C2-29	MW12_2046-004	MW11S4033-002/MW11S4020-001			
C2-29	MW12_2046-005	MW11S4033-002/MW11S4020-001		50	
C2-29	MW12_2046-006	MW11S4033-002/MW11S4020-001	100		
C2-29	MW12_2046-007	MW11S4033-002/MW11S4020-001	50/100		
C2-29	MW12_2046-008	MW11S4033-002/MW11S4020-001			
C2-29	MW12_2046-009	MW11S4033-002/MW11S4020-001			
C2-29	MW12_2046-010	MW11S4033-002/MW11S4020-001	100		
C2-29	MW12_2046-011	MW11S4033-002/MW11S4020-001	50/100		25
C2-29	MW12_2046-012	MW11S4033-002/MW11S4020-001			
C2-30	MW12_2048-001	MW11S4033-016/MW11S4026-014			
C2-30	MW12_2048-002	MW11S4033-016/MW11S4026-014			
C2-30	MW12_2048-003	MW11S4033-016/MW11S4026-014			
C2-30	MW12_2048-004	MW11S4033-016/MW11S4026-014			
C2-30	MW12_2048-005	MW11S4033-016/MW11S4026-014			
C2-30	MW12_2048-006	MW11S4033-016/MW11S4026-014			
C2-30	MW12_2048-007	MW11S4033-016/MW11S4026-014			
C2-30	MW12_2048-008	MW11S4033-016/MW11S4026-014			
C2-30	MW12_2048-009	MW11S4033-016/MW11S4026-014			
C2-30	MW12_2048-010	MW11S4033-016/MW11S4026-014			
C2-30	MW12_2048-011	MW11S4033-016/MW11S4026-014			
C2-30	MW12_2048-012	MW11S4033-016/MW11S4026-014			
C2-31	MW12_2049-001	MW11S4033-016/MW11S4060-010		50	
C2-31	MW12_2049-002	MW11S4033-016/MW11S4060-010		50	25
C2-31	MW12_2049-003	MW11S4033-016/MW11S4060-010			
C2-31	MW12_2049-004	MW11S4033-016/MW11S4060-010			
C2-31	MW12_2049-005	MW11S4033-016/MW11S4060-010			
C2-31	MW12_2049-006	MW11S4033-016/MW11S4060-010			
C2-31	MW12_2049-007	MW11S4033-016/MW11S4060-010			
C2-31	MW12_2049-008	MW11S4033-016/MW11S4060-010		50	25
C2-31	MW12_2049-009	MW11S4033-016/MW11S4060-010			
C2-31	MW12_2049-010	MW11S4033-016/MW11S4060-010			
C2-31	MW12_2049-011	MW11S4033-016/MW11S4060-010			
C2-31	MW12_2049-012	MW11S4033-016/MW11S4060-010			
C2-32	MW12_2051-001	MW11S4034-003/MW11S4029-003			
C2-32	MW12_2051-002	MW11S4034-003/MW11S4029-003			
C2-32	MW12_2051-003	MW11S4034-003/MW11S4029-003			
C2-32	MW12_2051-004	MW11S4034-003/MW11S4029-003			
C2-32	MW12_2051-005	MW11S4034-003/MW11S4029-003			
C2-32	MW12_2051-006	MW11S4034-003/MW11S4029-003			
C2-32	MW12_2051-007	MW11S4034-003/MW11S4029-003			

C2-32	MW12_2051-008	MW11S4034-003/MW11S4029-003			
C2-32	MW12_2051-009	MW11S4034-003/MW11S4029-003			
C2-32	MW12_2051-010	MW11S4034-003/MW11S4029-003			
C2-32	MW12_2051-011	MW11S4034-003/MW11S4029-003			
C2-32	MW12_2051-012	MW11S4034-003/MW11S4029-003		50	
C2-33	MW12_2052-001	MW11S4034-003/MW11S4038-003			
C2-33	MW12_2052-002	MW11S4034-003/MW11S4038-003			
C2-33	MW12_2052-003	MW11S4034-003/MW11S4038-003			
C2-33	MW12_2052-004	MW11S4034-003/MW11S4038-003			
C2-33	MW12_2052-005	MW11S4034-003/MW11S4038-003			
C2-33	MW12_2052-006	MW11S4034-003/MW11S4038-003			
C2-33	MW12_2052-007	MW11S4034-003/MW11S4038-003			
C2-33	MW12_2052-008	MW11S4034-003/MW11S4038-003			
