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The genetic basis of partial resistance to powdery mildew in Norwegian wheat

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Abstract

Powdery Mildew caused by (*Blumeria graminis)* is a major problem for cereal production, especially wheat (*Tritium aestivum),* and is an ever-occurring pathogen in Norway. One way for developing wheat cultivars with effective and long-lasting resistance to powdery mildew is to incorporate different Quantitative Trait Loci (QTL) conveying partial resistance. In this study, 296 spring wheat, and 103 winter wheat lines from a collection of wheat lines and cultivars that cover all current and historically important Norwegian cultivars were used. The main objective of the study was to find QTL associated with powdery mildew resistance in the wheat and identify which QTL provides the best resistance. The collected data was from four different localities in different years ranging from 2012 to 2019. The collection was previously genotyped with 35k Affymetrix-SNP array. A total of 14136 and 14089 markers were used for the spring and winter wheat lines respectively, to perform a genome-wide association study. This resulted in identification of QTL shown to be significantly associated with powdery mildew infection, eleven in spring wheat experiments and seven in winter wheat experiments. These QTL were compared with previously documented genes and QTL to establish if the QTL found in present study are previously described or possibly novel that can possibly be used in resistance breeding. In Spring wheat, the 7DS (55 Mbp) QTL is possibly the same as the described *Pm38/Lr34/Yr18* gene. The 7BL (709-713 Mbp) QTL is possibly the same as *Pm5a*. The 2BS (9-19 Mbp), 3AL (621-623 Mbp), 6AL (602-609 Mbp) and 7BL (637 Mbp) QTL are the most important against powdery mildew in MASBASIS lines, moreover, the 7BL and 6AL QTL are possibly pleiotropic to yellow rust, and the same is possible for 6AL with regard to fusarium head blight. In winter wheat, the QTL on 6AL (446-454 Mbp), 7AS (26-30 Mbp) and the second QTL on 7AS (28-33 Mbp) are also recommended for improving powdery mildew resistance.

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Contents

Abbreviations

- PM: Powdery mildew
- APR: Adult plant resistance
- MAS: Marker assisted selection
- RIL: Recombinant inbred lines
- ANOVA: Analysis of variance
- SSR: Simple sequence repeat
- SNP: Single nucleotide polymorphism
- KASP: competative bioscience allele specific
- QTL: Quantitative trait loci
- MIM: Multiple interval mapping
- IWGSC: International wheat genome sequencing consortium
- CIMMYT: International maize and wheat improvement center
- DNA: Deoxyribonucleic acid
- EST: Expressed sequence tag
- Mbp: Mega base pair(s)
- bp: base pair(s)
- cM: centimorgan
- cDNA: complementary DNA
- dNTP: 2'-deoxynucleoside 5'-triphosphate
- PCR: Polymerase chain reaction
- MAS: Marker-assisted selection
- FHB: Fusarium head blight
- Lsmeans: least square means
- LSMAE: least square means for disease severity over all environments
- YR: Yellow rust
- SNB: Septoria nodurum blotch
- Vb : Vollebekk
- St: Staur
- Sa: Sande
- Hs: Holmenstrand
- *Bgt: Blumeria. graminis* f. sp. *tritici*

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Figure 15: Boxplots showing the effects of different haplotypes on powdery mildew severity quantitative trait loci (QTL) on 5A chromosome. Groups are significantly different from groups with a different letter (on top of the plot) based on Tukey's HSD test. The horizontal line in each box represents the median, n= number of lines that had this haplotype.

INTRODUCTION

Wheat

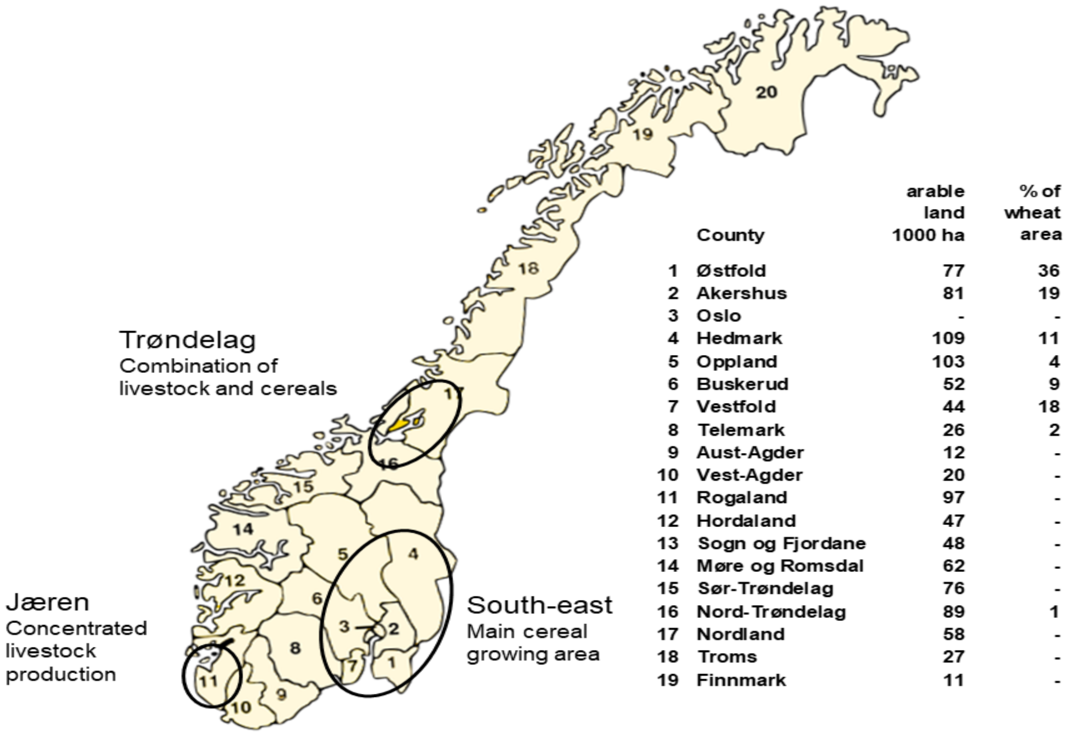
The wheat plant (*Triticum* spp.) has over the years become the most widely cultivated cereal across the globe. This is due to its ability to provide large quantities of food and feed resources to humans and animals in a wide range of products; from flour for breads, biscuits and other baked products to pasta, semolina and the likes (Curtis et al., 2002). A typical wheat grain may consist of about 13% water, 71% carbohydrates, 13% protein, and 1.5% fat. This makes it an important source for multiple nutrients: carbohydrates, vegetal protein and dietary fibre. In addition, non-food products like livestock bedding are also obtained from the whole-wheat plant. Advances in fields like plant genetics and physiology have immensely contributed to improving breeding, production and management of the crop. This has consequently resulted in the wheat plant's dominance and occupancy of the current vast areas of cereal production in the world.

Archaeological record claims that wheat was cultivated first in Fertile Crescent of southwest Asia around 9600 BCE. Even if the crop is most successful in latitudes between 30° and 60°N and 27° and 40°S (Nuttonson, 1955), it can be grown further north and at high elevations near the equator (Curtis et al., 2002). Many wheat species make up the *Triticum* genus. The most widely grown and most economically important is the common bread wheat, *T. aestivum.*

The genetics of wheat is more complicated than most domesticated crops; this is because the genus consists of species with various sets of chromosomes. Some species are diploid, meaning they have two sets of seven chromosomes (2n=14) such as *T. monococcum*. However, the majority of them are polypoid, and have four sets of chromosomes (tetraploid) or six sets of chromosomes (hexaploid). In addition, the wild emmer and durum are typical tetraploids, which developed as a result of hybridisation between two diploid wild grasses driven by natural selection. The hexaploids, like the common wheat (*T. aestivum*) result from crossing between either a domesticated emmer or durum wheat with another wild diploid grass (*Aegilops tauschii*) (Ellstrand et al., 1999).

Norwegian agriculture

Norway is located northwest of the continent of Europe in western Scandinavia between latitudes 57º58' and 71º10'N. Out of a total land area of about 324,000 km2, 3% is arable land, given the cold climate, thin soils, mountainous terrain (44%), forests (38%), lakes (6%) and wetlands (6%). About half of the agricultural production in the country occurs in the south-eastern part of the country, it is an area with fairly mild climate with less rain compared to the other parts of the country, while western and northern parts of Norway has some livestock raising and dairy farming. The area around Trondheim is the next important in terms of cereal production (Lillemo & Dieseth, 2011). The leading crops are cereals—particularly barley, wheat, and oats. Total output in 2017 was 1.307 million metric tons(Statistics Norway, 2019). These regions and the distribution of wheat cultivation in Norway is shown in Figure 1(Lillemo & Dieseth, 2011).



	County	arable land 1000 ha	% of wheat area
1	Østfold	77	36
2	Akershus	81	19
3	Oslo	-	-
4	Hedmark	109	11
5	Oppland	103	4
6	Buskerud	52	9
7	Vestfold	44	18
8	Telemark	26	2
9	Aust-Agder	12	-
10	Vest-Agder	20	-
11	Rogaland	97	-
12	Hordaland	47	-
13	Sogn og Fjordane	48	-
14	Møre og Romsdal	62	-
15	Sør-Trøndelag	76	-
16	Nord-Trøndelag	89	1
17	Nordland	58	-
18	Troms	27	-
19	Finnmark	11	-

Figure1: Distribution of arable land and wheat cultivation in Norway divided per county. The main agricultural areas are indicated by circles. (Lillemo & Dieseth, 2011)

Unstable and rainy spring and autumn weather make climatic conditions one of the most difficult challenges to Norwegian production of wheat. It can cause problems for soil tillage, sowing and harvesting and can affect the quality, due to pre-harvest sprouting or other quality issues. In some years this in turn leads to large proportions of the harvest is downgraded to be used in feed concentrates for livestock, even if the aim is to produce wheat with potential for food for its population. This is affecting the national food security and self-sufficiency as well as resulting in a reduction in price and farmer income.

The Short summer forces many of the farmers to use facilities for drying the grains after harvest to secure and prevent quality losses under humid weather. Norwegian winter has another effect with the snow cover that could lead to snow mould in case when unfrozen ground is covered with snow, this condition can cause total failure of the winter wheat crop. 2018 was another case of unsteady weather with high temperature and low precipitation during the summer and spring. This led to yield losses of nearly 50% compared to a normal year, Figure 2 (Statistics Norway, 2019).

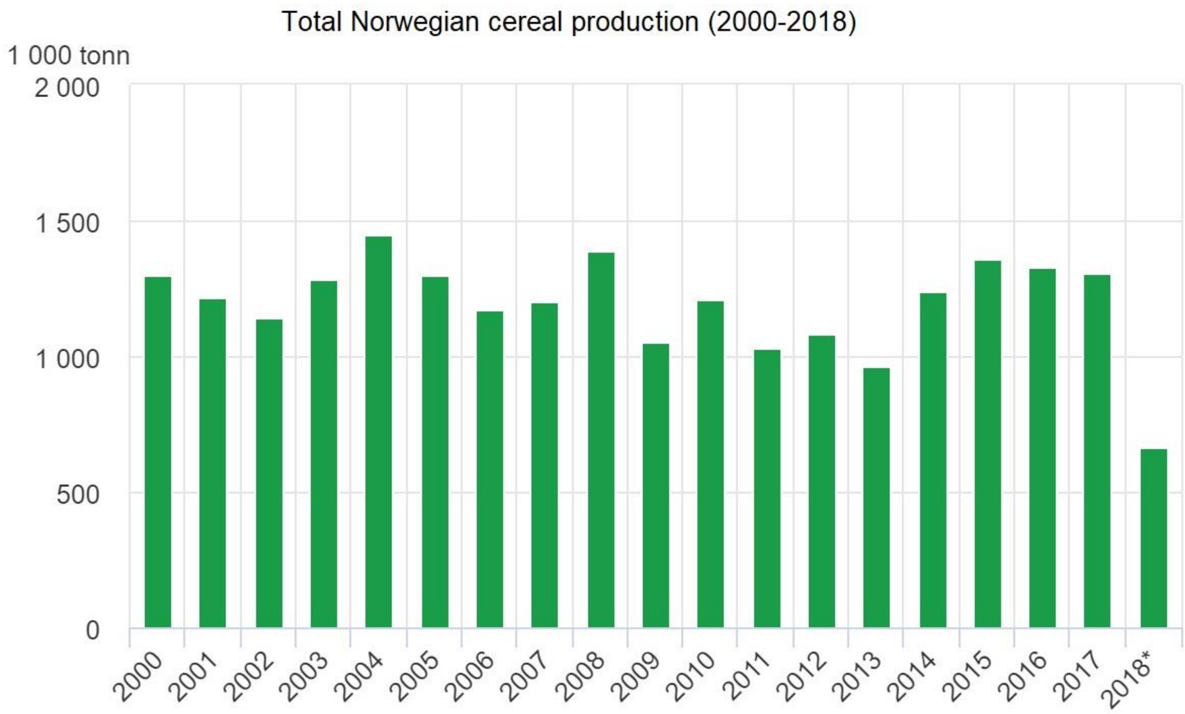


Figure2 : Total Norwegian cereal production (2000-2018), 2018 was according to prediction of Norske Felleskjøp 15.08.2018 (Statistics Norway, 2019)

Wheat in Norway

Norway is close to self-sufficiency for meat, milk and eggs according to Lillemo and Dieseth (2011). , but this can be debated because Norway relies on importing plant protein such as soya beans for production of livestock feed.

The Norwegian wheat production aim is to produce wheat for food and bread wheat is the second-largest cereal crop in Norway, after barley. However, due to quality issues, large quantities have in some years been downgraded to feed and used in concentrations for livestock (Lillemo & Dieseth, 2011). Therefore, it is important to intensify the efforts in reducing quality losses from the challenging weather so that more of the wheat can be used for human consumption to avoid a surplus of feed.

These efforts have their own barriers such as costs that are relatively higher than in most of other countries due to a general high national cost level, the small scale of many farms, challenging climatic conditions and diseases (Lillemo & Dieseth, 2011).

Several diseases attack wheat and have the potential to reduce yield or quality. Powdery mildew (PM) (*Blumeria graminis* f.sp. *tritici*), Septoria Nodorum Blotch (caused by *Parastagonospora nodorum*), Fusarium Head Blight (FHB) (caused by *Fusarium* SPP*)* and recently yellow rust (YR) (caused by *Puccinia striiformis* f.sp. *tritici*) are the most common diseases that threaten the wheat crop in Norway. Resistant host plants reduce the need to apply fungicides and give a better way for controlling diseases (Bennett, 1984; Hsam & Zeller, 2002).

History of Norwegian wheat breeding

The earliest identification of emmer wheat (*Triticum dicoccum*) in Norway is from around 2500 BC, in the form of an imprint of a grain in burnt clay that was found in remnants of a house wall at Kråkerøy in Østfold (Mikkelsen & Høeg, 1979). Since 19th century efforts has been made to improve wheat to suit our needs by breeding, and many new varieties of wheat have been developed.

In Norway Bastian Larsen started the systematic evaluation of Norwegian landraces of wheat in 1889 at the Agricultural University of Norway in Ås. His vital work and the essential contributions from many breeders after him have resulted in a vast array of cultivars that have been released at different times in the history of Norway.

Early wheat breeding in Norway focused on powdery mildew resistance and resulted in release of landmark cultivars like Fram I and Fram II with resistance from the landrace selection J03. Later, crosses were done with foreign cultivars like Pike, Marquis, Sopu and Diamant II to improve yield and quality (Hysing et al., 2007; Lillemo & Dieseth, 2011). A result of this was the cultivar Nora with slightly higher yield and better lodging resistance at that time. A breeding program that was initiated in 1959 for high yield, earliness selection, resistance for various diseases, lodging shattering and sprouting resulted in release of Rollo, Runar and Reno cultivars in the 1960s to 1970s. Semi-dwarf spring wheat lines from CIMMYT were also introduced in 1960s (Lillemo & Dieseth, 2011). Since 2001, seven spring wheat cultivars have been developed Berserk, Demonstrant, Krabat, Laban, Mirakel, Rabagast and Seniorit (Russenes et al., 2019).

The goal of current Norwegian wheat breeding program is to develop wheat of high quality, high yield potential, good agronomic performance, resistance to important diseases such powdery mildew, Leaf Blotch and Fusarium Head Blight (Lillemo & Dieseth, 2011). Graminor is the only company working with variety improvement for the Norwegian market, and is responsible for the Norwegian wheat breeding program. Their work is supported by research at NMBU and other research institutes, such as Nofima Mat (the former Norwegian Food Research Institute, MATFORSK), the Plant Health and Plant Protection Division, Norwegian Institute of Bioeconomy Research (NIBIO). It also has a close collaboration with international breeding companies such as Lantmännen SW seeds (Swedish company). Graminor experimental farm for wheat breeding is in

Bjørke close to the city of Hamar, about 120 km north of Oslo. Graminor goal is to develop marker assisted selection method for important traits and implement a new innovative technological solutions such as Genomic selection with virtual reality to develop methods that bring the field to human evaluation through a VR image (Graminor, 2017).

A collection of wheat cultivars and breeding lines (MASBASIS) that covers all current and historically important Norwegian wheat cultivars and breeding lines has been developed at the Norwegian University of Life Sciences in collaboration with Graminor. This collection contains more than 300 spring wheat cultivars/lines and over 100 winter wheat cultivars/lines. It can be considered as a small core collection of the Norwegian wheat breeding material.

Problem and Justification

Disease is an important factor that can cause reduction in yields and quality and lead to economic losses. The most important diseases that infect wheat in Norway are powdery mildew, Leaf Blotch, Fusarium Head Blight, and in recent years, yellow rust has also become a serious threat to the production (Abrahamsen et al., 2017; Lillemo & Dieseth, 2011).