C2-33	MW12_2052-009	MW11S4034-003/MW11S4038-003			
C2-33	MW12_2052-010	MW11S4034-003/MW11S4038-003			
C2-33	MW12_2052-011	MW11S4034-003/MW11S4038-003			
C2-33	MW12_2052-012	MW11S4034-003/MW11S4038-003			
C2-34	MW12_2053-001	MW11S4034-005/MW11S4060-004			
C2-34	MW12_2053-002	MW11S4034-005/MW11S4060-004			
C2-34	MW12_2053-003	MW11S4034-005/MW11S4060-004			
C2-34	MW12_2053-004	MW11S4034-005/MW11S4060-004			
C2-34	MW12_2053-005	MW11S4034-005/MW11S4060-004			
C2-34	MW12_2053-006	MW11S4034-005/MW11S4060-004	100		
C2-34	MW12_2053-007	MW11S4034-005/MW11S4060-004		50	25
C2-34	MW12_2053-008	MW11S4034-005/MW11S4060-004			
C2-34	MW12_2053-009	MW11S4034-005/MW11S4060-004			
C2-34	MW12_2053-010	MW11S4034-005/MW11S4060-004	100		
C2-34	MW12_2053-011	MW11S4034-005/MW11S4060-004			
C2-34	MW12_2053-012	MW11S4034-005/MW11S4060-004		50	
C2-35	MW12_2054-001	MW11S4035-001/MW11S4009-013			
C2-35	MW12_2054-002	MW11S4035-001/MW11S4009-013			
C2-35	MW12_2054-003	MW11S4035-001/MW11S4009-013			
C2-35	MW12_2054-004	MW11S4035-001/MW11S4009-013			
C2-35	MW12_2054-005	MW11S4035-001/MW11S4009-013			
C2-35	MW12_2054-006	MW11S4035-001/MW11S4009-013			
C2-35	MW12_2054-007	MW11S4035-001/MW11S4009-013			
C2-35	MW12_2054-008	MW11S4035-001/MW11S4009-013		50	25
C2-35	MW12_2054-009	MW11S4035-001/MW11S4009-013			
C2-35	MW12_2054-010	MW11S4035-001/MW11S4009-013			
C2-35	MW12_2054-011	MW11S4035-001/MW11S4009-013		50	
C2-35	MW12_2054-012	MW11S4035-001/MW11S4009-013			
C2-36	MW12_2055-001	MW11S4035-006/MW11S4025-012		50	25
C2-36	MW12_2055-002	MW11S4035-006/MW11S4025-012		50	
C2-36	MW12_2055-003	MW11S4035-006/MW11S4025-012			

C2-36	MW12_2055-004	MW11S4035-006/MW11S4025-012			
C2-36	MW12_2055-005	MW11S4035-006/MW11S4025-012			
C2-36	MW12_2055-006	MW11S4035-006/MW11S4025-012			
C2-36	MW12_2055-007	MW11S4035-006/MW11S4025-012			
C2-36	MW12_2055-008	MW11S4035-006/MW11S4025-012			
C2-36	MW12_2055-009	MW11S4035-006/MW11S4025-012			
C2-36	MW12_2055-010	MW11S4035-006/MW11S4025-012			
C2-36	MW12_2055-011	MW11S4035-006/MW11S4025-012	50/100		25
C2-36	MW12_2055-012	MW11S4035-006/MW11S4025-012			
C2-37	MW12_2057-001	MW11S4035-010/MW11S4060-002			
C2-37	MW12_2057-002	MW11S4035-010/MW11S4060-002	100		
C2-37	MW12_2057-003	MW11S4035-010/MW11S4060-002	100		
C2-37	MW12_2057-004	MW11S4035-010/MW11S4060-002			
C2-37	MW12_2057-005	MW11S4035-010/MW11S4060-002			
C2-37	MW12_2057-006	MW11S4035-010/MW11S4060-002			
C2-37	MW12_2057-007	MW11S4035-010/MW11S4060-002	100		
C2-37	MW12_2057-008	MW11S4035-010/MW11S4060-002	50/100		
C2-37	MW12_2057-009	MW11S4035-010/MW11S4060-002	100		
C2-37	MW12_2057-010	MW11S4035-010/MW11S4060-002	50/100		25
C2-37	MW12_2057-011	MW11S4035-010/MW11S4060-002	100		
C2-37	MW12_2057-012	MW11S4035-010/MW11S4060-002	100		
C2-38	MW12_2059-001	MW11S4035-013/MW11S4016-011	100	50	25