Powdery Mildew (PM)

Powdery Mildew of wheat is the most common, widespread and recognisable foliar disease that has been given most attention in Norwegian wheat breeding over time. This is because powdery mildew is an ever-occurring disease in the wheat production in Norway (Lillemo & Dieseth, 2011). The Norwegian summer season normally has temperatures between 15 and 25°C and is also characterised by rainfall and wind, which provide ideal conditions for the growth of the pathogen *Blumeria graminis* f.sp. *tritici*. As a result, heavy epidemics are observed on susceptible cultivars nearly every year (Lillemo & Dieseth, 2011). These mild temperatures, high relative humidity and dense stands of wheat provide favourable conditions for powdery mildew development (Agrios, 2005).

Alam et al. (2013) and Griffey et al. (1993) observed that the powdery mildew utilises the host nutrients, and reduces photosynthesis and yield, sometimes by as much as 13-34% and could reach up to 50% if the flag leaf becomes severely diseased by heading and grain filling stage without killing the host plant.

Powdery mildew is observed as white to grey spots or patches on young plant tissues or entire leaves, stems and heads. The fluffy tiny, pinhead-sized white pustules are first detected on the lowest leaves, which later turn into a yellow-brownish colour and finally in the older infections presents black cleistothecia. These are recognised as distinct round black dots within older, grey colonies of powdery mildew and comprise sexual spores (ascospores) that infect in the fall and early spring (Agrios, 2005).

Fungicides are extensively used to control diseases when susceptible cultivars are used and because of the unpredictable Norwegian weather. Therefore, breeding of resistant cultivars is a safer strategy for disease control due to economic and environmental reasons (Lillemo & Dieseth, 2011).

Resistance breeding methods

Major breeding aims include high grain yield, good quality, disease and insect resistance and tolerance to abiotic and biotic stresses. Disease resistance, in this case powdery mildew resistance has been focused in Norwegian breeding (Lillemo & Dieseth, 2011). Use of fungicides is not a durable solution because of the ability of the pathogens to develop fungicide resistance. Rather, resistant plants are a good solution and important to give reliable production of the food. Additionally, resistant plants will reduce the need to use fungicides and thereby avoid environmental side effects and concerns for the consumption of the plant products (Bennett, 1984). Two main types of resistance to powdery mildew have been documented, namely monogenic or race-specific (vertical) and partial or race non-specific (horizontal).

Race-specific resistance

One type of resistance that is governed by single major R *(Pm)* genes of relatively large effects is known as seedling or vertical resistance (Bennett, 1984). These different genes will encode variant plant proteins that are exhibited at the vegetative phase of the life cycle of wheat which identify specific effector molecules of pathogens. Consequently, those R-genes cause a very effective defence response, the hypersensitive response against pathogens upon invasion, which causes the host tissue to undergo a rapid, programmed cell death.

Race specific resistance genes are able to recognise the avirulence gene products of the pathogen in a gene for-gene system (Flor, 1956).

This type of resistance is easy to select for, reachable with simple genetics, provides complete protection against specific races of pathogens. Race-specific resistance works usually against only some isolates of powdery mildew, but is ineffective against others (Hsam & Zeller, 2002). A single mutation in the pathogen can leave the plant susceptible. In addition, airborne spores can be dispersed over a large area. Typically, *Blumeria graminis* has a short generation time, a big population size and sexual reproduction with the possibility of a pathogen surviving between the growing seasons. For all those reasons, the powdery mildew pathogen will evolve to overcome single race-specific resistance (Burdon et al., 1996). This results in short durability of race-specific resistance genes against the fungal pathogens (Hsam & Zeller, 2002; McDonald & Linde, 2002).

Here in Norway, the spring wheat cultivars Bastian, Polkka, Brakar and Avle were resistant at the time of their release, but became susceptible within 1-3 years due to rapid occurrence of new virulence, which demand release of new resistant cultivars continuously (Lillemo et al., 2010; Skinnes, 2002). Because of the lack of sustainability when it comes to race specific resistance genes to powdery mildew in Norway, research has focused on partial or race non-specific resistance in recent years.

Race non-specific resistance

Also called partial, horizontal, adult plant resistance (APR) (Griffey et al., 1993) and slow mildewing (Roberts & Caldwell, 1970), race non-specific resistance is reported to be the most sustainable of the two types of resistance. This because it is based on several resistance genes working together to reduce the infection efficiency of the pathogen. They also retard growth and reproduction of the pathogen, especially in adult plants stage (Shaner, 1973). Furthermore, partial resistance genes appear to be equally effective to different virulent strains, which makes it difficult for pathogen populations to adapt (Parlevliet & Zadoks, 1977). However, it is documented that a combination of both partial and race-specific resistance could achieve a more durable resistance in the wheat plant (Bennett, 1984; Shaner, 1973; Shaner & Finney, 1975).

Breeding for quantitative partial resistance is more effective and considered more durable to all races of powdery mildew pathogen. Due to the presence of race-specific genes that can mask the effect of race non-specific resistance genes during field selection it can be challenging to identify and select partial resistance genes in the field (Keller et al., 1999; Lillemo et al., 2010). It is therefore very important to understand the genetic architecture of partial resistance to improve the efficiency of wheat breeding for powdery mildew (Shaner & Finney, 1975).

Molecular markers

A molecular marker (identified as genetic marker) is a fragment of DNA that is linked with a specific DNA sequence with a known location on a chromosome within the genome. It is a variation that may arise due to mutation or alteration in the genomic loci that can be observed. For many years it was restricted to identifying organisms by traditional phenotype markers. Later, it has been used for many approaches such as characterise plant germplasm, marker-assisted introgression of favourable alleles and variety protection and gene isolation (Andersen & Lübberstedt, 2003).

Molecular genetic markers can be biochemical markers, which identify variation at the gene product level like changes in proteins and amino acids(Collard et al., 2005), or markers that detect difference at the DNA level like nucleotide changes, duplication, deletion, inversion or insertion. Markers can be successfully applied for tracing favourable alleles (dominant or recessive) across generations and detecting the most suitable individuals among the segregating progeny (Ibitoye & Akin-Idowu, 2010). If the genetic pattern of homozygotes can be distinguished from heterozygotes, then a marker is considered to be co-dominant. Generally co-dominant markers are more informative than the dominant markers (Huang & Röder, 2004; Mohan et al., 1997).

DNA markers arise from different types of mutation. Most markers are neutral because they are located in the DNA non-coding regions. Some markers are located within gene sequences and such markers are often referred to as "functional markers" (Yadav et al., 2016). DNA markers help to reveal differences between individuals (polymorphisms) of the same or different species by tracing a specific DNA sequence in a genome. Polymorphic DNA markers can easily expose the differences between individuals of a same or various species while monomorphic DNA markers cannot sort genotypes (Collard et al., 2005).

A genetic marker may be a short DNA sequence, such as a single base-pair change (single nucleotide polymorphism, SNP), or a longer one, like minisatellites. Different types of molecular markers have been used to localise 77 powdery mildew resistance genes in the wheat genome (Li et al., 2014).

Types of molecular markers:

- RFLP (or restriction fragment length polymorphism)
- AFLP (Amplified Fragment Length Polymorphism)
- SSR Microsatellite polymorphism, (Simple Sequence repeat)
- SNP (Single Nucleotide Polymorphism)
- KASP (Kompetitive Allele Specific PCR)

Simple Sequence Repeats SSRs (microsatellites)

The phenomenon of repetitions of a short DNA sequence tends to produce different numbers of repeat of the nucleotide bases (Adenine, Cytosine, Guanine and Thymine) called satellite DNA. These nucleotide bases have a different density from bulk DNA - such that they form a second or 'satellite' band when genomic DNA is separated on a density gradient.

Although the first microsatellite was characterised in 1984 at the University of Leicester by Weller and colleagues as a polymorphic GGAT repeat in the human myoglobin gene (Weller et al., 1984), the term "microsatellite" was introduced later by Litt and Luty (1989), also known as short tandem repeats (STRs), or simple sequence length polymorphism (SSLPs) (Litt & Luty, 1989).

In early 1990s the increasing availability of DNA amplification by PCR, microsatellite genetic markers became the workhorse for genome-wide analyses to locate any gene responsible for a given phenotype or disease because of their high level of polymorphism, abundance, high detection ability, co-dominant inheritance and good genome coverage (Powell et al., 1996).

Although the rise of higher quantity and cost-effective single-nucleotide polymorphism (SNP) platforms led to the era of the SNP markers for genome scans, SSRs remain highly informative measures of genomic variation for linkage and association studies (Ganal & Röder, 2007). Their continued advantage lies in their greater allelic diversity than biallelic SNPs, thus microsatellites can differentiate alleles within a SNP-defined linkage disequilibrium block of interest.

Single Nucleotide Polymorphisms

Abbreviated to SNP is a single nucleotide (A,T,G,C) at specific position in the genome that has been substituted with another nucleotide. In principle, any of the four alleles can be present at each nucleotide position because of four existing nucleotide types, but in practice, only two allelic variants occur (Syvånen et al., 1999). Therefore, because of the mutation bias or unequal concurrency of the nucleotide transition (A/G, T/C) and transversions (A/ C, A/ T, G/ C, G /T), SNP markers are bi-allelic in nature (Khlestkina & Salina, 2006). These substitutions of bi-allelic markers can differentiate the minority individuals from the majority.

SNP markers are abundant, co-dominant and evenly distributed across the genome. Consequently, a huge number of SNP markers may occur within coding sequences of genes, non-coding regions of genes or in the intergenic regions across the genome. The high-density genotyping arrays in wheat breeding further expand the improvement of resources for SNP markers and the construction of high-resolution genetic maps can give a better understanding of the genetics of complex traits. Nonetheless, due to the redundancy of the genetic code (Degeneracy) SNPs within a coding sequence do not necessarily change the amino acid sequence of the protein that is produced.

Utilisation of SNP markers is useful and can offer enormous quantity of useful and cost-effective markers for genotype–phenotype association studies that make SNP an ideal marker method. Several articles have underlined the interest of developing and identifying SNP markers for resistance in plants (Zhang et al., 2003). In hexaploid wheat, Cavanagh et al. (2013) developed high throughput Infinitum iSelect 9K SNP genotyping array and constructed high density SNP map. Wang et al. (2014) developed high-density 90K SNP genotyping array and used it to characterise genetic variation in allotetraploid and allohexaploid wheat populations. Allen et al. (2017) characterised Affymetrix 35K as a wheat breeders' array suitable for high-throughput SNP genotyping of global accessions of hexaploid bread wheat.

Kompetitive Allele Specific PCR (KASP)

KASP is one of the numerous uniplex SNP genotyping platforms that combine a variety of chemistries and has advanced to be a global benchmark technology(Semagn et al., 2014).

KASP is a homogeneous, fluorescence-based genotyping technology, developed initially by KBioscience (Kumpatla et al., 2012), the high rates of the ability to design an assay make it the most used uniplex SNP genotyping platforms (Semagn et al., 2014). Few numbers of markers can provide scalable flexibility for mapping of quantitative trait locus QTL in bi-parental populations (Semagn et al., 2014).

SNP rates (the ability to design an assay) vary from 50 to 97% and have highly successful conversion rates from one platform to another (Fan et al., 2003). Genomics service labs in North America and Europe (LGC) have stated that KASP achieves higher rates of successful assay design (98–100 %) and conversion to successful working assays (93–94 %) than for instance TaqMan (72 and 61 %, respectively) (www.biosearchtech.com)

There are three components in a KASP reaction: KASP primer mix, KASP master mix and template DNA. KASP primer mix consists of two alleles specific forward primers and one common reverse primer, each forward primer contains a simple unlabelled tail sequence, which is an additional string of bases that are not complementary to the target DNA at the 5' end but corresponds with a universal FRET cassette. The KASP master mix contains all other components that are necessary for the PCR, it also contains two florescent labelled reporter cassettes, each cassette is comprised of two oligoneoclutides , one of which is labelled with fluorophore (FAM, HEX) and the other which includes the quencher. The third component consists of the taq DNA polymerase, free nucleotide and Magnesium dichloride (MgCl2). (www.biosearchtech.com)

Association mapping

A quantitative trait locus (QTL) is a locus (a region of DNA) which is associated with variation of a quantitative trait in the phenotype. Within this region, there are one or a few genes which are responsible and can explain variation in a phenotypic trait. In other words, it is a "genetic locus where functionally different alleles segregate and cause significant effects on a quantitative trait" (Salvi & Tuberosa, 2005). QTL can be found on different chromosomes, and the number of QTL can vary for the various traits, i. e some QTL may indicate that resistance to a disease is controlled by many genes with small effect, or few genes with large effect, or combination of genes with varying effects. DNA and molecular revolution has made it possible to identify many QTL that are responsible for economic traits in wheat.

Association mapping is one of the methods used to detect QTL. It takes advantage of a historic linkage disequilibrium to link observable phenotypic characteristics to the genotypes, uncover marker-trait associations, and map quantitative trait loci QTL with high resolution in a way that is statistically very powerful. Marker-trait associations identify molecular markers (such as SNPs or SSR markers) significantly correlated with a phenotypic trait by conducting Genome-wide association analysis (Gupta et al., 2014).

Genome Wide Association Study (GWAS) is useful to identify SNPs and other molecular markers associated with a disease or other traits, but this method cannot specify which genes are causal. However, it requires extensive knowledge of SNPs within the genome of the organism of interest, and is therefore difficult to perform in species that have not been well studied or do not have well-annotated genomes (Gupta et al., 2019). Fortunately, the whole genome of hexaploid wheat of the cultivar Chinese Spring was sequenced and released in 2018 (IWGSC, 2018), which serves as a reference genome, GWAS can be more easily applied in research of this species.

Marker-assisted selection

Marker assisted selection or marker aided selection (MAS) is the ability to select important phenotypic traits using markers tightly linked to genes controlling the trait (e.g. productivity, disease resistance, stress tolerance, and quality). Young expressed his vision ”Even though marker-assisted selection now plays a prominent role in the field of plant breeding, examples of successful, practical outcomes are rare” (Dale Young, 1999) as of 2011, "To date, more than 2500 studies on mapping in plants have been published. Yet, Young’s (1999) optimistic vision has still not become a reality, and breeding programs based on DNA markers for improving quantitative traits in plants are rare." (Altman & Hasegawa, 2011). Now, as of 2019, genomic selection is changing the circumstances and is on its full way into plant breeding programs, especially big companies have already fully implemented this technology, and many plant breeders such as Graminor are doing research and planning to implement it.

Genomic selection (GS)

GS is a method that uses genome-wide molecular marker data to predict the genetic value of untested lines in breeding programs. The aim of GS is to define the genetic potential of an individual instead of identifying the specific QTL (Heffner et al., 2011). GS method was originally developed in livestock breeding to predict breeding values using simulated data of individuals based on genome-wide markers (Xu, Y. et al., 2020). It should be pointed out that plant breeders already developed similar concepts such as genome-wide dense marker maps (Meuwissen et al., 2001) before GS was established.

The data used to train GS models has proven to have big effects on the accuracy of GS results such as the size of the training population, relationships between individuals, marker density, and use of pedigree information (Jannink et al., 2010). Though, the optimal strategy for enforcement of GS in a plant-breeding program is still uncertain (Robertsen et al., 2019), but GS method has assured to outperform the deficiency of MAS by utilising both large- and small-effect QTL with large numbers of genome-wide molecular markers to predict complex traits. (Heffner et al., 2011).

Fortunately, all of the relevant markers in MAS studies can be used as a database in GS panels and can give better estimation to predict the perfect phenotype. (Arruda et al., 2016)

Mapping of powdery mildew resistance genes

The first powdery mildew resistance gene *Pm1* was described in 1953 (Pugsley & Carter, 1953). Since then, more than 82 powdery mildew resistance genes or alleles have been characterised at 54 loci and assigned to specific chromosomes and chromosome arms in common wheat (McIntosh RA et al., 2017), but most of them are race-specific and are easily overcome by new *B. graminis* f. sp. *tritici* (*Bgt)* isolates (Li et al., 2014). On the contrary, some of them are race-non-specific resistance genes such as *Pm38* and *Pm39* that were described by Lillemo et al. (2008) by using SSR markers, which show strong partial resistance to powdery mildew and are pleiotropic to the rust resistance genes, *Pm38* is pleiotropic to Lr34/Yr18 and *Pm39* is pleiotropic to Lr46/Yr29.

Project Aim

The main aim of this master thesis project was to find the QTL for powdery mildew resistance in Norwegian spring and winter wheat, and verify the QTL that provide best resistance.

Specific aims:

- Identify the markers that are linked to interesting QTL.
- Compare the identified QTL with the documented ones.
- Recommend new QTL that were found.

Materials and Methods

Plant Material

The Norwegian wheat cultivars were the plant material of interest. A collection of wheat cultivars and breeding lines known as 'MASBASIS' was used for this project. The 'MASBASIS' covers all current and historically important Norwegian wheat cultivars. The set contain 296 spring wheat lines and 103 winter wheat lines. Full lists of MASBASIS lines are attached in Appendix Table 1 and 2. These lines include significant sources of disease resistance (race specific and non specific) and quality traits, crossing parents and advanced breeding lines from Graminor (Norwegian plant breeding company). MASBASIS has been genotyped with SNP markers (Affymetrix 35K wheat array)(Allen et al., 2017)as a part of ongoing collaborative wheat projects between Graminor and NMBU (Norwegian University of Life Sciences), and was used for this study.

Previously tested SSR and KASP markers were also added to the data set. As described in the following section, statistical methods were used to find associations between markers and powdery mildew resistance, correcting for population structure and kinship.

Field orientation

The study was conducted at four locations in south-eastern Norway. Vollebekk (Vb) research farm at the Norwegian University of Life Sciences, Ås (59°N, 90 m above sea level), Staur research farm close to Hamar (60°N, 153 m above sea level), Sande (Sa) research field (NLR viken) in Vestfold (59°N, 25 m above sea level) and Bringaker field close to Holmenstrand (Hs) (59°N, 123 m above sea level) in Vestfold. All four locations experience natural epidemics of powdery mildew, but Ås and Hamar have been described as being characterised with different *B. graminis* f. sp. *tritici* virulence compositions (Skinnes, 2002). The hill plot method was adopted for this project using alpha lattice block design (12 plots per blocks) with at least two replications for each cultivar/line at each location. For the spring wheat trials, Avocet (susceptible) was used as a border and Bastian (moderately susceptible) was used as a barrier between the susceptible border and the trial plots. For the winter wheat trials, Kanzler (susceptible) and Bjørke (moderately susceptible) were used as borders in a similar fashion. Each trial was planted with 50 cm between plots and 40 cm between each row.

Powdery mildew for the spring wheat was evaluated in Ås and Staur since 2012. Sande field was evaluated just in 2018 and Holmestrand just in 2019, while for the winter wheat; powdery mildew was evaluated just in Ås since 2014. All of the disease scoring data was done for projects supervised by Morten Lillemo and this data has been granted from him for the purpose of this project, while I did the powdery mildew scoring of the 2018 field trials in Vollebekk, Staur and Sande. Powdery mildew disease severity was scored on leaves as the percentage of leaf area infected, using a modified Cobb scale (0 to 100% infected leaf area) (Peterson et al., 1948) at the time when the susceptible checks (Avocet and Kanzler for spring and winter wheat, respectively) obtained their maximum severity. Due to the high epidemic variance in Vb -2016 winter field, the scoring was done twice with a period in between, these scores have been considered as two fields (1-Vb16, 2-Vb16)

Statistical analysis

Phenotypic analysing

Least Squares Means (lsmeans) can be defined as a linear combination (sum) of the estimated effects from a linear model. These means are based on the used model. Lsmeans are preferred because they reflect the model that is being fit to the data and will adjust according to the field variability between blocks in alpha-lattice models. Therefore, PROC MIXED was used to statistically analyse the disease severity to calculate lsmeans. Each lsmean is computed as $\mathbf{L}\hat{\boldsymbol{\beta}}$, where $\mathbf{L}$ is the coefficient matrix associated with the least squares mean and $\hat{\boldsymbol{\beta}}$ is the estimate of the fixed-effects parameter vector.

Lsmeans of powdery mildew severity from each line was used and calculated to estimate disease severity in each environment (location/year). The SAS statistical package (SAS 9.4) and mixed linear model PROC MIXED was used with lines as fixed effects, replicates and blocks within replicates, as random factors.

For spring wheat, lsmeans were calculated for all environments defining lines as fixed effects and environments as random effects. Furthermore, lsmeans for all locations were also calculated for three different periods 2012-13-14, 2015-16 and 2017-18-19. Lsmeans were also calculated for Staur and Vollebekk separately, for each location by itself defining years as random effects and lines as fixed effects.

Additionally, winter wheat’s lsmeans were calculated for each line in each environment and over all environments.

Unscrambler X was used to perform Principal Component Analyses (PCA) of the phenotypic data.

Population structure

The combined evolutionary processes such as mutation, genetic drift, isolation, natural selection and recombination will lead to the formation of subpopulations; these subpopulations will have systematic difference in allele frequency between them.

I used the population structure that Camille Branchereau provided in her master thesis: "The population structure was calculated with a subset of 938 single nucleotide polymorphism (SNP) markers for both winter and spring wheat populations and estimated with STRUCTURE v2.3.4 with a Bayesian clustering method (Pritchard et al., 2000). The analysis was performed for K from 1 to 10, 5 000 burnin length, 50 000 repetitions (numbers of Markov chain Monte Carlo, MCMC) and 3 iterations per run. Output results are then analysed using Structure Harvester (http://taylor0.biology.ucla.edu/structureHarvester/). This program processes STRUCTURE results and, by using the Evanno method (provided there is at least 3 replicates (Evanno et al., 2005), detects the number of K groups that best fit the dataset (Earl, 2012). With these results, R-Studio was then used to perform principal component analyses (PCA), often used in population genetics (Engelhardt & Stephens, 2010; Patterson et al., 2006)."

Branchereau (2018)described that the population stratification could be explained by the origin of the lines. The 103 winter wheat set (population) was divided in two subpopulations; the first subpopulation mainly contained German and English lines, while the second composed of lines from Norway and Sweden.

The 299 spring wheat panel was also divided in two subpopulations; the first subpopulation contained lines from the northern European countries (Norway, Sweden, Germany and Finland), whereas the second subpopulation contained lines from the international maize and wheat improvement centre (CIMMYT), Australia, China and the USA.

Genetic diversity

The markers for the study were chosen based on the Affymetrix 35k SNP chip(Allen et al., 2017). A total of 14136 markers for spring wheat and 14089 for winter wheat were chosen as the respective markers to be used in further analyses. Markers with minor allele frequency >=5% were filtered out and heterozygosity were treated as missing. The total of markers consisted of a combination of SNP markers, SSR markers and KASP markers.

Genotypic analysis

Association mapping analysis can be a helpful method in identifying the molecular markers significantly linked to traits of interest. In this case mixed linear modelling (MLM) was used to perform the association mapping analyses. MLM includes both population structure and kinship, and reduces type I error due to relatedness and population structure. Both genotype data including SNP markers and phenotype data from the field trials were used in the statistical software Tassel v.5.2.7 (Bradbury et al., 2007) along with a kinship matrix constructed from the genotypic data and population structure results from STRUCTURE v. 2.3.4 .

Association mapping

Markers that associated with powdery mildew were identified using mixed linear model (MLM) in TASSEL v.5.2.7 with regression model: MLM + kinship matrix (K) + population structure matrix derived from (Branchereau, 2018). SNP markers were filtered for allele frequencies over 0.05 and heterozygosity were treated as missing. A p-value was calculated for each SNP marker based on MLM that has the form $y = Xb + Qv + u + e$, where y is the vector of the phenotypic values (best linear unbiased predictors), X is the vector of SNP marker genotypes, b is the vector of marker fixed effects to be estimated, Q is the population structure matrix derived from structure analysis, v is a vector of fixed effects due to population structure, u is the vector of random effects, and e is the vector of residuals.

Significance threshold

To study partial resistance which include many QTL with minor effect with about 14 thousand markers, Bonferroni correction will not fit with my data with $\alpha = 0.05$, giving a threshold of $-\log10 (0.05/14136) = 5.451$ for the spring and almost the same for winter wheat $-\log10 (0.05/14097) =5.541$. Therefore, an arbitrary threshold of $-\log10(p)=3$ was chosen to detect potential QTL involved in powdery mildew resistance in this study, which is more relevant for capturing most of the relevant QTL governing the trait. However, with this threshold, one cannot exclude the possibility of also detecting some false positive marker-trait associations and results should therefore be interpreted with care. (Gupta et al., 2014)

Allele Stacking and Haplotype Analysis

TASSEL output were analysed in R Studio (R studio 1.2.1335) with 'Tidyverse' package for allele stacking. To examine the effect of accumulated resistance alleles in cultivars/lines, they were assigned to groups according to their number of resistance alleles. The resistant allele was detected from TASSEL results based on the predicted effect of significant markers associated with the QTL from the environments. Significant difference between the groups were determined by a Tukey's HSD test.

R studio was also used with 'MultcompView' package for haplotypes analysing. Two different QTL were further studied on 5AL chromosome (one for spring wheat and one for winter wheat) by haplotype analysis, these QTL were chosen due to their high value for –log10 (p-value) for PC1 and their stability across environments. Three markers were used for haplotype construction based on their location near the significant peak marker of the QTL and their high – log10 (p-value). Also, significant difference between the groups were determined by a Tukey's HSD test.

QTL Comparison with previous researches

The studied SNP markers that showed association with powdery mildew were assigned to chromosomes with the accurate physical position from a comparison of SNP sequences with the Chinese spring reference genome RefSeq 1.0 (IWGSC, 2018). SSR markers were also assigned to chromosomes based on comparison of SSR primers with the Chinese Spring sequence based on public BLASTn.

https://urgi.versailles.inra.fr/blast/?dbgroup=wheat_iwgsc_refseq_v1_chromosomes&program=blastn

A high percentage of the previous researchers used SSR markers in their reports and few of them have published the primer sequence for the flanking marker. Unpublished SSR primer sequences were obtained from a digital platform that serves small grains research communities (GrainGenes) and assigned them in the Chinese Spring sequence to get physical position.
https://wheat.pw.usda.gov/cgi-bin/GG3/browse.cgi?class=marker

A meta-analysis of partial resistance loci to powdery mildew in wheat was presented by Lillemo and Lu (2015), an overview and application of QTL for Adult Plant Resistance to Leaf Rust and Powdery Mildew in Wheat was published by Li et al. (2014). A collection for genes associated with powdery mildew resistance with the source of identification and their chromosomal location were collected by Shah et al. (2018). All above sources were also used as a database to compare with the SNP markers detected here. In addition, many studies are using SNP markers and it is relevantly easier to compare with, such as (Leonova, 2019; Xu, X. et al., 2020).

RESULTS

Phenotypic analysis of Powdery Mildew (PM) resistance

Disease severity distributions for MASBASIS spring wheat lines (at Staur and Sande) and winter wheat lines (at Vollebekk) from 2018 are shown in Figure 3 below.

The severity of powdery mildew was low for both Sande and Vollebekk (Vb). In 2018, however, the crops in Sande (Sa) and Vollebekk experienced less favourable conditions for powdery mildew infestation than Staur (St), due to very warm temperatures. Maximum powdery mildew severity in winter wheat in Vollebekk was approximately 30% and that was registered for 'Ellvis'. In spring wheat, the maximum severity in Sande was 80% registered for 'Reno, Sirius, and 512-87', while in Staur the maximum of 80 % was registered for 'T10014, Chara and Avocet YrA'.

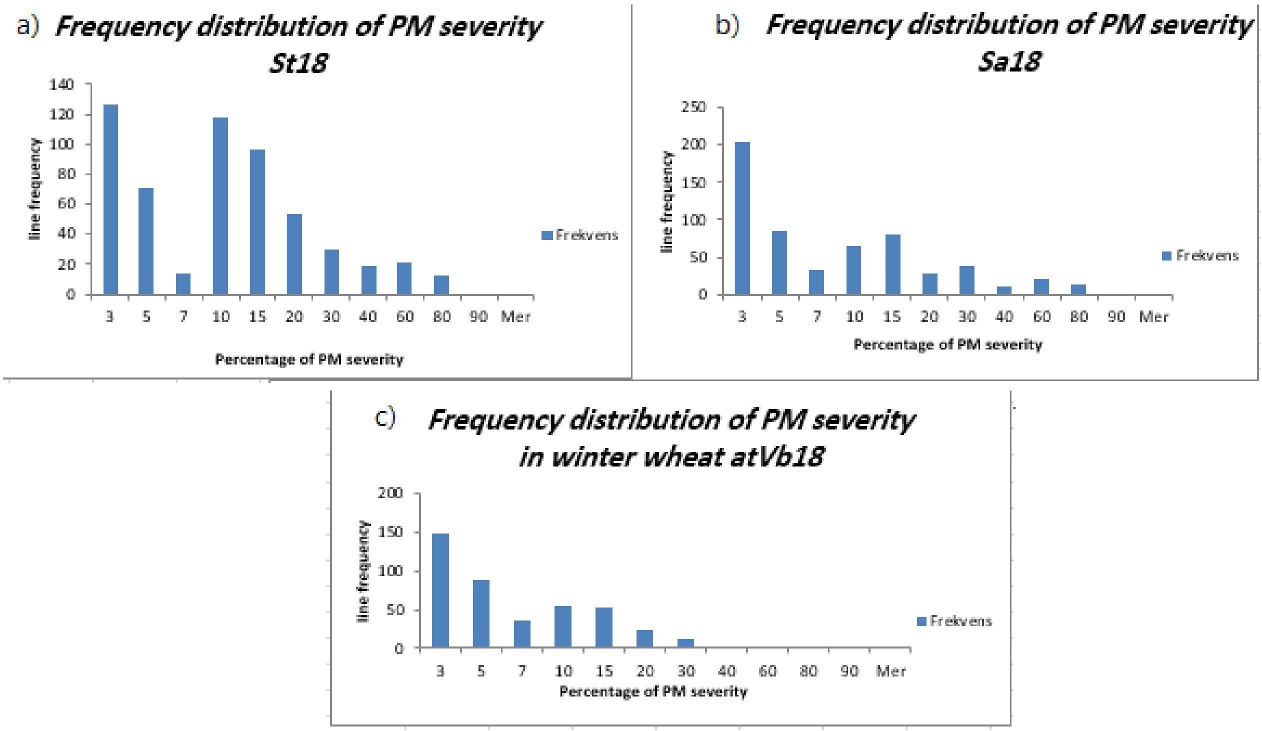


Figure 3 : Frequency distribution of powdery mildew severity in 2018 for MASBASIS at three different localities a) Sande spring wheat field, b) Sande spring wheat field and c) Vollebekk winter wheat field.

All of the phenotypic data for both winter (2014-2019) and spring wheat (2012-2019) were run in SAS package (SAS 9.4) mixed linear model PROC MIXED to statistically analyse the disease severity to calculate least square means (Lsmeans) for the phenotypes with lines as fixed effects. SAS outputs with the estimated covariance parameter for the random effects and results of tests for the fixed effects are presented in Table1 and 2 for Sande spring field (2018), Table 3 and 4 for Staur spring fields (2018), Table5 and 6 for all spring environments, Table 7 and 8 for Vollebekk winter field

(2018) and Table 9 and 10 for all winter wheat environments. These Tables show that line effects were significant in all environments. Which means that the data is useful for association mapping. Also, that in some environments there was variability within the field that was used by statistical model to estimate the lsmeans of the line effects. Some of these effects were in blocks level (Sande 2018 Table1 and Vollebekk 2018 Table 7), or in the replications within the blocks (sande 2018 Table1 and Vollebekk Table 7) or of the column (Vollebekk 2018 Table 7).

Table1: Covariance parameter Estimate for spring wheat Sande 2018

Covariance Parameter Estimates				
Cov Parm	**Estimate**	**Standard Error**	**Z Value**	**Pr > Z**
Rep	9.3408	13.8580	0.67	0.2501
Block(Rep)	4.5648	3.4535	1.32	0.0931
Column	0	.	.	.
Residual	71.7293	6.6211	10.83	<.0001

Table2: Test of fixed effect for spring wheat Sande 2018

Type 3 Tests of Fixed Effects				
Effect	**Num DF**	**Den DF**	**F Value**	**Pr > F**
Line	299	217	4.76	<.0001

Table3: Covariance parameter estimate for spring wheat Staur 2018

Covariance Parameter Estimates				
Cov Parm	**Estimate**	**Standard Error**	**Z Value**	**Pr > Z**
Rep	0.1292	0.4247	0.30	0.3805
Block(Rep)	0	.	.	.
Column	0	.	.	.
Residual	45.6849	3.9174	11.66	<.0001

Table4: Test of fixed effect for spring wheat Staur 2018

Type 3 Tests of Fixed Effects				
Effect	**Num DF**	**Den DF**	**F Value**	**Pr > F**
Line	300	215	9.21	<.0001

Table5: Covariance parameter estimate for all spring environments

Covariance Parameter Estimates				
Cov Parm	**Estimate**	**Standard Error**	**Z Value**	**Pr > Z**
Environment	13.5714	5.1074	2.66	0.0039
Residual	110.04	2.4830	44.32	<.0001

Table6: Test of fixed effect for all spring environments

Type 3 Tests of Fixed Effects				
Effect	**Num DF**	**Den DF**	**F Value**	**Pr > F**
Line	302	3928	19.71	<.0001

Table7: Covariance parameter Estimate for Winter wheat Vollebekk 2018

Covariance Parameter Estimates				
Cov Parm	**Estimate**	**Standard Error**	**Z Value**	**Pr > Z**
Rep	0.9641	1.3290	0.73	0.2341
Block(Rep)	1.9458	1.3566	1.43	0.0757
Column	0.1186	0.6255	0.19	0.4248
Residual	26.1234	2.4778	10.54	<.0001

Table8: Test of fixed effect for winter wheat Vb 2018

Type 3 Tests of Fixed Effects				
Effect	**Num DF**	**Den DF**	**F Value**	**Pr > F**
Line	135	226	2.21	<.0001

Table9: Covariance parameter Estimate for all winter environments

Covariance Parameter Estimates				
Cov Parm	**Estimate**	**Standard Error**	**Z Value**	**Pr > Z**
Environment	8.5835	5.0889	1.69	0.0458
Residual	20.4440	1.2284	16.64	<.0001

Table10: Test of fixed effect for all winter environments

Type 3 Tests of Fixed Effects				
Effect	**Num DF**	**Den DF**	**F Value**	**Pr > F**
Line	103	554	11.42	<.0001

Lsmeans disease score for some of the main spring cultivars in 2018 are shown in Figure 4. Naxos (German) and Saar (CIMMYT) cultivars are known for their partial resistance against powdery mildew, they showed a higher disease resistance under 2018 condition in both Sande and Staur fields. Avocet YrA is known as a susceptible cultivar showed a higher susceptibility in 2018 than the lsmeans for all environments. Mirakel (47.9% of Norwegian market shares in 2019,Norway) and the newly released Seniorita (0.04 of Norwegian market shares, Norway) (Strand, 2019) showed a higher powdery mildew severity in Sande than Staur and all environments.