C2-38	MW12_2059-002	MW11S4035-013/MW11S4016-011			
C2-38	MW12_2059-003	MW11S4035-013/MW11S4016-011			
C2-38	MW12_2059-004	MW11S4035-013/MW11S4016-011			
C2-38	MW12_2059-005	MW11S4035-013/MW11S4016-011	50/100		
C2-38	MW12_2059-006	MW11S4035-013/MW11S4016-011	50/100		
C2-38	MW12_2059-007	MW11S4035-013/MW11S4016-011	50/100		25
C2-38	MW12_2059-008	MW11S4035-013/MW11S4016-011	50/100		
C2-38	MW12_2059-009	MW11S4035-013/MW11S4016-011	100	50	
C2-38	MW12_2059-010	MW11S4035-013/MW11S4016-011			
C2-38	MW12_2059-011	MW11S4035-013/MW11S4016-011			
C2-38	MW12_2059-012	MW11S4035-013/MW11S4016-011			
C2-39	MW12_2060-001	MW11S4035-015/MW11S4034-005			
C2-39	MW12_2060-002	MW11S4035-015/MW11S4034-005	100		
C2-39	MW12_2060-003	MW11S4035-015/MW11S4034-005			
C2-39	MW12_2060-004	MW11S4035-015/MW11S4034-005			
C2-39	MW12_2060-005	MW11S4035-015/MW11S4034-005			
C2-39	MW12_2060-006	MW11S4035-015/MW11S4034-005			
C2-39	MW12_2060-007	MW11S4035-015/MW11S4034-005			
C2-39	MW12_2060-008	MW11S4035-015/MW11S4034-005	100		
C2-39	MW12_2060-009	MW11S4035-015/MW11S4034-005			
C2-39	MW12_2060-010	MW11S4035-015/MW11S4034-005			
C2-39	MW12_2060-011	MW11S4035-015/MW11S4034-005			

C2-39	MW12_2060-012	MW11S4035-015/MW11S4034-005			
C2-40	MW12_2064-001	MW11S4036-007/MW11S4030-010			
C2-40	MW12_2064-002	MW11S4036-007/MW11S4030-010			
C2-40	MW12_2064-003	MW11S4036-007/MW11S4030-010	100		
C2-40	MW12_2064-004	MW11S4036-007/MW11S4030-010	100		
C2-40	MW12_2064-005	MW11S4036-007/MW11S4030-010	50/100	50	25
C2-40	MW12_2064-006	MW11S4036-007/MW11S4030-010	50/100		
C2-40	MW12_2064-007	MW11S4036-007/MW11S4030-010	50/100		
C2-40	MW12_2064-008	MW11S4036-007/MW11S4030-010			
C2-40	MW12_2064-009	MW11S4036-007/MW11S4030-010	50/100		
C2-40	MW12_2064-010	MW11S4036-007/MW11S4030-010			
C2-40	MW12_2064-011	MW11S4036-007/MW11S4030-010	50/100		
C2-40	MW12_2064-012	MW11S4036-007/MW11S4030-010			
C2-41	MW12_2067-001	MW11S4036-013/MW11S4047-016	50/100		25
C2-41	MW12_2067-002	MW11S4036-013/MW11S4047-016			
C2-41	MW12_2067-003	MW11S4036-013/MW11S4047-016			
C2-41	MW12_2067-004	MW11S4036-013/MW11S4047-016			
C2-41	MW12_2067-005	MW11S4036-013/MW11S4047-016			
C2-41	MW12_2067-006	MW11S4036-013/MW11S4047-016			
C2-41	MW12_2067-007	MW11S4036-013/MW11S4047-016	50/100		
C2-41	MW12_2067-008	MW11S4036-013/MW11S4047-016			
C2-41	MW12_2067-009	MW11S4036-013/MW11S4047-016			
C2-41	MW12_2067-010	MW11S4036-013/MW11S4047-016			
C2-41	MW12_2067-011	MW11S4036-013/MW11S4047-016	50/100		
C2-41	MW12_2067-012	MW11S4036-013/MW11S4047-016	100		
C2-42	MW12_2068-001	MW11S4036-016/MW11S4020-012		50	
C2-42	MW12_2068-002	MW11S4036-016/MW11S4020-012			
C2-42	MW12_2068-003	MW11S4036-016/MW11S4020-012			
C2-42	MW12_2068-004	MW11S4036-016/MW11S4020-012			
C2-42	MW12_2068-005	MW11S4036-016/MW11S4020-012			