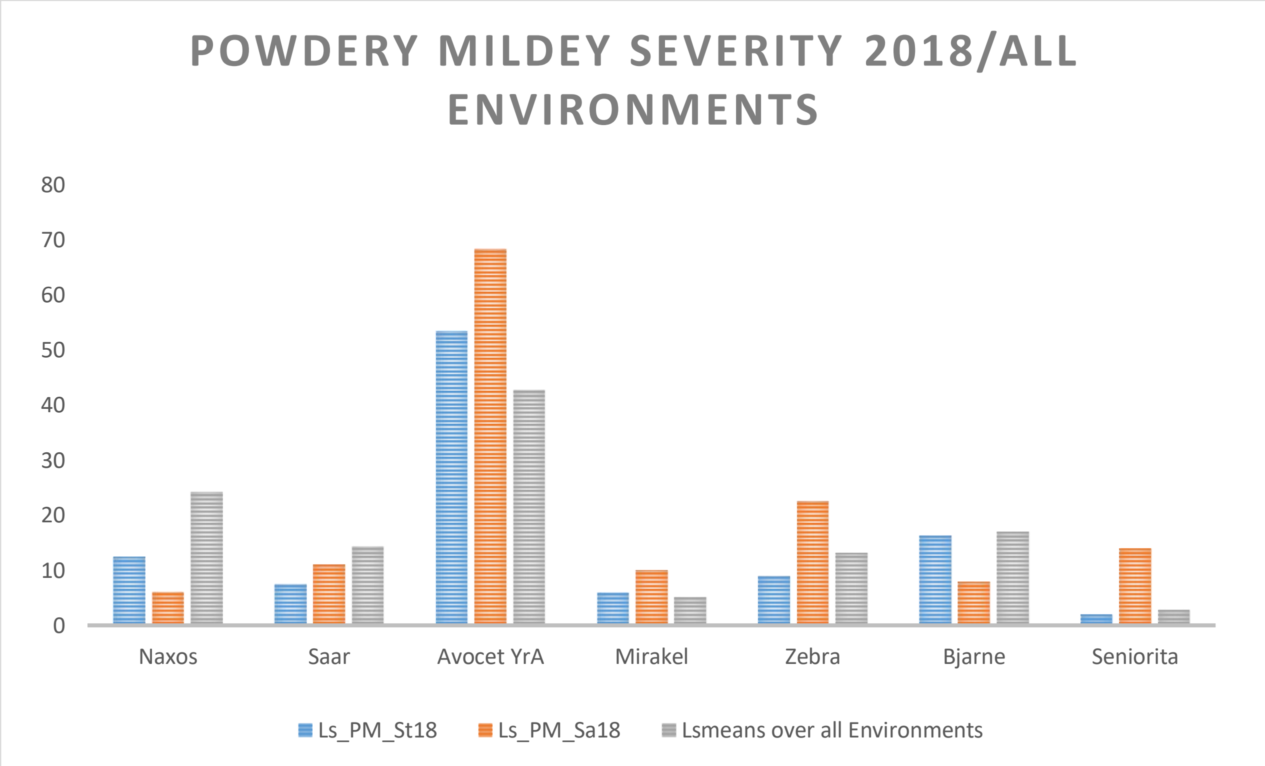


Figure 4: Lsmeans for powdery mildew severity in main spring cultivated cultivars (Mirakel, Zebra, Bjarne and Seniorita), important sources of partial resistance (Naxos and Saar) and susceptible check (Avocet YrA) in Staur 2018 (blue bars), Sande 2018 (orange bars) and all environments in (grey bars).

In like manner, in winter wheat lsmeans for some of the main winter cultivars in 2018 are shown in Figure 5. Massey (USA) and Fenman (UK) cultivars with high levels of partial resistance, Bjørke (Norwegian) is a moderately susceptible cultivar to powdery mildew. Ellvis (61.7% of Norwegian market shares, Germany), Kuban (16.3% of Norwegian market shares, Germany), Magnifik (3.6% of Norwegian market shares, Sweden), Olivin (3.9% of Norwegian market shares, Germany) are good example of the cultivars that are cultivated in Norway (Strand, 2019). Kanzler (Germany) is a susceptible check to powdery mildew. All of them showed a less powdery mildew severity in 2018 compared with the lsmeans over all years.

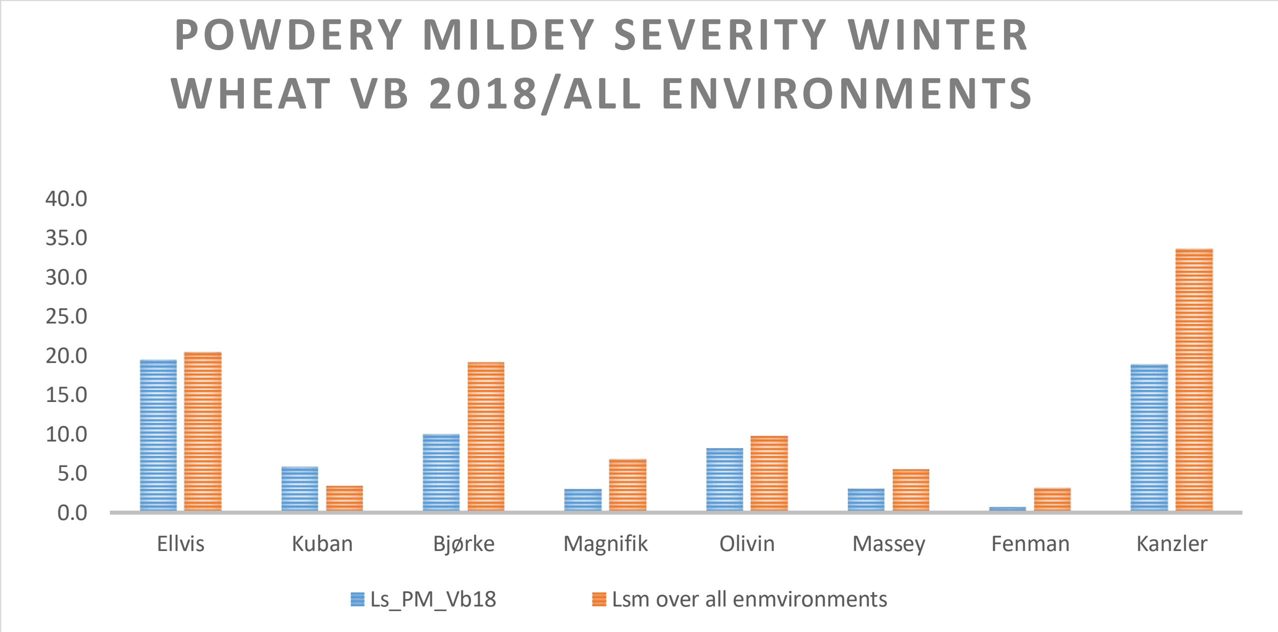


Figure 5: Lsmeans for powdery mildew severity in main spring cultivated cultivars (Ellvis, Magnifik, Olivin, and Kuban), important sources of partial resistance (Massey and Fenman), moderately susceptible (Bjørke) and susceptible check (Kanzler) in Vollebekk 2018 (blue bars) and all environments in (orange bars).

Then all of SAS data were run in Unscrambler X to perform Principal Component Analyses (PCA) and define powdery mildew resistance in 297 spring and 103 winter lines displaying PC1 against PC2. PC1 could explain 89% of the variance for the spring wheat all over the 16 environments (location/year) in between 2012-2019 (6) and could explain 78% of the variance in winter wheat lines all over 6 environments in between 2014-2019 (Figure 7).

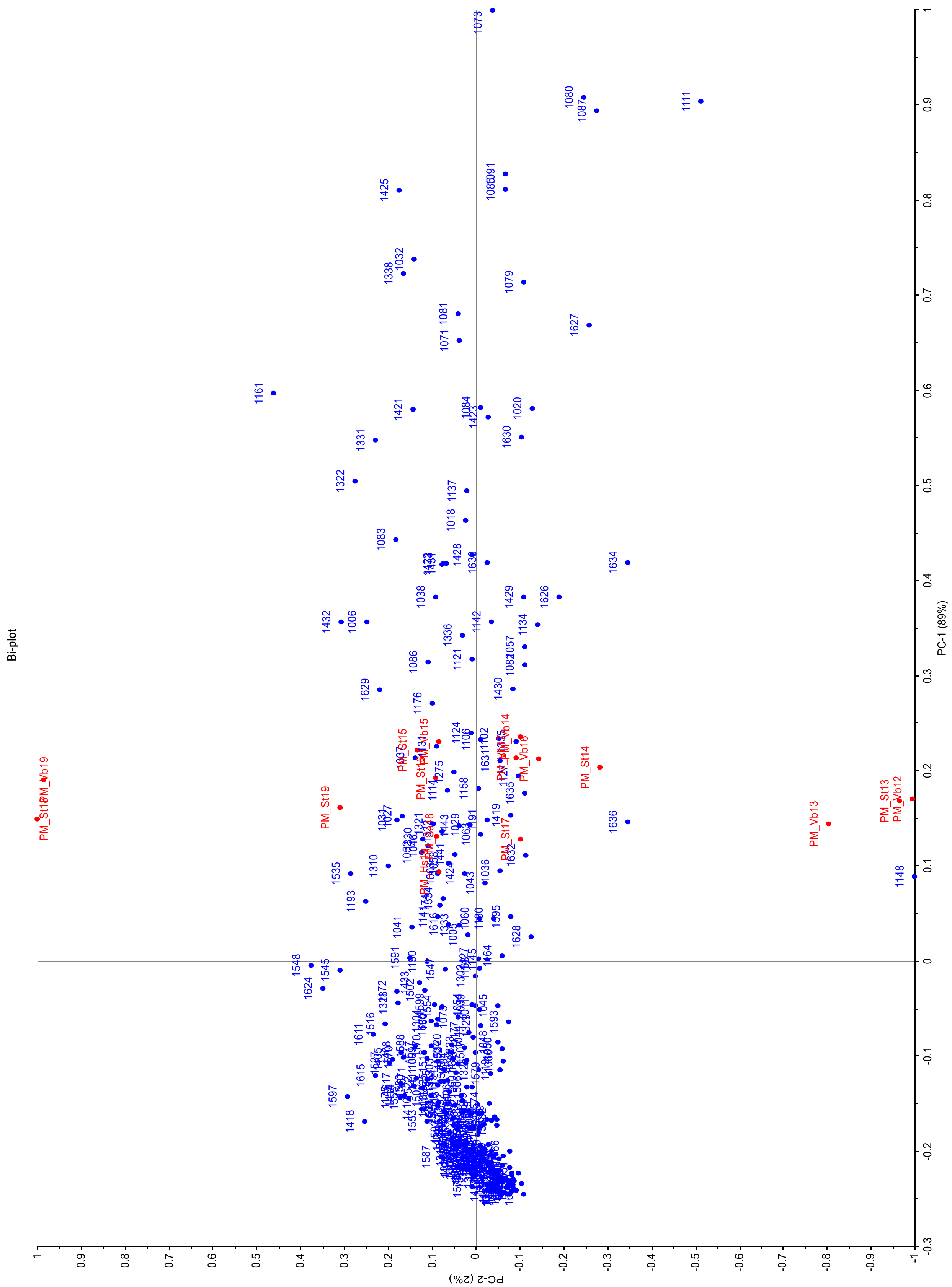


Figure 6: Powdery mildew resistance defined by principal component analysis in unscramble X for 297 spring MASBASIS lines displaying PC1 against PC2 for 16 different environments in between 2012-2019, each blue data point represents a genotype, each red data point represents an environment.

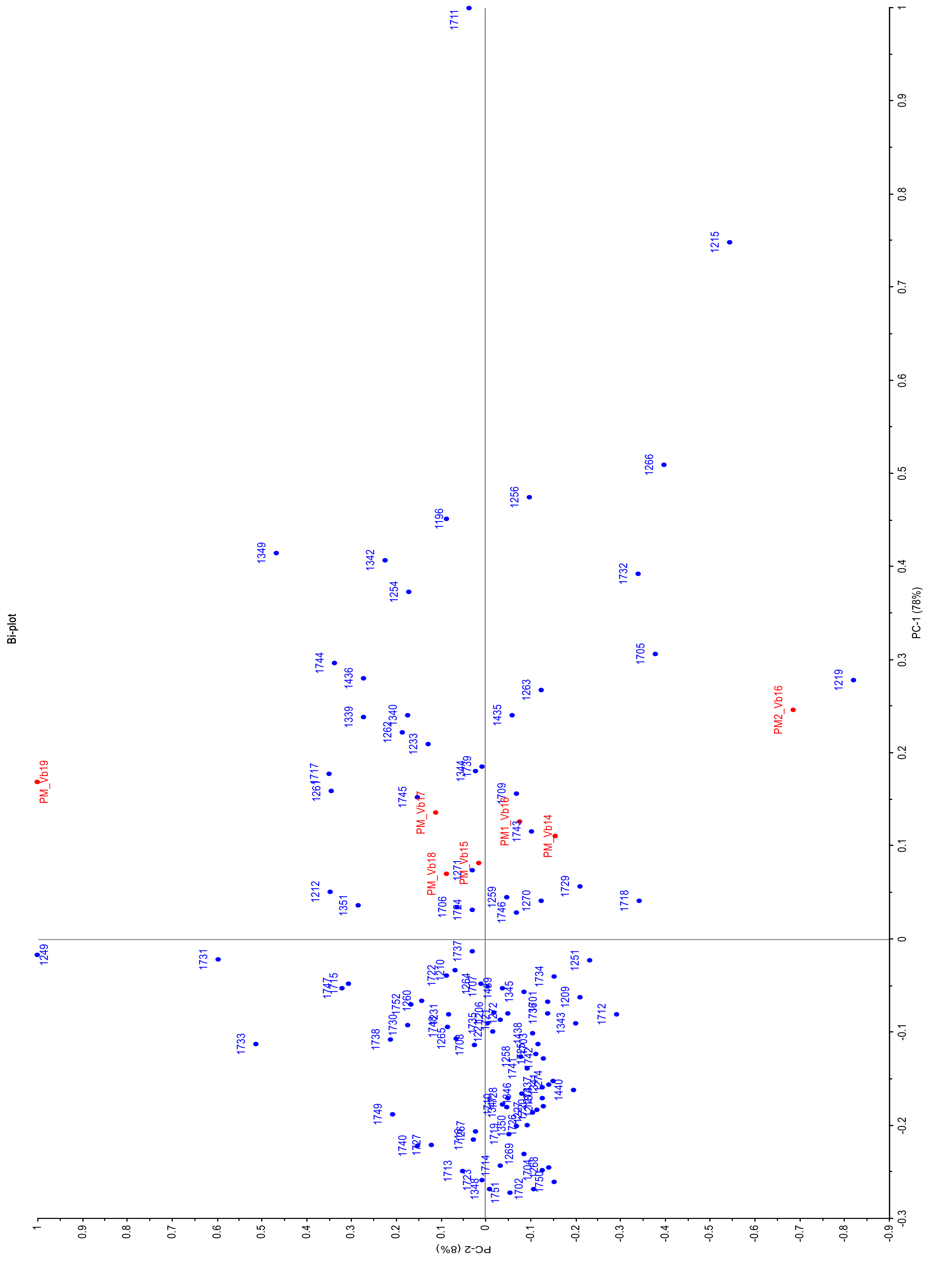


Figure 7: Powdery mildew resistance defined by principal component analysis in unscramble X for 103 winter MASBASIS lines displaying PC1 against PC2 for 6 different environments in between 2014-2019, each blue data point represents a genotype, each red data point represents an environment.

Table 11 shows the disease severity lsmeans for main spring wheat cultivars (Mirakel, Zebra, Bjarne and Seniorita), important sources of partial resistance (Saar and Naxos), susceptible checks (Avocet) and those lines that have clear changes in their powdery mildew severities over the time periods (AC Somerset).

Table 11: Disease severity Lsmeans for selected spring wheat lines covering locations with a single trial (Sande 2018 and Holmenstrand 2019) and Staur 2018, locations with many trials (Staur and Vollebekk over all years), over all environments, PC1, PC2 and over three different time periods.

Cultivar	Staur 2018	Sande 2018	Holmenstrand 2019	Staur all years	Vollebekk all years	Over all environments	PC1	PC2	Over period (2012-13-14)	Over period (2015-16)	Over period (2017-18-19)
Mirakel	10.0	6.0	4.8	3.9	3.2	5.2	-41.4	4.0	1.8	3.5	5.1
Zebra	9.0	22.6	4.1	9.1	12.2	13.2	-11.2	-0.6	9.8	13.3	10.2
Bjarne	16.3	7.9	5.2	15.4	16.4	17.0	6.2	1.4	13.6	21.2	11.6
Seniorita	2.0	14.0	0.5	2.4	1.5	2.8	-45.1	-4.6	2.1	2.2	3.6
Saar	7.5	11.1	3.2	8.9	10.0	12.7	-18.8	-3.6	8.1	10.4	8.4
Naxos	12.5	6.1	4.5	15.0	19.6	22.6	8.0	10.7	12.3	18.8	15.0
Avocet	68.3	53.5	41.2	69.8	73.5	52.3	221.0	-2.8	71.6	73.2	64.8
AC Somerset	4.5	3.1	5.3	10.9	24.5	23.3	19.7	-73.8	45.2	10.5	6.6

Table 12 shows the disease severity lsmeans for main winter wheat cultivars (Ellvis and Kuban, Magnifik, Olivin), important sources of partial resistance (Massey, Fenman), moderately susceptible cultivar (Bjørke) and susceptible check (kanzler).

Table12: Disease severity Lsmeans for winter wheat Vollebekk in 2018 and over all years, PC1 and PC2

Cultivar	Vollebekk 2018	Over all environments	PC1	PC2
Ellvis	**19.5**	**20.5**	**30.23168**	**10.58885**
Kuban	5.9	3.4	-11.8	-4.5
Magnifik	3.0	6.8	-2.4	1.5
Olivin	8.2	9.8	3.8	7.9
Massey	3.1	5.5	-7.2	-0.4
Fenman	0.7	3.2	-13.5	-2.4
Bjørke	10.0	19.2	32.9	2.0
Kanzler	18.9	33.6	72.8	0.85

Association mapping of powdery mildew resistance

Association mapping of powdery mildew resistance for PC1 for 13 environments for spring wheat (2012-2018)

For detecting significant markers associated with powdery mildew resistance, PC1 was chosen as the main trait to analyse since it captured well the differences in overall resistance levels between the lines and could explain 89% and 78% of the phenotypic variance for both spring and winter wheat, respectively. The mixed linear model in TASSEL was used and the significant markers for powdery mildew are displayed in Manhattan plot 9. Full lists of significant markers are attached in Appendix Table 3 and 4.

To check the p-value data Quantile- Quantile plot (Q-Q plot) was used which is a scatter plot for comparing two distributions. In genome-wide association study (GWAS) it is of interest to compare the distribution of observed probability (P value) with reference probability under null hypothesis (no association). If the p-values match the expected distribution of expected p-values it is an indicator of good management of false positives (Type I error). Deviations from the trend line for the markers with the lowest p-values indicate association between the phenotype and the genetic markers. The QQ-plot in Figure8 illustrates that calculated p-value matches the expected one up to -log10 (P-value) 1.8 and then start to deviate and show inflation for calculated –log10(p-value) which means the mixed linear model did not sufficiently correct for kinship and population structure and using a significance threshold of –log10 (P-value) (P= 0.000316) will better avoid the false positive markers.

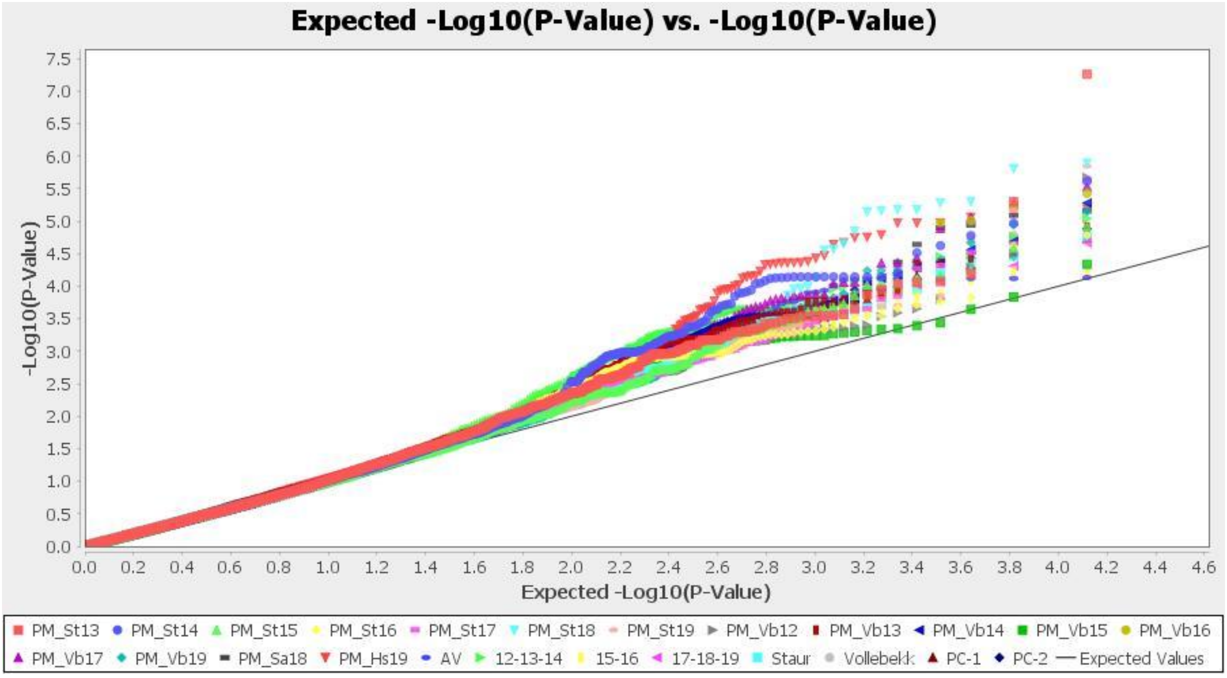


Figure 8: QQplot for spring wheat, horizontal axis indicate expected – log10 (p-value). Vertical axis indicates calculated – log10 (p-value). The box shows the symbols that used to represent the environments, lsmeans for spring environments (AV), lsmeans for 3 different periods over all fields, lsmeans for each field over all years, PC1 and PC2.

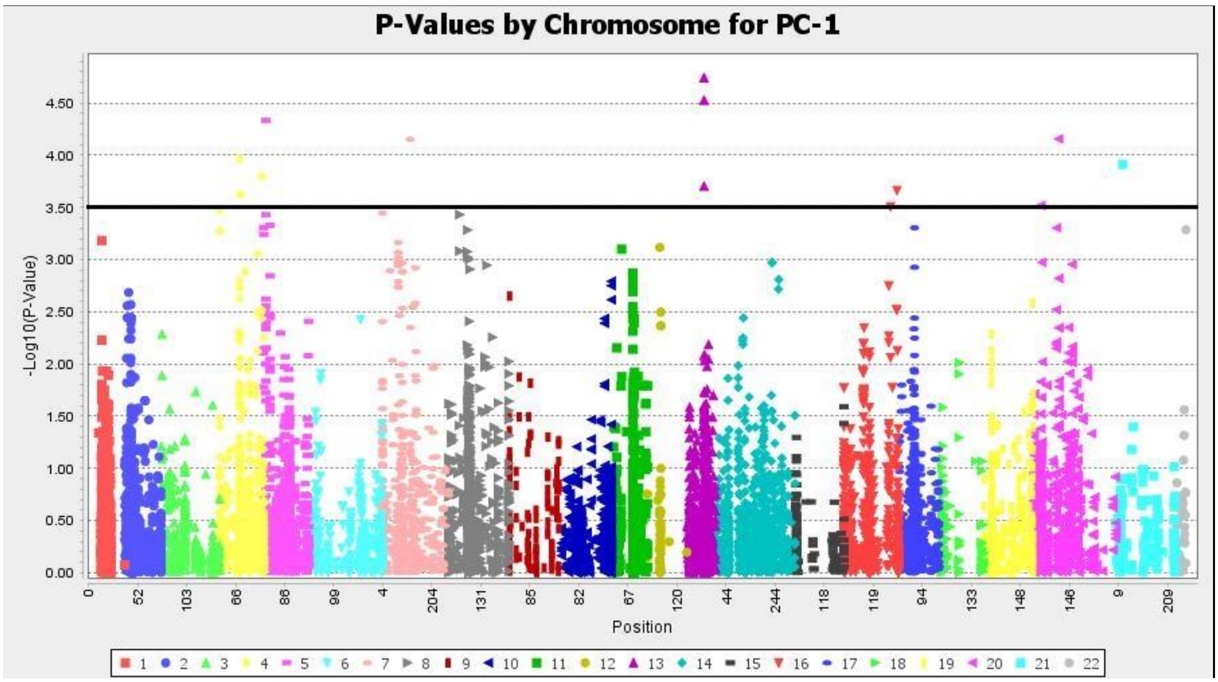


Figure 9: Manhattan plot displaying the markers for PC1 in spring wheat derived from TASSEL with markers position on chromosomes and significance threshold at –log10 (P-value) 3.5.

Following Figure 9 a total of 13 markers were found to be over –log10 (P-value) 3.5 (P= 0.000316). Clusters of 3 significant markers were found on chromosome 2A and 5A, 2 significant markers were found on chromosomes 6A and 7B, and 3 individuals markers were found on 3 different chromosomes 2B, 3A and 7B. There were a total of 37 markers with –log10 (P-value) >3.0 (P=0.001). The highest significant marker was found on chromosome 5A with –log10 (P-value) 4.742321 (*AX-94525543*) at position 70 cM (Allen et al., 2017) on the consensus map(Allen et al., 2017), and physical position 702750297 base pair bp on the Chinese Spring reference genome.

To identify interesting markers in addition to those that were significant for PC1, association mapping was run in TASSEL for each environment using a significance threshold of –log10 (P-value) over 3.0. Markers with at least one significant environment was considered interesting (appendix 3 and 4). Significant QTL have at least one marker that is significant for PC1 over 3.5, and may also contain additional interesting markers which have one environment with at least – log10 (p-value) over 3.0 and with a maximum distance of 10 Mega base pair (Mbp) (if available) or 10 cM (Allen et al., 2017)to a marker significant for PC1. These QTL and interesting QTL that contain markers with – log10 (p-value) between 3-3.5 are presented in Table 13. Total of “interesting environments” in Table 13 counting the environments with – log10 (p-value) over 3. The marker clusters in chromosome 6AL were sorted according to their physical position even though their cM positions on the consensus map were different.

Table 13: Significant QTL for powdery mildew resistance in spring wheat. Each QTL were categorised with: Chromosome, cM position(Allen et al., 2017), physical position, number of markers for each QTL, peak marker, number of interesting environments, highest –log10 (p-value) for single trial ,–log10 (p-value) for PC1 and known markers in the same physical position. C refers to unknown chromosome*

Chr	cM	Physical position Mbp	# of markers	PEAK MARKER	# of interesting Env.	HIGHEST -LOG(P)	-LOG 10 (P) FOR PC1	Known markers in the same physical position
1AS	54-57	2-9	3	*AX-94955419*	6	4.27(St17)	3.18	*K_c11891_1015*
2AS	2	3	2	*AX-95188522*	8	5.15(Vb19)	3.48	-
2AL	82-83	515-524	10	*AX-95238660*	10	4.74(HS19)	3.97	-
2AL	85	605	3	*AX-95160643*	7	5.01(VB16)	3.62	-
2A	156-157	739	3	*AX-95102130*	5	5.3(St13)	3.05	-
2A	173	757	1	*AX-94802107*	7	3.69(Vb17)	3.79	-
2BS	0-10	9-19	9	*AX-95017965*	12	4.94(Vb19)	4.33	-
2BS	27	26-30	5	*AX-94483531*	6	3.44(Vb17)	3.33	-
3AS	3-5	7-16	8	*AX-94555538*	9	5.67(Vb12)	3.45	*barc12/wmc11/Xbarc310*
3AS	67-72	67-69	9	*AX-94441567*	6	5.89(St18)	3.16	*gwm2*
3AL	116-117	621-623	2	*AX-94623333*	10	5.85(St19)	4.15	-
3B	45	NA	2	*AX-95197805*	6	3.59(Vb17)	3.43	-
3BS	76-78	46-51	3	*AX-95245849*	8	5.16(Sa18)	3.28	-
3BL	85	556	5	*AX-94681037*	5	3.46(ST13)	3	-
4BL	41	642	1	*AX-94636050*	4	3.5(Vb16)	3.1	*gwm6*
4DS	50-54	40	4	*AX-94719086*	7	3.7(Vb16)	3.12	-
5AL	70-79	700-708	10	*AX-94525543*	14	5.43(Vb16)	4.74	-
6AL	216	428	1	*AX-95201760*	8	5.61(St14)	3.66	-
6AL	190-218	602-609	5	*AX-94643574*	11	4.51(ST14)	3.5	*wmc621/AX-94411794*
6BL	60-63	622-631	7	*AX-94424805*	5	4.75(Hs19)	3.31	-
7BL	30-34	709-713	2	*AX-95217260*	7	5.28(St18)	3.52	*Xwmc581*
7BL	94	654-655	2	*AX-95154008*	5	3.54(St16)	3.3	*wmc517*
7BL	102-104	637	5	*AX-95156242*	10	5.63(St17)	4.15	*AX-95156242*
7DS	27	55	1	*AX-94435697*	10	5.53(Vb17)	3.91	*gwm130/ csLV34/ gwm295*
7C*	39	NA	1	*Terp_Syn*	6	5.24(Vb16)	3.29	-

The data shown in red colour (Table13) were used to analyse the effect of different numbers of the examined quantitative trait loci (QTL) on the Lsmeans of powdery mildew severity. These QTL clusters were chosen according to the number of interesting environments and to their –log10 (p-value) for PC1.

It is clearly seen in the boxplot (Figure 10) that the individual lines that carried six to seven of examined resistance-associated alleles were significantly more resistant to powdery mildew than lines with 5 or less resistance alleles. Continuously, the individual lines that carried 5 resistance alleles were significantly more resistant to powdery mildew than lines with 4 or less resistance alleles.

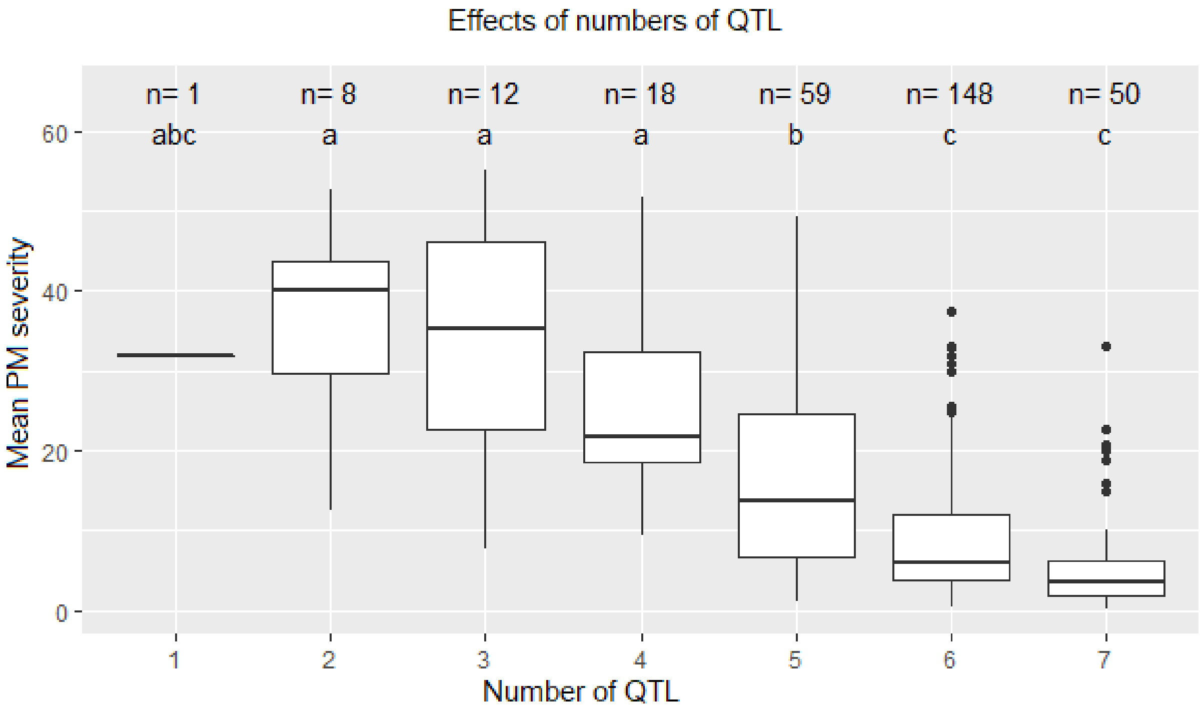


Figure 10: Boxplot showing the effect of different numbers of resistance alleles at quantitative trait loci (QTL) based on the lsmeans of powdery mildew severity. Groups are significantly different from groups with a different letter (on top of the plot) based on Tukey's HSD test. The horizontal line in each box represents the median, n= number of lines that had this number resistance allele at the examined QTL.

Table 14 shows how many resistant alleles are found in the main spring wheat cultivars of special interest. Full list of resistant alleles for studied QTL are attached in Appendix Table 6.

Table 14 Allele stacking dataset for the main spring cultivars/lines of special interest, lsmeans over all environments, Sum number of resistant alleles in each line, (+) present resistant allele in the line and (-) absent of the resistant allele in the line.

Line	Lsmeans	Nr of resistance alleles	2AL	2BS	3AL	5AL	6AL	7BL	7DS
Mirakel	5.2	6	+	-	+	+	+	+	+
Zebra	13.9	5	+	-	+	+	-	+	+
Bjarne	20.8	6	+	-	+	+	+	+	+
Seniorita	2.8	7	+	+	+	+	+	+	+
Saar	14.4	6	+	-	+	+	+	+	+
Naxos	24.2	5	+	+	+	+	+	-	-
Naxos/2*Saar	6.2	7	+	+	+	+	+	+	+
Avocet YrA	42.8	2	+	-	-	+	-	-	-
AC Somerset	23.7	4	-	-	-	+	+	+	+

Haplotype Analysis

Four haplotypes were analysed based on three markers on chromosome 5A (*AX-95018258* with –log10 (p-value) = 4.53, *AX-94525543* with –log10 (p-value) = 4.74 and *AX-94771047* with –log10 (p-value) = 3.70) that were significantly associated with powdery mildew resistance. Figure 11 shows the effect of each haplotype based on the lsmeans for powdery mildew. Haplotype (1-1-0) is significantly different from the haplotype (0-0-1). The peak marker for this QTL was the middle one and the 1 was the resistant allele. Only two of the lines carry the (1-0-1) and (1-1-1) haplotypes; therefore, there was little statistical power to detect significant differences from the other haplotypes. Table 15 shows group of line that have rare haplotypes.

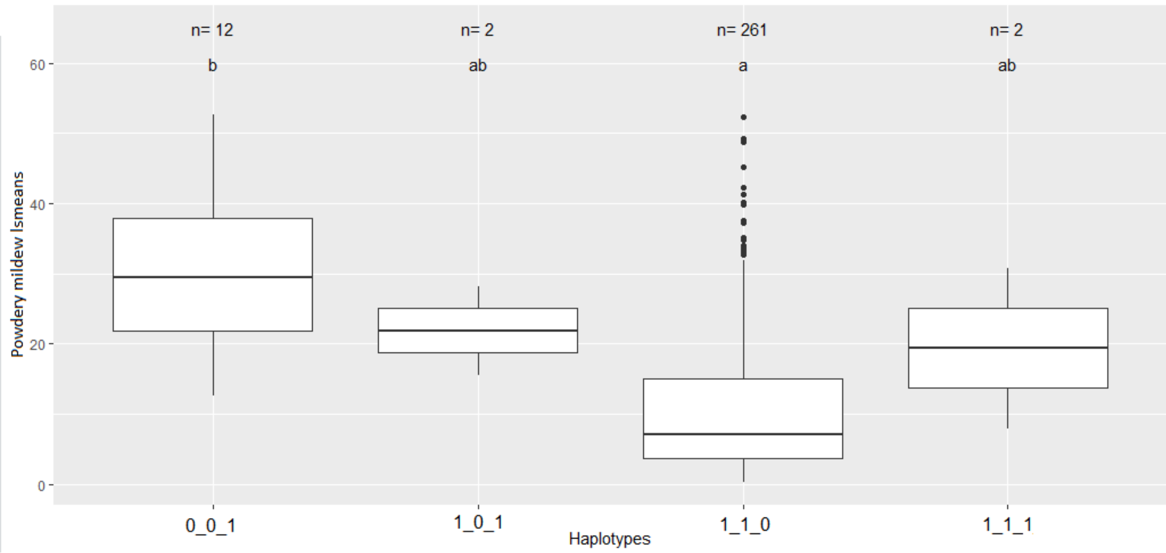


Figure 11: Boxplots showing the effects of different haplotypes on powdery mildew severity quantitative trait loci (QTL) on 5A chromosome. Groups are significantly different from groups with a different letter (on top of the plot) based on Tukey's HSD test. The horizontal line in each box represents the median, n= number of lines that had this haplotype.