C2-42	MW12_2068-006	MW11S4036-016/MW11S4020-012			
C2-42	MW12_2068-007	MW11S4036-016/MW11S4020-012			
C2-42	MW12_2068-008	MW11S4036-016/MW11S4020-012			
C2-42	MW12_2068-009	MW11S4036-016/MW11S4020-012			
C2-42	MW12_2068-010	MW11S4036-016/MW11S4020-012			
C2-42	MW12_2068-011	MW11S4036-016/MW11S4020-012		50	
C2-42	MW12_2068-012	MW11S4036-016/MW11S4020-012			
C2-43	MW12_2069-001	MW11S4036-016/MW11S4035-008			
C2-43	MW12_2069-002	MW11S4036-016/MW11S4035-008			
C2-43	MW12_2069-003	MW11S4036-016/MW11S4035-008			
C2-43	MW12_2069-004	MW11S4036-016/MW11S4035-008			
C2-43	MW12_2069-005	MW11S4036-016/MW11S4035-008			
C2-43	MW12_2069-006	MW11S4036-016/MW11S4035-008			
C2-43	MW12_2069-007	MW11S4036-016/MW11S4035-008			

C2-43	MW12_2069-008	MW11S4036-016/MW11S4035-008			
C2-43	MW12_2069-009	MW11S4036-016/MW11S4035-008			
C2-43	MW12_2069-010	MW11S4036-016/MW11S4035-008			
C2-43	MW12_2069-011	MW11S4036-016/MW11S4035-008			
C2-43	MW12_2069-012	MW11S4036-016/MW11S4035-008			
C2-44	MW12_2070-001	MW11S4038-002/MW11S4025-008			
C2-44	MW12_2070-002	MW11S4038-002/MW11S4025-008			
C2-44	MW12_2070-003	MW11S4038-002/MW11S4025-008			
C2-44	MW12_2070-004	MW11S4038-002/MW11S4025-008			
C2-44	MW12_2070-005	MW11S4038-002/MW11S4025-008			
C2-44	MW12_2070-006	MW11S4038-002/MW11S4025-008			
C2-44	MW12_2070-007	MW11S4038-002/MW11S4025-008			
C2-44	MW12_2070-008	MW11S4038-002/MW11S4025-008		50	25
C2-44	MW12_2070-009	MW11S4038-002/MW11S4025-008		50	25
C2-44	MW12_2070-010	MW11S4038-002/MW11S4025-008			
C2-44	MW12_2070-011	MW11S4038-002/MW11S4025-008			
C2-44	MW12_2070-012	MW11S4038-002/MW11S4025-008			
C2-45	MW12_2071-001	MW11S4038-003/MW11S4046-016			
C2-45	MW12_2071-002	MW11S4038-003/MW11S4046-016			
C2-45	MW12_2071-003	MW11S4038-003/MW11S4046-016			
C2-45	MW12_2071-004	MW11S4038-003/MW11S4046-016			
C2-45	MW12_2071-005	MW11S4038-003/MW11S4046-016		50	
C2-45	MW12_2071-006	MW11S4038-003/MW11S4046-016			
C2-45	MW12_2071-007	MW11S4038-003/MW11S4046-016		50	25
C2-45	MW12_2071-008	MW11S4038-003/MW11S4046-016			
C2-45	MW12_2071-009	MW11S4038-003/MW11S4046-016			
C2-45	MW12_2071-010	MW11S4038-003/MW11S4046-016			
C2-45	MW12_2071-011	MW11S4038-003/MW11S4046-016			
C2-45	MW12_2071-012	MW11S4038-003/MW11S4046-016			
C2-46	MW12_2072-001	MW11S4038-005/MW11S4039-013	100	50	
C2-46	MW12_2072-002	MW11S4038-005/MW11S4039-013			
C2-46	MW12_2072-003	MW11S4038-005/MW11S4039-013		50	25
C2-46	MW12_2072-004	MW11S4038-005/MW11S4039-013			
C2-46	MW12_2072-005	MW11S4038-005/MW11S4039-013			
C2-46	MW12_2072-006	MW11S4038-005/MW11S4039-013	100		
C2-46	MW12_2072-007	MW11S4038-005/MW11S4039-013	100		
C2-46	MW12_2072-008	MW11S4038-005/MW11S4039-013	50/100		
C2-46	MW12_2072-009	MW11S4038-005/MW11S4039-013	100		
C2-46	MW12_2072-010	MW11S4038-005/MW11S4039-013			
C2-46	MW12_2072-011	MW11S4038-005/MW11S4039-013			