Table 15 Group of lines that have rare haplotypes

Lines that have(0-0-1) haplotype	**Lines that have (1-0-1) haplotype**	**Lines that have (1-1-1) haplotype**
CJ9403 Catbird-2 N894037 NG8675/CBRD//SHA5/WEAVER, Nanjing 7840 - Pl.4 CBRD/KAUZ, GUAM92//PSN/BOW NG8675/CBRD SHA3/CBRD SHA5/WEAVER//80456/YANGMAI 5 SABUF/5/BCN/4/RABI//GS/CRA/3/AE.SQUARROSA (190) IVAN/6/SABUF/5/BCN/4/RABI//GS/CRA/3/AE.SQUARROSA(190)	Tjalve TJALVE/Purpur seed	Kukri DH20097

Association mapping of powdery mildew resistance for PC1 for 6 environments for winter wheat (Vollebekk 2014-2019)

The mixed linear model in Tassel gave as well significant marker for powdery mildew resistance in the winter wheat panel. The significant markers for powdery mildew are displayed in Manhattan plot (Figure 12). Full lists of significant and interesting markers are attached in Appendix Table 5. The significant markers for PC1 were considered associated with powdery mildew resistance since PC1 could explain the variance with 78% for winter wheat. The significance threshold was set to –log10 (P-value) 3.0 (P= 0.001).

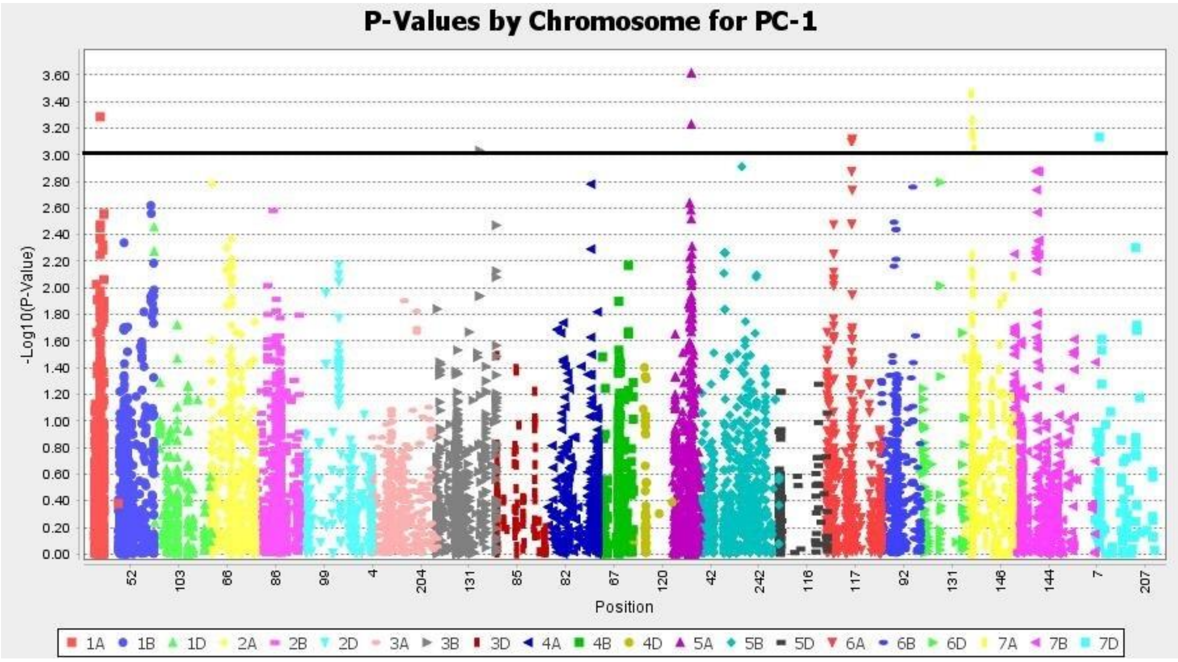


Figure 12: Manhattan plot displaying the markers for PC1 in winter wheat derived from Tassel with markers position on chromosomes and significance threshold at –log10 (P-value) 3.0.

Following Figure 12 a total of 12 markers were found to be over –log10 (P-value) 3.0 (P= 0.001). A cluster of 5 significant markers were found on chromosome 7A, 2 significant markers were found on chromosome 5A and 6A, and 3 individuals markers were found on 3 different chromosomes 1A, 3B and 7D. There were 32 markers with –log10 (P-value) >2.5 (P=0.003154). The highest significant marker was found on chromosome 5A with –log10 (P-value) = 3.614733 (*AX-94966165*) at position 79 cM (Allen et al., 2017), with a physical position (475268568 bp) on the Chinese Spring reference genome.

To check the p-value distribution QQ-plot was used. The QQ-plot in Figure 13 illustrate that calculated p-value matches the expected one up to 2.0 and then start to deviate at the top tail for one of the environments (the first disease score from Vollebekk in 2016), but for most of the other environments and the PC1 the p-values follow the expected distribution quite well up to –log10 (P-value) 3.0. Therefore, a significance threshold at –log10 (P-value) 3.0 (P= 0.001) could be applied.

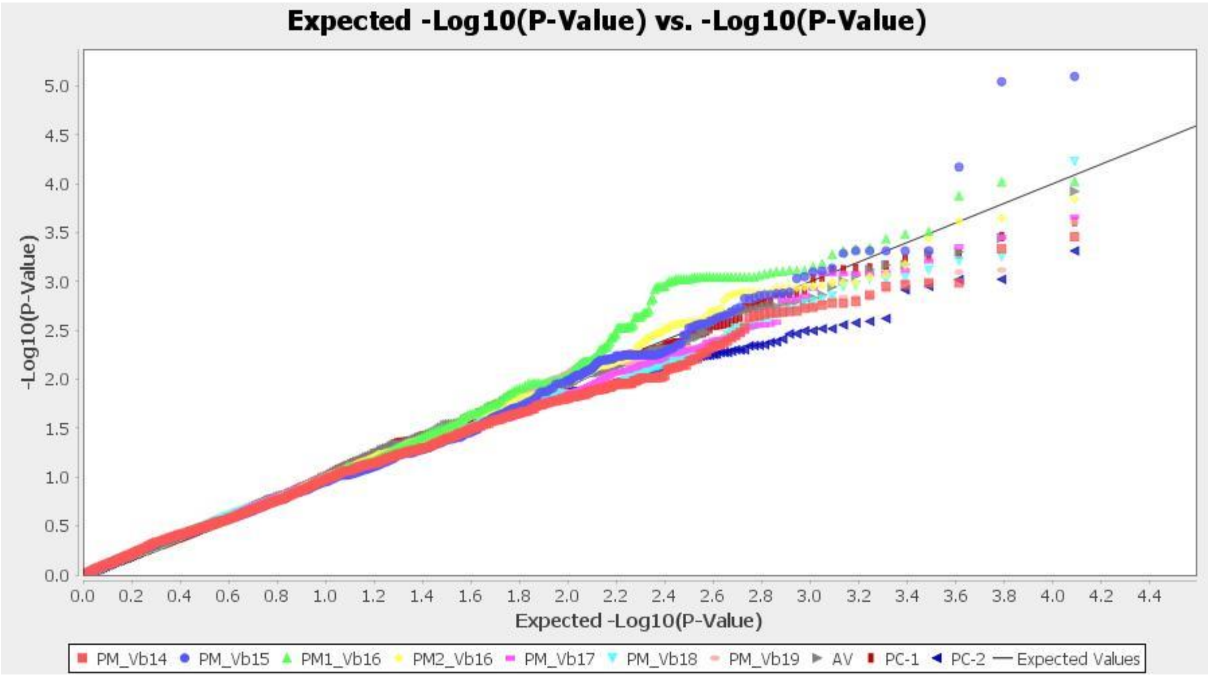


Figure 13: QQ plot for winter wheat, horizontal axis indicates expected – log10 (p-value). Vertical axis indicates calculated – log10 (p-value). The box shows the symbols that used to represent the environments, lsmeans of all winter wheat environments (AV), PC1 and PC2.

To identify additional interesting markers that were not significant for PC1, association mapping was run in TASSEL for single environments using a significance threshold of –log10 (P-value) over 3.0. Markers with at least one significant environment was considered interesting. Full list of these interesting markers are attached in Appendix Table 5. Interesting QTL that have at least one marker that is significant for PC1, and may also contain additional interesting marker significant for at least one environment and with a maximum distance of 10Mbp (if available) or 10 cM (Allen et al., 2017) to a marker significant for PC1. These QTL are presented in Table 16.

Table 16 Significant QTL for powdery mildew resistance in winter wheat. Each QTL were categorised with: Chromosome, cM position (Allen et al., 2017), physical position, peak marker, number of significant trials for at least one marker, number of significant trials for all markers, significant PCA, highest –log10 (p-value) for single trial ,–log10 (p-value) for PC1 and known genes in the same position.

Chr	cM	Physical position (Mbp)	Number of markers	PEAK MARKER	Number of significant Environments	HIGHEST –LOG10 (P)	-LOG10 (P) FOR PC1	Known markers in the same physical position
1AS	74	42	1	*AX-94526630*	2	3.62(2_Vb16)	3.28	barc148
3BL	176	775	1	*AX-94652021*	3	3.34(Vb14)	3.03	*BE489472*
5AL	79	473-475	3	*AX-94966165*	4	3.25(Vb18)	3.61	gwm 186
6AL	101-102	446-454	3	*AX-94688926*	2	5.09(Vb15)	3.12	-
7AS	26-30	78	3	*AX.94890346*	4	3.65(2_Vb16)	3.46	-
7AS	33-38	28-33	2	*AX-94395845*	3	3.84(2_Vb16)	3.14	-
7DS	18	44	1	*AX-94412216*	1	3.44(2_Vb16)	3.13	gwm130/ csLV34/ gwm295

All data in this Table were used for boxplot showing the effect of several resistance quantitative trait loci (QTL) based on the lsmeans powdery mildew severity (Figure 12). 5AL data were used to check the difference haplotypes and their effects on powdery mildew severity. Figure 14.

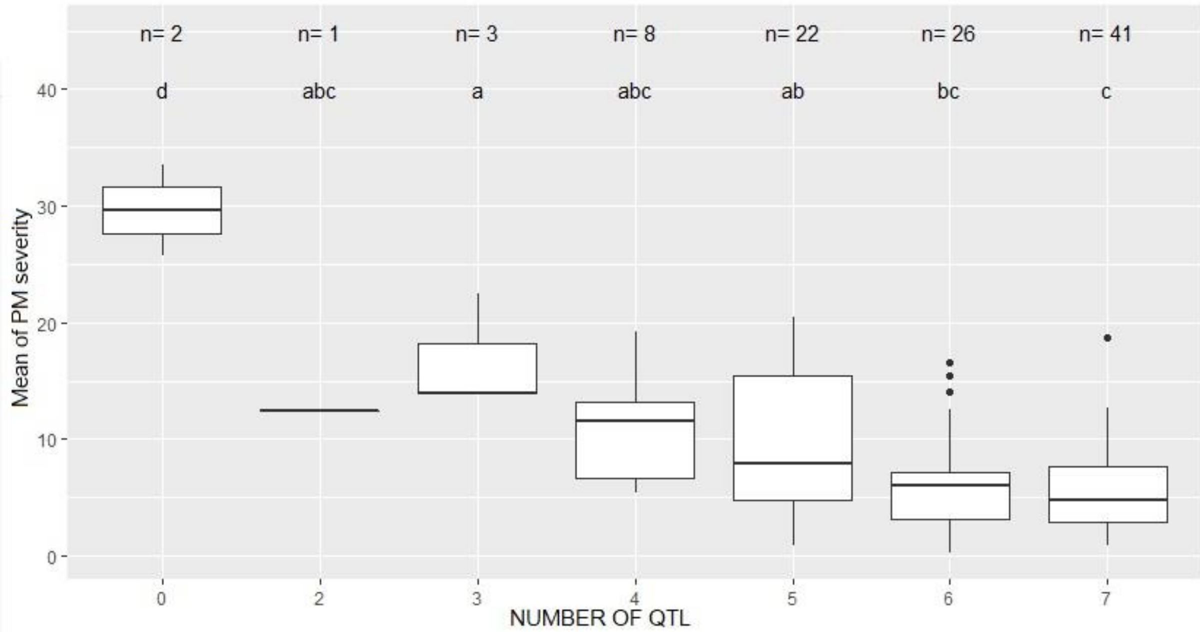


Figure 14: boxplot showing the effect of different numbers of resistance alleles at quantitative trait loci (QTL) based on the lsmeans of powdery mildew severity. Groups are significantly different from groups with a different letter (on top of the plot) based on Tukey's HSD test.The horizontal line in each box represents the median, n= number of lines that had this number of resistance allele at the examined QTL.

From Figure 14 it is evident that increasing number of resistance-associated alleles in a line will enhance its resistance to powdery mildew infection significantly. It is also evident that many of the majority of the winter wheat lines are found in the groups with 5 or more resistant alleles. The number of lines in each category affects the ability to detect significant differences, but it is evident that lines with 6 or more resistant alleles are significantly more resistant than those with 3 or 0 resistant alleles. The two lines with 0 resistant alleles (Kanzler and Finans) were significantly more susceptible than all the others.

Table 17 shows how many resistant alleles are found in the main winter wheat cultivars of special interest. Full list of resistant alleles for studied QTL are attached in Appendix Table 7.

Table 17 Allele stacking dataset for the main winter cultivars of special interest, lsmeans over all environments, Sum number of resistant alleles in each line, (+) present resistant allele in the line and (-) absent of the resistant allele in the line.

Line	Lsmeans	Nr of resistance alleles	1AS	3BL	5AL	6AL	7AS	7AS	7DS
Ellvis	20.5	5	+	-	-	+	+	+	+
Kuban	3.4	7	+	+	+	+	+	+	+
Magnifik	6.8	6	+	+	-	+	+	+	+
Olivin	9.8	7	+	+	+	+	+	+	+
Massey	5.5	7	+	+	+	+	+	+	+
Fenman	3.1	7	+	+	+	+	+	+	+
Bjørke	19.1	5	+	+	-	-	+	+	+
Folke (Sweden)	6.5	6	+	+	-	+	+	+	+
Kanzler	33.6	0	-	-	-	-	-	-	-

Haplotype Analysis

Three haplotypes were analysed based on three markers on chromosome 5AL: *AX-94691627* with –log10 (p-value) = 3.22, *AX-94966165* with –log10 (p-value) = 3.61 that were significantly associated with powdery mildew resistance and *AX-94400860* with –log10 (p-value) = 2.52. These markers are different from the spring 5AL markers that have been used for haplotypes Figure and they are different QTL. Winter wheat markers are located between 473-475 Mbp while the spring wheat markers are between 700-708 Mbp. Figure 15 shows the effect of each haplotype based on the lsmeans of powdery mildew severity. Haplotype (1-1-0) and (1-1-1) are significantly different from the haplotype (0-0-0). The significant markers for this QTL were *AX-94966165* and *AX-94400860* have 1 as resistance allele; therefore, there was no significant difference between (1-1-0) and (1-1-1) haplotypes.

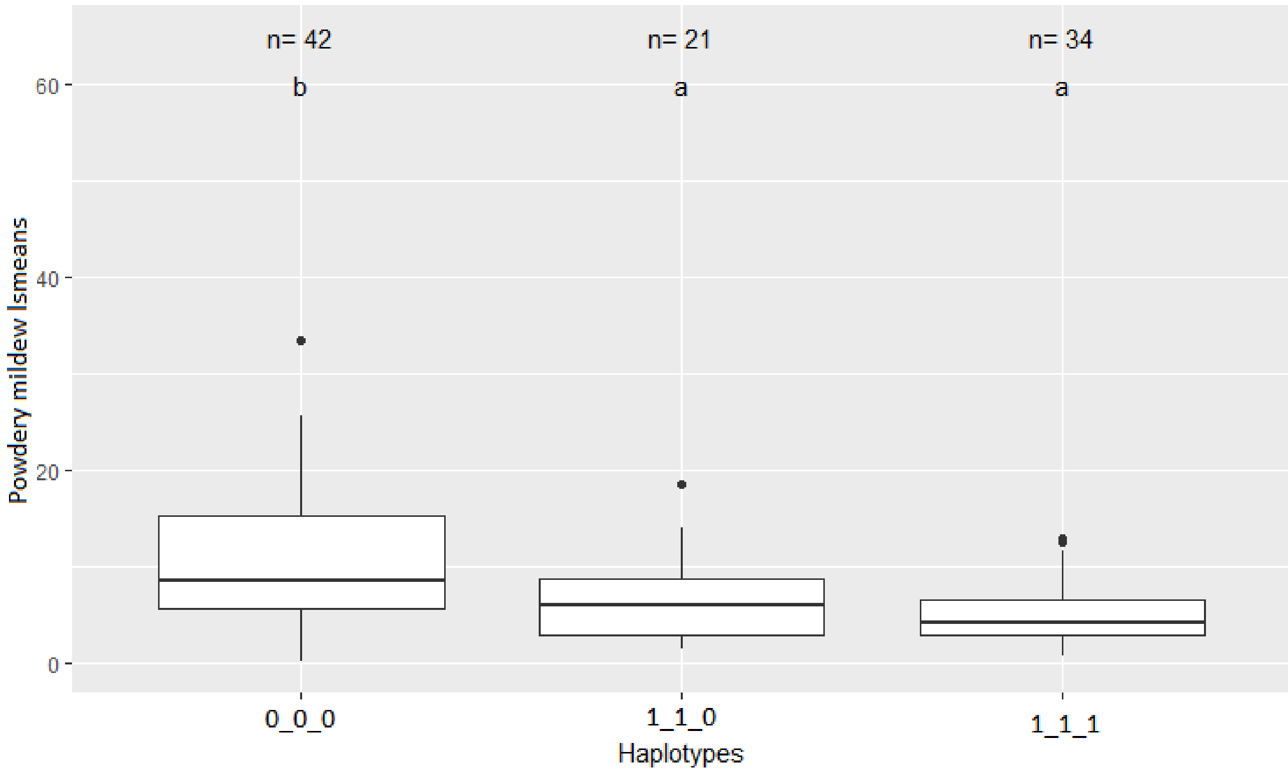


Figure 15: Boxplots showing the effects of different haplotypes on powdery mildew severity quantitative trait loci (QTL) on 5A chromosome. Groups are significantly different from groups with a different letter (on top of the plot) based on Tukey's HSD test. The horizontal line in each box represents the median, n= number of lines that had this haplotype.