C2-46	MW12_2072-012	MW11S4038-005/MW11S4039-013	50/100		25
C2-47	MW12_2073-001	MW11S4038-008/MW11S4053-005			
C2-47	MW12_2073-002	MW11S4038-008/MW11S4053-005			
C2-47	MW12_2073-003	MW11S4038-008/MW11S4053-005			

C2-47	MW12_2073-004	MW11S4038-008/MW11S4053-005			
C2-47	MW12_2073-005	MW11S4038-008/MW11S4053-005			
C2-47	MW12_2073-006	MW11S4038-008/MW11S4053-005			
C2-47	MW12_2073-007	MW11S4038-008/MW11S4053-005			
C2-47	MW12_2073-008	MW11S4038-008/MW11S4053-005			
C2-47	MW12_2073-009	MW11S4038-008/MW11S4053-005			
C2-47	MW12_2073-010	MW11S4038-008/MW11S4053-005			
C2-47	MW12_2073-011	MW11S4038-008/MW11S4053-005			
C2-47	MW12_2073-012	MW11S4038-008/MW11S4053-005			
C2-48	MW12_2075-001	MW11S4038-010/MW11S4016-014			
C2-48	MW12_2075-002	MW11S4038-010/MW11S4016-014		50	
C2-48	MW12_2075-003	MW11S4038-010/MW11S4016-014			
C2-48	MW12_2075-004	MW11S4038-010/MW11S4016-014			
C2-48	MW12_2075-005	MW11S4038-010/MW11S4016-014			
C2-48	MW12_2075-006	MW11S4038-010/MW11S4016-014	50/100		25
C2-48	MW12_2075-007	MW11S4038-010/MW11S4016-014			
C2-48	MW12_2075-008	MW11S4038-010/MW11S4016-014			
C2-48	MW12_2075-009	MW11S4038-010/MW11S4016-014			
C2-48	MW12_2075-010	MW11S4038-010/MW11S4016-014			
C2-48	MW12_2075-011	MW11S4038-010/MW11S4016-014			
C2-48	MW12_2075-012	MW11S4038-010/MW11S4016-014			
C2-49	MW12_2076-001	MW11S4038-012/MW11S4009-003			
C2-49	MW12_2076-002	MW11S4038-012/MW11S4009-003			
C2-49	MW12_2076-003	MW11S4038-012/MW11S4009-003			
C2-49	MW12_2076-004	MW11S4038-012/MW11S4009-003			
C2-49	MW12_2076-005	MW11S4038-012/MW11S4009-003			
C2-49	MW12_2076-006	MW11S4038-012/MW11S4009-003			
C2-49	MW12_2076-007	MW11S4038-012/MW11S4009-003			
C2-49	MW12_2076-008	MW11S4038-012/MW11S4009-003			
C2-49	MW12_2076-009	MW11S4038-012/MW11S4009-003			
C2-49	MW12_2076-010	MW11S4038-012/MW11S4009-003			
C2-49	MW12_2076-011	MW11S4038-012/MW11S4009-003			
C2-49	MW12_2076-012	MW11S4038-012/MW11S4009-003			
C2-50	MW12_2082-001	MW11S4038-016/MW11S4047-016			
C2-50	MW12_2082-002	MW11S4038-016/MW11S4047-016			
C2-50	MW12_2082-003	MW11S4038-016/MW11S4047-016			
C2-50	MW12_2082-004	MW11S4038-016/MW11S4047-016			
C2-50	MW12_2082-005	MW11S4038-016/MW11S4047-016			
C2-50	MW12_2082-006	MW11S4038-016/MW11S4047-016			
C2-50	MW12_2082-007	MW11S4038-016/MW11S4047-016			
C2-50	MW12_2082-008	MW11S4038-016/MW11S4047-016			
C2-50	MW12_2082-009	MW11S4038-016/MW11S4047-016			
C2-50	MW12_2082-010	MW11S4038-016/MW11S4047-016			
C2-50	MW12_2082-011	MW11S4038-016/MW11S4047-016			

C2-50	MW12_2082-012	MW11S4038-016/MW11S4047-016			
C2-51	MW12_2084-001	MW11S4039-005/MW11S4035-001			
C2-51	MW12_2084-002	MW11S4039-005/MW11S4035-001			
C2-51	MW12_2084-003	MW11S4039-005/MW11S4035-001			
C2-51	MW12_2084-004	MW11S4039-005/MW11S4035-001			
C2-51	MW12_2084-005	MW11S4039-005/MW11S4035-001			
C2-51	MW12_2084-006	MW11S4039-005/MW11S4035-001			
C2-51	MW12_2084-007	MW11S4039-005/MW11S4035-001			
C2-51	MW12_2084-008	MW11S4039-005/MW11S4035-001			
C2-51	MW12_2084-009	MW11S4039-005/MW11S4035-001			
C2-51	MW12_2084-010	MW11S4039-005/MW11S4035-001			
C2-51	MW12_2084-011	MW11S4039-005/MW11S4035-001			
C2-51	MW12_2084-012	MW11S4039-005/MW11S4035-001			
C2-52	MW12_2085-001	MW11S4039-011/MW11S4030-012			
C2-52	MW12_2085-002	MW11S4039-011/MW11S4030-012			
C2-52	MW12_2085-003	MW11S4039-011/MW11S4030-012			
C2-52	MW12_2085-004	MW11S4039-011/MW11S4030-012			
C2-52	MW12_2085-005	MW11S4039-011/MW11S4030-012			
C2-52	MW12_2085-006	MW11S4039-011/MW11S4030-012			
C2-52	MW12_2085-007	MW11S4039-011/MW11S4030-012			
C2-52	MW12_2085-008	MW11S4039-011/MW11S4030-012			
C2-52	MW12_2085-009	MW11S4039-011/MW11S4030-012			
C2-52	MW12_2085-010	MW11S4039-011/MW11S4030-012			
C2-52	MW12_2085-011	MW11S4039-011/MW11S4030-012			
C2-52	MW12_2085-012	MW11S4039-011/MW11S4030-012	100		
C2-53	MW12_2086-001	MW11S4039-012/MW11S4036-010			
C2-53	MW12_2086-002	MW11S4039-012/MW11S4036-010			
C2-53	MW12_2086-003	MW11S4039-012/MW11S4036-010			
C2-53	MW12_2086-004	MW11S4039-012/MW11S4036-010			
C2-53	MW12_2086-005	MW11S4039-012/MW11S4036-010			
C2-53	MW12_2086-006	MW11S4039-012/MW11S4036-010			
C2-53	MW12_2086-007	MW11S4039-012/MW11S4036-010			
C2-53	MW12_2086-008	MW11S4039-012/MW11S4036-010		50	25
C2-53	MW12_2086-009	MW11S4039-012/MW11S4036-010			
C2-53	MW12_2086-010	MW11S4039-012/MW11S4036-010			
C2-53	MW12_2086-011	MW11S4039-012/MW11S4036-010			
C2-53	MW12_2086-012	MW11S4039-012/MW11S4036-010			
C2-54	MW12_2087-001	MW11S4039-015/MW11S4009-006			
C2-54	MW12_2087-002	MW11S4039-015/MW11S4009-006			
C2-54	MW12_2087-003	MW11S4039-015/MW11S4009-006		50	25
C2-54	MW12_2087-004	MW11S4039-015/MW11S4009-006			
C2-54	MW12_2087-005	MW11S4039-015/MW11S4009-006			
C2-54	MW12_2087-006	MW11S4039-015/MW11S4009-006			
C2-54	MW12_2087-007	MW11S4039-015/MW11S4009-006			

C2-54	MW12_2087-008	MW11S4039-015/MW11S4009-006		
C2-54	MW12_2087-009	MW11S4039-015/MW11S4009-006		
C2-54	MW12_2087-010	MW11S4039-015/MW11S4009-006		
C2-54	MW12_2087-011	MW11S4039-015/MW11S4009-006		
C2-54	MW12_2087-012	MW11S4039-015/MW11S4009-006		
C2-55	MW12_2088-001	MW11S4039-016/MW11S4049-009		
C2-55	MW12_2088-002	MW11S4039-016/MW11S4049-009		
C2-55	MW12_2088-003	MW11S4039-016/MW11S4049-009	50	25
C2-55	MW12_2088-004	MW11S4039-016/MW11S4049-009		
C2-55	MW12_2088-005	MW11S4039-016/MW11S4049-009		
C2-55	MW12_2088-006	MW11S4039-016/MW11S4049-009		
C2-55	MW12_2088-007	MW11S4039-016/MW11S4049-009		
C2-55	MW12_2088-008	MW11S4039-016/MW11S4049-009		
C2-55	MW12_2088-009	MW11S4039-016/MW11S4049-009		
C2-55	MW12_2088-010	MW11S4039-016/MW11S4049-009		