Table 18 shows the main MASBASIS winter lines of special interest that have different types of 5AL haplotypes. Haplotypes for all winter MASBASIS lines are attached in Appendix Table 9.

Table 18 Main winter MASBASIS cultivars that have different 5AL haplotypes.

Line	Lsmeans	AX.94691627	AX.94966165	AX.94400860
Ellvis	20.5	0	0	0
Kuban	3.4	1	1	1
Magnifik	6.8	0	0	0
Olivin	9.8	1	1	1
Massey	5.5	1	1	1
Fenman	3.1	1	1	1
Bjørke	19.1	0	0	0
Folke	6.5	0	0	0
Kanzler	33.6	0	0	0
Solist (Denmark)	6.5	1	1	0
Torp (Denmark)	8.8	1	1	0
Vlasta (Czech)	4.6	1	1	0
KWS Ozon (Germany)	1.5	1	1	0

DISCUSSION

Association mapping revealed many significant markers in various chromosomes associated with powdery mildew severity in both spring and winter wheat. This study could detect several QTL were stable in many of the studied environments. Many of them were confirmed by previous studies and others were new and have not been described before.

Phenotypic evaluation

The favourable condition for powdery mildew is when it rains early in the season and where temperatures are moderately cool; and conidia will germinate most rapidly with relative humidity at 97 to 100% (Curtis et al., 2002). The 2018 season in Sande and Vollebekk experienced less favourable conditions for powdery mildew epidemics than Staur due to heat and drought which lead to small plants making it difficult to score disease severity. Drought stress on the plants also hampered disease development. Thus, loose wheat stands, heat and drought in spring prevented good development of powdery mildew epidemics.

By comparing the spring wheat histograms in Figure 3, the lower severity in Sande compared to Staur it is noticeable. However, the continuous distribution and low disease severity in all three environments indicate that more than one gene (polygenic effects) control resistance (partial resistance) to powdery mildew in some lines in MASBASIS. Figures 4 and 5 show lsmeans for disease scores over all environments and in 2018 for some of the main cultivars, well-characterised sources of partial resistance (Lillemo et al., 2010) and susceptible checks. The lsmeans over all environments were relatively lower with some exceptions, especially for commonly cultivated cultivars when they were grown under unfavourable conditions.

Principal components analysis with high explanation by PC1 for both spring and winter wheat clarify that most of the variation among lines is caused by genetic rather than environmental variation which suggested that the environmental influence did not affect the resistance phenotype to a great extent.

Spring wheat

The current study identified 11 significant (>3.5 for PC1) QTL on different chromosomes in spring wheat, see Table 13. Three on 2AL, two on each 6AL and 7BL and one on 2BS, 3AL, 5AL and 7DS.

Comparison between significant QTL and previous research

QTL on 6AL

The current study located a minor (significant >3.5-4< for PC1) QTL that was stable (interesting over half of the environments, ≥8) on 6AL with 5 SNP markers (peak marker *AX-94643574*) at physical position 602-609 Mbp which were interesting in 11 environments (-log10 (p-value)>3) with the significance threshold –log10 (p-value) = 3.5. Malihipour et al. (2017) detected a QTL associated with disease severity to Fusarium Head blight explaining 11.8% of phenotypic variation in the same region (611 Mbp). The Authors explained that there is a possibility for pleiotropic QTL conferring resistance to several diseases at this position. Another master thesis in NMBU for Christopher Frøiland (Frøiland, unpublished) also found a QTL with SNP marker *AX-94411794* associated with the resistant against yellow rust at physical position 609 Mbp indicating that this genomic region confers resistance to multiple pathogens. Based on the data in this thesis, it is not possible to determine whether the different disease resistances are due to the same gene or a cluster of linked genes. Zebra cultivar is lacking 2BS and 6AL QTL and has lsmeans over all environments (LSMAE) = 13.9. Comparing Zebra with Seniorita that has all 7 QTL with LSMAE = 2.8 shows the important effect of these QTL, Table14.

BJY/COC//CLMS/GEN, C80.1/3* QT4522//2*ATTILA, GN04526, HAHN/PRL//AUS1408 and BCN*2//CROC_1/AE.SQUARROSA (886) are lines lacking 2BS and 6AL QTL out of the seven studied QTL and have LSMAE 49.2, 23,9, 26,1, 21.9 and 21,9 respectively. see Appendix Table 6.

QTL on 7BL

Lillemo et al. (2008) revealed a minor QTL on 7BL in the CIMMYT bread wheat line Saar close to SSR marker *Xwmc581* (712 Mbp). It was ignored because it was barely significant and had low contribution in multiple regression. Nematollahi et al. (2008) used the same marker and published that it is a neutral marker and showed it to be a useful variation for distinguishing the different *Pm5* alleles. The presence of *Pm5a* in Saar was confirmed by QTL mapping (Lillemo et al., 2008; Lillemo et al., 2010).

This current study identified in the same genetic region a QTL in the MASBASIS lines. It was detected with 2 SNP markers (peak marker *AX-95217260*) at physical position 709-713 Mbp with significant threshold – log10 (p-value) = 3.52 and was interesting in 7 environments. Since significant markers are found in the same genetic region in current and previous studies, and was also found to be present in Saar in both of them, it indicates that this QTL is likely *Pm5a* and still playing a role in partial resistance of this cultivar and the SNP markers of this study can be likely used to flank *Pm5a*. The peak marker of this QTL was not significant in winter wheat, but the possibility of Bjørke having *Pm5a* (Hysing et al., 2007) is still possible, since Bjørke have the resistant allele of the peak marker.

A major and stable QTL was also found in this study with –log10 (p-value) = 4.15. This QTL was detected with 5 SNP markers (peak marker *AX-95156242*) at physical position 637 Mbp and was interesting in 10 different environments. The same peak marker was also significant to yellow rust (YR) in Christopher Frøiland master thesis (Frøiland, unpublished). This QTL was one of the seven studied QTL in Figure10. Adding this QTL and 7DS QTL to Naxos (lacking 7BL and 7DS) by crossing with Saar raised the partial resistance of Naxos from 24.2 to 6.2 lsmeans disease severity over all environments (LSMAE). Therefore, 7BL and 7DS is likely playing a main role in the combination of partial resistance to powdery mildew, especially for the partial resistance of Saar.

QTL on 7DS

This current study detected a minor QTL by one SNP marker (*AX-94435697*) at physical position 55 Mbp with – log10 (p-value) = 3.91 for PC1. This QTL was interesting in 10 different environments and is therefore considered to be stable. This QTL is one of the seven studied QTL in Figure 10. Lillemo et al. (2008) described and published that the *Lr34/Yr18* is pleiotropic to powdery mildew and named it *Pm38*. The Authors mapped *Pm38* with many markers such as *csLV34* at physical position 51 Mbp and *gwm295* at physical position 53 Mbp in Norwegian cultivars. Spielmeyer et al. (2005) described the association of the *Lr34/Yr18* gene to powdery mildew by using SSR marker *gwm130 at physical position 58 Mbp.* This study also detected a QTL in winter wheat in the same genetic region with SNP marker (*AX-94412216*) at physical position 44 Mbp.

Lu et al. (2012) detected a minor QTL associated with powdery mildew by SSR marker *wmc463* (38 Mbp) in the German spring wheat Naxos. The Authors described that this QTL is likely not *Pm38* (Lillemo et al., 2008; Spielmeyer et al., 2005) because it should show more stable resistance across environments. The QTL in this study was not present in Naxos and, furthermore, it was stable across many environments. Malla (2014) also studied Naxos and did not find any QTL on 7DS.

Windju et al. (2017) also researched Naxos and indicated the same QTL as (Lu et al., 2012) and could not find another QTL on 7DS.

The markers that detected *Pm38* is located closer to the studied QTL within 4 Mbp distance, and have 13 Mbp distance from Naxos QTL. The data in this thesis and previous studies indicate that the QTL in this study is probably *Pm38* gene. This would mean that Naxos does not have *Pm38*.

Comparison between interesting QTL under threshold and previous research

The present study documented many significant QTL in different chromosomes. On the contrary, many interesting QTL in the spring wheat are hidden under the significant threshold but still showing –log10 (p-value) over 3.0. Partial resistance stands for quantitative trait with a small effect from each loci and all of these effects will contribute to resistance against the pathogen. Therefore, the results under the threshold cannot be ignored; they are still interesting and may affect the resistance, although it is not possible to distinguish them from false positive marker-trait associations.

QTL on 1AS

Windju et al. (2017) studied Naxos and mapped a major and stable on 1AS in some of the same fields (Vollebekk and Staur) by SNP maker *K_c11891_1015* (12 Mbp). In the present study QTL in 1AS was detected with 3 SNP markers (peak marker *AX-94955419*) in the same region between (2-9 Mbp) with interesting results across 6 environments. Those results include –log10 (p-value) = 3.18 for PC1, –log10 (p-value) = 3.22 for Vollebekk over all years and – log10 (p-value) = 3.45 in the time period 2015 and 2016. Naxos cultivar does not have the resistant allele of the peak marker of this QTL. Therefore, this QTL is not the same as the published one, but is still interesting results, although being under the threshold.

QTL on 3AS

The current study identified a QTL on 3AS with –log10 (p-value) = 3.45, which was stable across 9 environments and different periods. This QTL was mapped with peak marker *AX-94555538* and 7 another SNP markers in between (7-16 Mbp). The resistant allele of the peak marker was found in Saar cultivar. Lillemo et al. (2008) reported that the resistance of Saar is controlled by three major QTL, out of them one on 3AS with SSR markers *Xbarc310* that has physical position 7 Mbp. It is more likely that this QTL is the same as the studied on and is still playing a role in partial resistance of Saar. In the same genetic region, SSR marker *barc12* (15 Mbp) was flanked by the Septoria

Tritici Blotch resistance gene *StbSm3* (Cuthbert, 2011). Another SSR marker *WMC11* (17 Mbp) was also used to map yellow rust resistance gene *YR76* in Tyee/Avocet by Xiang et al. (2016).

Another QTL was detected on this chromosome at physical position 67-69 Mbp. This QTL was mapped with 9 SNP markers (peak marker *AX-94441567*) with – log10 (p-value) = 3.16 for PC1 and has interesting results across 6 environments. Naxos cultivar has the resistant allele of the peak marker for this QTL. Lu and Lillemo (2014) described a minor QTL on 3AS that contributed to resistance against *Parastagonospora nodorum* leaf blotch in bread wheat lines 'Shanghai-3/Catbird' and 'Naxos'. This QTL was mapped with *gwm2* SSR marker at physical position 60 Mbp. It is likely the same QTL as the studied one, since Naxos has both of the QTL. Hence, this QTL could be pleiotropic to different diseases. Another study also used SSR marker *gwm2* to map tan spot resistance gene *tsr4* (Tadesse et al., 2010).

Based on the data in this thesis, it is not possible to determine whether the different disease resistances are due to the same gene or a cluster of linked genes.

QTL on 7BL

Azzimonti et al. (2014) reported a marker on 7BL at 651 Mbp associated with resistance to leaf rust and gave low to moderate epidemics under all epidemics stages and this marker did not localise with markers for Lr68 on 7BL. The authors questioned it since the marker could not be attributed with certitude, and because of a large confidence interval. In this study a QTL was found at the same genetic region by 2 SNP markers (peak marker *AX-95154008, 654-655Mbp*) but under the threshold with – log10 (p-value) = 3.3 which was interesting in 5 environments. This QTL is interesting, although being under the threshold with a possibility of pleiotropic to several diseases with low partial resistance effect.

Based on the data in this thesis, it is not possible to determine whether the different disease resistances are due to the same gene or a cluster of linked genes.

Evaluation of new QTL

QTL on 2AL

This study could determine three QTL on 2AL chromosome, the first QTL was stable and detected with 10 SNP markers (peak marker *AX-95238660*) at physical position (515-524 Mbp) with –log10 (p-value) = 3.97 for PC1. It was interesting in 10 environments with up to 31 interesting marker-trait associations as a total for all of these 10 markers over all environments. However, it failed to defend the susceptible cultivar Avocet YrA with 5AL QTL (602-609 Mbp) against powdery mildew. This QTL was one of the seven studied QTL, see Figure10 and Table 14. The susceptible allele of this QTL is found in 27 lines out of 297 MASBASIS lines. Almost half of these 27 lines has Runar, which has the susceptible allele, and is susceptible to powdery mildew, as one of the parents. Most of the rest are either foreign lines or multi-crossing lines with relatively high susceptibility to powdery mildew. Therefore, these finding can propose that this QTL is possibly associated with another phenotypic trait (e.g. headings date) and powdery mildew.

The second QTL on the same chromosome was detected with 3 SNP markers (peak marker *AX-95160643*) at physical position 605 Mpb with – log10 (p-value) = 3.62 for PC1. It was interesting in 7 environments. The resistant allele is lacking in 30 lines from different origins with relatively high susceptibility to powdery mildew (e.g. Avocet YrA and Reno). Avocet YrA was the only one that is lacking this QTL out of the showed cultivars/lines in Table 14. This QTL is valuable because of its significant association to powdery mildew and can be used in GS panel.

The third QTL was detected on chromosome 2AL by just one marker (*AX-94802107*, 757Mbp) with – log10 (p-value) =3.79 for PC1. This QTL was interesting across 7 environments. Out of the studied cultivar/lines in Table 14, Avocet YrA was the only one lacking this QTL out of showed cultivar/lines in Table14 with another 20 lines from different origins. Because this QTL show significant association to powdery mildew, it can be recommended to be used in GS panel.

QTL on 2BS

The present study could detect a major and stable QTL on 2BS with nine SNP markers (peak marker *AX-95017965*) at physical position 9-19 Mbp with – log10 (p-value) = 4.33. This QTL was interesting in twelve environments. Comparing Saar (LSMAE= 14.4) and Bjarne (LSMAE =20.8), both of them lacking this QTL out of the seven studied QTL in Figure10 and Table 14 with Seniortia (LSMAE =2.8) has all of the studied QTL, indicate that this QTL has a major effect in partial resistance.

Crossing Saar and Naxos produced offspring (Naxos/2*Saar) having all of the seven studied QTL showed improved partial resistance to powdery mildew Table 14. Examples of lines lacking 2BS and 6AL QTL is BJY/COC//CLMS/GEN, C80.1/3* QT4522//2*ATTILA, GN04526, HAHN/PRL//AUS1408 and BCN*2//CROC_1/AE.SQUARROSA (886) have LSMAE of 49.2, 23,9, 26,1, 21.9 and 21,9 respectively, see Appendix Table 6. This indicates that both 2BS and 6AL QTL are associated with powdery mildew resistance.

QTL on 3AL

This current study revealed a new major and stable QTL on chromosome 3AL with two SNP markers (peak marker *AX-94623333*) at physical position 621-623 Mbp with – log10 (p-value) = 4.15. This QTL was interesting in 10 different environments. In comparison between Saar (lacking just 2BS QTL) with LSMAE = 14.4 and AC Somerset (LSMAE =23.3) is lacking this and 2AL QTL, see Table 14. The 2AL QTL did not shows any effects in the susceptible cultivar Avocet YrA (have 2AL and 5AL QTL). Therefore, 3AL is likely playing a main role in the partial resistance of Saar. However, Lillemo et al. (2008) crossed Avocet with Saar and could not detect any QTL at 3AL in Saar. A possible reason could be poor marker coverage on chromosome 3AL between 621-623 Mbp with the DArT and SSR markers that was used at that time.

QTL on 5AL

The present study identified a major (significant over 4 for PC1) and stable (over half of environments) QTL on 5AL with 10 SNP markers, two of them were significant (peak marker *AX-94525543*) at physical position 700-708 Mbp. This QTL was interesting in almost all environments (14 out of 16 environment) with high – log10 (p-value) = 4.74 for PC1.

On the contrary, although Avocet YrA cultivar has this QTL, it is still highly susceptible to powdery mildew. This QTL failed to defend the Avocet YrA with 2AL QTL (515-524 Mbp) without an accumulated effect from the other studied QTL to reach a good partial resistance, Table 14 and Figure10.

The haplotype analysis Figure 11 shows the difference between different haplotypes and gave a better understanding that almost all of MASBASIS spring wheat lines have this haplotype. Many of the lines that have been listed in Table 15 as having the rare (0-0-1) haplotype are CIMMYT lines. This raised the possibility that vernalisation gene *Vrn-A1* (located on 5AL) commonly found in CIMMYT lines (van Beem et al., 2005) could be causing the *5AL* QTL . Mapping the primers of *Vrn-A1* that obtained from *(Fu et al., 2005)* shows that the gene is located at 580 Mbp with a 120 Mbp physical distance from the studied QTL and eliminate the intervention between this QTL and *Vrn-A1* gene.

QTL on 6AL

This current study detected two significant QTL on chromosome 6AL; the first QTL was located at the same physical position as QTL associated with FHB and YR in other studies. The second QTL was minor and stable, detected by one SNP marker (*AX-95201760*) with – log10 (p-value) = 3.66 for PC1 at physical position 428 Mbp. This QTL was interesting in 8 different environments, with highest – log10 (p-value) = 5.61 in Staur 2014.