C2-55	MW12_2088-011	MW11S4039-016/MW11S4049-009		
C2-55	MW12_2088-012	MW11S4039-016/MW11S4049-009		
C2-56	MW12_2089-001	MW11S4039-016/MW11S4060-010		
C2-56	MW12_2089-002	MW11S4039-016/MW11S4060-010		
C2-56	MW12_2089-003	MW11S4039-016/MW11S4060-010		
C2-56	MW12_2089-004	MW11S4039-016/MW11S4060-010		
C2-56	MW12_2089-005	MW11S4039-016/MW11S4060-010		
C2-56	MW12_2089-006	MW11S4039-016/MW11S4060-010	50	25
C2-56	MW12_2089-007	MW11S4039-016/MW11S4060-010		
C2-56	MW12_2089-008	MW11S4039-016/MW11S4060-010		
C2-56	MW12_2089-009	MW11S4039-016/MW11S4060-010	50	
C2-56	MW12_2089-010	MW11S4039-016/MW11S4060-010		
C2-56	MW12_2089-011	MW11S4039-016/MW11S4060-010		
C2-56	MW12_2089-012	MW11S4039-016/MW11S4060-010		
C2-57	MW12_2090-001	MW11S4046-016/MW11S4053-005		
C2-57	MW12_2090-002	MW11S4046-016/MW11S4053-005		
C2-57	MW12_2090-003	MW11S4046-016/MW11S4053-005		
C2-57	MW12_2090-004	MW11S4046-016/MW11S4053-005		
C2-57	MW12_2090-005	MW11S4046-016/MW11S4053-005		
C2-57	MW12_2090-006	MW11S4046-016/MW11S4053-005		
C2-57	MW12_2090-007	MW11S4046-016/MW11S4053-005		
C2-57	MW12_2090-008	MW11S4046-016/MW11S4053-005		
C2-57	MW12_2090-009	MW11S4046-016/MW11S4053-005		
C2-57	MW12_2090-010	MW11S4046-016/MW11S4053-005		
C2-57	MW12_2090-011	MW11S4046-016/MW11S4053-005		
C2-57	MW12_2090-012	MW11S4046-016/MW11S4053-005		
C2-58	MW12_2091-001	MW11S4047-016/MW11S4035-008		
C2-58	MW12_2091-002	MW11S4047-016/MW11S4035-008		
C2-58	MW12_2091-003	MW11S4047-016/MW11S4035-008		

C2-58	MW12_2091-004	MW11S4047-016/MW11S4035-008			
C2-58	MW12_2091-005	MW11S4047-016/MW11S4035-008			
C2-58	MW12_2091-006	MW11S4047-016/MW11S4035-008			
C2-58	MW12_2091-007	MW11S4047-016/MW11S4035-008			
C2-58	MW12_2091-008	MW11S4047-016/MW11S4035-008			
C2-58	MW12_2091-009	MW11S4047-016/MW11S4035-008			
C2-58	MW12_2091-010	MW11S4047-016/MW11S4035-008			
C2-58	MW12_2091-011	MW11S4047-016/MW11S4035-008			
C2-58	MW12_2091-012	MW11S4047-016/MW11S4035-008		50	25
C2-59	MW12_2092-001	MW11S4049-002/MW11S4025-015			
C2-59	MW12_2092-002	MW11S4049-002/MW11S4025-015			
C2-59	MW12_2092-003	MW11S4049-002/MW11S4025-015			
C2-59	MW12_2092-004	MW11S4049-002/MW11S4025-015			
C2-59	MW12_2092-005	MW11S4049-002/MW11S4025-015			
C2-59	MW12_2092-006	MW11S4049-002/MW11S4025-015			
C2-59	MW12_2092-007	MW11S4049-002/MW11S4025-015			
C2-59	MW12_2092-008	MW11S4049-002/MW11S4025-015			
C2-59	MW12_2092-009	MW11S4049-002/MW11S4025-015			
C2-59	MW12_2092-010	MW11S4049-002/MW11S4025-015			
C2-59	MW12_2092-011	MW11S4049-002/MW11S4025-015			
C2-59	MW12_2092-012	MW11S4049-002/MW11S4025-015			
C2-60	MW12_2094-001	MW11S4049-009/MW11S4026-007			
C2-60	MW12_2094-002	MW11S4049-009/MW11S4026-007			
C2-60	MW12_2094-003	MW11S4049-009/MW11S4026-007			
C2-60	MW12_2094-004	MW11S4049-009/MW11S4026-007			
C2-60	MW12_2094-005	MW11S4049-009/MW11S4026-007			
C2-60	MW12_2094-006	MW11S4049-009/MW11S4026-007			
C2-60	MW12_2094-007	MW11S4049-009/MW11S4026-007			
C2-60	MW12_2094-008	MW11S4049-009/MW11S4026-007			
C2-60	MW12_2094-009	MW11S4049-009/MW11S4026-007			
C2-60	MW12_2094-010	MW11S4049-009/MW11S4026-007			
C2-60	MW12_2094-011	MW11S4049-009/MW11S4026-007			
C2-60	MW12_2094-012	MW11S4049-009/MW11S4026-007			
C2-61	MW12_2095-001	MW11S4053-005/MW11S4030-012			
C2-61	MW12_2095-002	MW11S4053-005/MW11S4030-012			
C2-61	MW12_2095-003	MW11S4053-005/MW11S4030-012			
C2-61	MW12_2095-004	MW11S4053-005/MW11S4030-012			
C2-61	MW12_2095-005	MW11S4053-005/MW11S4030-012	100		
C2-61	MW12_2095-006	MW11S4053-005/MW11S4030-012			
C2-61	MW12_2095-007	MW11S4053-005/MW11S4030-012			
C2-61	MW12_2095-008	MW11S4053-005/MW11S4030-012		50	25
C2-61	MW12_2095-009	MW11S4053-005/MW11S4030-012			
C2-61	MW12_2095-010	MW11S4053-005/MW11S4030-012	50/100		25
C2-61	MW12_2095-011	MW11S4053-005/MW11S4030-012			

C2-61	MW12_2095-012	MW11S4053-005/MW11S4030-012	
C2-62	MW12_2097-001	MW11S4060-001/MW11S4038-011	
C2-62	MW12_2097-002	MW11S4060-001/MW11S4038-011	
C2-62	MW12_2097-003	MW11S4060-001/MW11S4038-011	
C2-62	MW12_2097-004	MW11S4060-001/MW11S4038-011	
C2-62	MW12_2097-005	MW11S4060-001/MW11S4038-011	
C2-62	MW12_2097-006	MW11S4060-001/MW11S4038-011	
C2-62	MW12_2097-007	MW11S4060-001/MW11S4038-011	
C2-62	MW12_2097-008	MW11S4060-001/MW11S4038-011	
C2-62	MW12_2097-009	MW11S4060-001/MW11S4038-011	
C2-62	MW12_2097-010	MW11S4060-001/MW11S4038-011	
C2-62	MW12_2097-011	MW11S4060-001/MW11S4038-011	
C2-62	MW12_2097-012	MW11S4060-001/MW11S4038-011	
C2-63	MW12_2099-001	MW11S4060-004/MW11S4009-015	
C2-63	MW12_2099-002	MW11S4060-004/MW11S4009-015	
C2-63	MW12_2099-003	MW11S4060-004/MW11S4009-015	
C2-63	MW12_2099-004	MW11S4060-004/MW11S4009-015	
C2-63	MW12_2099-005	MW11S4060-004/MW11S4009-015	
C2-63	MW12_2099-006	MW11S4060-004/MW11S4009-015	
C2-63	MW12_2099-007	MW11S4060-004/MW11S4009-015	
C2-63	MW12_2099-008	MW11S4060-004/MW11S4009-015	
C2-63	MW12_2099-009	MW11S4060-004/MW11S4009-015	
C2-63	MW12_2099-010	MW11S4060-004/MW11S4009-015	
C2-63	MW12_2099-011	MW11S4060-004/MW11S4009-015	
C2-63	MW12_2099-012	MW11S4060-004/MW11S4009-015	
C2-64	MW12_2101-001	MW11S4060-014/MW11S4020-012	
C2-64	MW12_2101-002	MW11S4060-014/MW11S4020-012	
C2-64	MW12_2101-003	MW11S4060-014/MW11S4020-012	
C2-64	MW12_2101-004	MW11S4060-014/MW11S4020-012	
C2-64	MW12_2101-005	MW11S4060-014/MW11S4020-012	
C2-64	MW12_2101-006	MW11S4060-014/MW11S4020-012	50
C2-64	MW12_2101-007	MW11S4060-014/MW11S4020-012	
C2-64	MW12_2101-008	MW11S4060-014/MW11S4020-012	
C2-64	MW12_2101-009	MW11S4060-014/MW11S4020-012	
C2-64	MW12_2101-010	MW11S4060-014/MW11S4020-012	
C2-64	MW12_2101-011	MW11S4060-014/MW11S4020-012	
C2-64	MW12_2101-012	MW11S4060-014/MW11S4020-012	