Spring wheat QTL analysis

Seven out of the eleven QTL found to be significant were studied further and showed in Figure10 and Table 13 (2AL, 2BS, 3AL, 5AL, 6AL, 7BL and 7DS QTL). Avocet YrA (Susceptible cultivar) has two of these QTL (2AL and 5AL QTL) with LSMAE = 42.8. Seniorita cultivar has all of these QTL with LSMAE = 2.8. AC Somerset line does not have the first three QTL (2AL, 2BS and 3AL) but its resistance has increased over the years, see Table 11, indicating a change in the virulence composition of the pathogen population and AC Somerset might have a race-specific resistance gene.

The 7DS (55 Mbp) QTL is possibly *Pm38/Lr34/Yr18* gene which is a pleiotropic gene to many diseases. The 7BL (709-713 Mbp) QTL is possibly *Pm5a* and was shown to be associated with powdery mildew resistance.

The 2BS (9-19 Mbp), 3AL (621-623 Mbp), 6AL (602-609 Mbp) and 7BL (637 Mbp) QTL are the most important QTL for powdery mildew resistance in MASBASIS spring lines and, moreover, the 7BL and 6AL QTL are possibly pleiotropic to yellow rust. In addition, 6AL is possibly pleiotropic to fusarium head blight.

In addition, other QTL were also found to be significant to powdery mildew 2AL (515-524 Mbp), 2AL (605 Mbp), 2AL (757 Mbp), 5AL (700-708 Mbp) and 6AL (428 Mbp).

Some of the interesting QTL showed that they are important and likely not false positive marker-trait associations. The 3AS (7-16 Mbp) QTL possibly play a role in the partial resistance of Saar, and may also be pleiotropic to *Septoria tritici* blotch and yellow rust. Also the 3AS (67-69 Mbp) QTL possibly play a role in partial resistance of Naxos and to be pleiotropic to *Parastagonospora nodorum* leaf blotch and tan spot resistance. The 7BL (654-655 Mbp) QTL is possibly associated with powdery mildew resistance and pleiotropic to leaf rust.

A cross that could be recommended is one between Mirakel and Seniorita. Mirakel has 6 out of the 7 QTL that has been significant in this study, good resistance to powdery mildew, very good protein quality (class 1), but is prone to lodging due to long weak straw. Seniorita has all seven QTL and very good resistance to powdery mildew, good protein quality (class 2), and relatively good lodging resistance compared to Mirakel. Both varieties have similar yield potential, Mirakel is somewhat more resistant against Leaf blotch diseases than Seniorita, while the latter is somewhat stronger than Mirakel against yellow rust (Strand, 2019). By combining traits from these two parents, it could be possible to develop high-yielding varieties in protein class 1 with very good resistance against powdery mildew (all seven QTL), better resistance against yellow rust and Leaf blotch diseases and better lodging resistance than that found in Mirakel. If these traits was combined in a variety it would be a good alternative to Mirakel, which is currently the only variety in protein class 1. The question is if this would represent an economically significant improvement with regard to powdery mildew resistance, since Mirakel already have a better powdery mildew resistance than most of the spring wheat in the Norwegian market at this point in time.

Even if partial resistance shown to be more durable, also race-specific resistance genes can be part of the total resistance when several genes are incorporated in a genotype. By combining race-specific genes and partial resistance QTL in the genotype, if the race-specific resistance overcome by the pathogen the plant will still have residual resistance. AC Somerset has had an increase in resistance which is probably due to a race-specific resistance gene, which makes it interesting to further investigate the genetic basis for resistance in this cultivar. AC Somerset should be tested for susceptibility to relevant isolates of powdery mildew races at the seedling stage. To further establish the effect of different resistance QTL and possibly identify race-specific resistance that is probably presented in AC Somerset, a bi-parental cross could be done with Naxos/2* Saar line as the second parent. This cross would be recommended since neither Saar or Naxos have any race-specific resistance against powdery mildew (Lillemo et al., 2010), so any race-specific resistance in the offspring would come from AC Somerset.

Winter wheat

The current study identified 7 significant QTL for winter wheat with –log10 (p-value) above significant threshold 3.0 on different chromosomes, Table 16 Figure 14. Two significant QTL on 7AS and one single significant QTL on 1AS, 3BL, 5AL, 6AL and 7DS.

Comparison between significant QTL and previous research

QTL on 1AS

Lan et al. (2009) detected a QTL on 1AS for Adult-Plant Resistance to powdery mildew in Chinese wheat cultivar Bainong 64 with SSR marker *brac148*, this marker located at 52 Mbp. In the same genetic region at position 42 Mbp this study found a SNP marker in winter wheat (*AX-94526630*) which was significant in 2 environments and has – log10 (p-value) = 3.28 for PC1. 9 lines have the susceptible allele of the marker (e.g. susceptible cultivar Kanzler). Relatively few lines have the susceptible allele of this QTL, increasing the chance of false positive marker-trait associations. Because this QTL is possibly the same as the one described before this strength the confidence that this QTL is associated with powdery mildew.

QTL on 3BL

In the current study, a QTL was found on chromosome 3BL with one SNP marker *AX-94652021* at physical position 775 Mbp. This QTL was significant with – log10 (p-value) = 3.03 for PC1 and was significant in 3 environments. Comparing Ellvis (LSMAE = 20.5) which is lacking this and 5AL QTL, to Kuban (LSMAE = 3.4) that have all of the significant QTL indicate that this QTL is possibly playing a role for the resistance of Kuban, see Table 17.

Li et al. (2009) detected *Pm41* on 3BL using many markers, among them the STS marker *BE489472*, the Authors described that this marker was located within 0.8 cM distance from the gene in emmer wheat. This marker is located at 763 Mbp in the Chinese spring sequence (IWGSC, 2018) with a 12 Mbp physical distance from the detected SNP marker in this study. This distance is relatively large and comparison was done between different genomes, and based on the data in this study it is not possible to determine whether they are the same QTL.

QTL on 5AL

This QTL was detected with 3 SNP markers (peak marker *AX-94966165*) at physical position 473-475 Mbp with –log10 (p-value) = 3.25 for PC1, and was significant over four environments. The effects of different haplotypes were also investigated for this QTL, Figure14. Results show a significant variance between haplotypes having the resistance allele of the significant markers and those having the susceptible,see Table18, Figure 14. This QTL was shown to be associated with powdery mildew infection. Comparing Bjørke (lacking this and 6AL QTL, LSMAE = 19.1), Ellvis (lacking this and 3BL QTL, LSMAE = 20.5), Folke (lacking this QTL, LSMAE= 6.5) and Magnifik (lacking this QTL, LSMAE = 6.8), to Kuban (LSMAE = 3.4) that have all of the significant QTL indicate that this QTL is possibly playing a role for the resistance of Kuban, see Table 17.

In the same genetic region, Lillemo et al. (2012) detected a QTL with DArT marker *wPt-2426* marker with a 5.5 cM distance from SSR marker *gwm186* SSR which has physical position 471 Mbp. The Authors described that this QTL explained from 4.0 to 9.7% of the phenotypic variation in Folke cultivar, but Folke have the susceptible allele for the QTL in this study. *Gwm186* marker is located in close proximity (2 Mbp) to the QTL in this study with. Because cM is not a measurement of the physical distance, the physical distance between the QTL in this study and the marker *wPt-2426* is very uncertain. These factors suggest that the published QTL and the studied QTL on 5AL are different, Table 17.

QTL on 7DS

Spielmeyer et al. (2005) described the association of *Lr34/Yr18* gene to powdery mildew by using SSR marker *gwm130* at physical position 58 Mbp in this chromosome. Lillemo et al. (2008) described and published that the *Lr34/Yr18* is pleiotropic to powdery mildew and named it *Pm38* by using *SSR* marker *Xgwm295* at physical position 53 Mbp and *csLV34* marker (51 Mbp). *Pm38* was likely detected in the spring wheat of this study with a peak marker *AX-94435697*. Lu et al. (2012) detected a minor QTL associated with powdery mildew by SSR marker *wmc463* (38 Mbp) in the German spring wheat Naxos. The Authors described that this QTL is likely not *Pm38* (Lillemo et al., 2008; Spielmeyer et al., 2005) because it should show more stable resistance across environments.

This study detected a QTL on 7DS in winter wheat which was mapped with one SNP marker *AX-94412216* at 44 Mbp, this QTL was significant with –log10 (p-value) =3.13 for PC1, especially at Vollebekk 2016. This QTL is closer to the QTL in Naxos (Lu et al., 2012) with 6 Mbp distance, than *Pm38* With 7-14Mbp distance to the markers that been used by Lillemo et al. (2008) and up to 14 Mbp to the marker that been used by Spielmeyer et al. (2005). The peak marker of this QTL was not significant or interesting in the spring wheat study, but Naxos has the resistant allele of this marker. These findings establish that this QTL is probably not *Pm38*, rather it is likely the same QTL that been found on Naxos.

Evaluation of new QTL

QTL on 6AL

This QTL was detected with three SNP markers (peak marker *AX-94688926*) at physical position (446-454 Mbp) with – log10 (p-value) = 3.12 for PC1. This QTL was significant in two environments. Comparing Bjørke (LSMAE = 19.1) which is lacking this and 5AL QTL, to Kuban (LSMAE = 3.4) that have all of the significant QTL indicate that this QTL is possibly playing a role for the resistance of Kuban, see Table 17. Further research can help to give a better understanding of the effects of this QTL.

QTL on 7AS

The current study detected two QTL in winter wheat on 7AS. The first QTL was detected with 3 SNP markers (peak marker *AX-94890346*) with – log10 (p-value) = 3.46 for PC1. and was significant in four environments.

The second QTL was detected with two SNP markers (peak marker *AX-94395845*) at physical position (28-33 Mbp) with – log10 (p-value) = 3.14 for PC1, and was significant in three environments.

Both of 7AS QTL are found in all of the studied cultivars in Table 17 except the susceptible check Kanzler. Based on the stability of the QTL over environments and significance –log10 (p-value) PC1 indicate that these QTL are likely important and useful when breeding for powdery mildew resistance. Further research can help to give a better understanding of the effects of this QTL.

Winter wheat QTL analysis

Seven QTL were studied in Figure14 (1AS, 3BL, 5AL, 6AL, 7AS, 7AS and 7DS). Kanzler (susceptible check, LSMAE = 33.6) does not have any of these QTL. Olivin, Maasey, Fenman and Kuban have all of the significant QTL and have LSMAE 9.8, 5.5, 3.1 and 3.4 respectivly.

The resistant allele of the 5AL QTL (peak marker *AX-94966165*) was lacking in many of MASBASIS lines and gave a significant difference from the susceptible allele in haplotype analysis, Figure 15. In addition, based on the stability of the QTL over environments and significance –log10 (p-value) PC1 indicate that the QTL on 3BL (*AX-94652021*, 775Mbp) and two on 7AS (*AX-94623333* (621-623 Mbp) and *AX-94643574* (602-609 Mbp)) are potentially important and useful when breeding for powdery mildew resistance. QTL on 1AS, 6AL (peak marker *AX-94688926*, 446-454 Mbp) and 7DS

(*AX-94412216*, 18Mbp) are significant but was less stable over environments than the others therefore are not as interesting as more stable QTL when breeding for powdery mildew.

Having 6 or 7 QTL in a genotype made a significant improvement of resistance, but the size of the MASBASIS winter wheat panel and fewer environments than spring wheat did not give the chance for a major QTL or marker to be determined. Therefore, the elite lines that contain all seven QTL can be used as a panel for further studies to give a better understanding and determine other QTL associated with powdery mildew resistance.

CONCLUSION

The aim of this study was to find markers that are linked to interesting QTL for powdery mildew resistance in Norwegian wheat and verify the QTL that provide best resistance and compare the identified with QTL published in previous studies as well as recommending new QTL that were found.

SNP markers associated with powdery mildew have been very useful to identify QTL in both winter and spring wheat population. Powdery mildew resistance was shown to be controlled by many different QTL located on most of the chromosomes.

The study on spring wheat could effectively detect 11 significant QTL on different chromosomes in spring wheat. Four major QTL on 2BS, 3AL, 5AL and 7BL. In addition, seven minor QTL two on each 2AL and 6AL, one on 7BL and 7DS. The winter wheat study could also detect 7 significant QTL on different chromosomes. Two QTL on 7AS and one QTL on each 1AS, 3BL, 5AL, 6AL and 7DS. By using the sequenced reference genome of Chinese Spring to locate the physical positions of the QTL, many QTL of this study could be confirmed by previous research. In addition, some of the interesting QTL that were not significant in this study were also confirmed by previous studies. Additionally, many new QTL associated with partial resistance were presented her and may also potentially be useful for improving powdery mildew resistance in the Norwegian wheat breeding programs.

The new spring wheat QTL on 2BS with peak marker *AX-95017965* (9-19 Mbp), 3AL with peak marker *AX-94623333* (621-623 Mbp), 6AL with peak marker *AX-94643574* (602-609 Mbp) and 7BL with peak marker *AX-95156242* (626-637 Mbp). These QTL and SNP markers are recommended for improving powdery mildew resistance in wheat breeding programs. Further study is needed to apply these markers in resistance breeding and to assess their effectiveness in improving powdery mildew resistance when applied in genomic selection breeding programs.

The new winter wheat QTL on 6AL (peak marker *AX-94688926,* 446-454 Mbp), 7AS (peak marker *AX-94890346,* 26-30 Mbp) and the second QTL on 7AS (peak marker *AX-94395845*, 28-33 Mbp) are also recommended for improving powdery mildew resistance. Based on the stability of the QTL over environments and significance –log10 (p-value) PC1 indicate that the QTL on 3BL and two on 7AS are potentially important and useful when breeding for powdery mildew resistance.

By comparing physical positions of QTL detected in previous studies with the QTL in this study, it was possible to determine that some regions contain QTL that are pleiotropic to many diseases.

Further follow-up studies of these genetic regions can give a better understanding whether these QTL are the same and have pleiotropic effects to several diseases or they several different genes conveying resistance to different diseases located in close proximity to each other.

Crosses have been recommended between Mirakel and Seniorita to produce offspring with desirable yield, quality and agronomical traits in addition to improved resistance to powdery mildew. Another cross has been suggested between AC Somerset and Naxos/2*Saar is to further investigate the race-specific resistance that been indicated as a results of this study.

This study has fulfilled its objectives, and hopefully it has provided results that can be valuable to future research on durable resistance against powdery mildew in wheat and breeding program aimed at improving such resistance.

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APPENDIX

Table 1 Spring MASBASIS lines with lsmeans for disease severity in each environment, PC1 and over all environments.

Name	Vb12	Vb13	Vb14	Vb15	Vb16	Vb17	Vb19	St13	St14	St15	St16	St17	St18	Sa18	Hs19	PC1	All env.
Bastian	12.4	8.4	22.3	24.4	6.4	30.0	31.8	13.7	21.7	34.2	25.0	11.2	10.0	10.8	6.6	20.5	17.2
Bjarne	14.0	5.7	21.4	23.6	16.1	13.9	20.2	14.3	12.8	27.3	17.7	11.3	16.3	7.9	5.2	6.2	20.8
Tjalve	28.6	29.4	42.9	30.4	33.7	30.9	39.9	27.5	20.6	37.2	43.0	18.6	60.0	48.0	17.9	78.9	26.1
Avle	6.6	2.1	17.6	9.6	2.5	5.8	28.6	5.1	4.0	12.2	8.1	2.9	7.0	2.9	2.0	-22.6	14.3
Zebra	12.1	6.6	16.2	15.6	10.7	10.6	13.9	5.8	8.2	16.0	10.7	3.3	9.0	22.6	4.1	-11.2	13.9
Berserk	2.0	1.6	5.4	1.0	1.5	0.0	0.5	4.8	6.3	5.2	4.8	0.8	15.0	13.0	0.0	-40.3	20.2
Brakar	18.8	30.8	47.9	51.1	35.8	49.8	45.1	63.5	20.1	59.5	47.4	28.8	40.0	22.9	14.1	102.4	29.8
Runar	48.1	38.6	67.4	69.4	40.2	55.2	54.5	46.4	46.5	49.9	47.9	40.1	35.0	14.6	35.9	128.4	32.3
T2038	25.8	8.7	27.7	35.8	18.7	24.8	40.6	11.4	22.7	30.7	18.9	20.2	30.0	9.1	9.7	33.9	22.9
T9040	29.8	12.4	22.6	44.5	26.2	19.1	36.0	11.5	9.6	29.2	31.1	8.7	9.0	27.5	6.7	31.9	11.7
T9040 (1995)	19.1	19.9	25.5	24.8	17.5	26.2	33.8	24.2	12.9	23.2	26.6	8.9	50.0	25.8	6.4	33.0	21.4
T10014	52.9	37.1	67.3	65.2	65.3	69.4	62.5	53.4	54.3	66.3	49.8	40.0	75.0	17.5	36.3	163.3	37.3
NK93602 (1995)	24.6	15.5	20.4	24.9	12.4	12.6	24.2	13.4	26.9	34.2	27.4	14.0	15.0	12.6	10.9	21.2	23.9
MS 273-150	29.8	27.4	42.6	45.4	36.6	40.3	48.6	25.5	30.2	45.3	49.1	26.2	30.0	23.3	26.7	84.7	32.1
DH 49-18 Bastian/Adder	17.0	5.9	5.6	15.3	12.4	17.1	21.7	7.9	6.2	18.0	7.8	6.8	9.5	14.7	3.9	-10.2	25.4
Naxos (x3)	14.2	9.5	23.2	22.9	14.1	19.6	33.7	4.1	10.5	13.0	25.0	6.2	12.5	6.1	4.5	8.0	24.2
Paros	16.9	17.8	22.8	31.4	17.8	15.9	28.0	12.8	15.3	27.3	24.5	5.9	8.5	15.8	13.7	18.1	14.4
Paros/NK93602	14.2	5.7	8.1	19.7	5.4	5.1	17.8	5.9	4.6	8.0	12.3	10.3	10.0	16.4	6.0	-17.5	14.9

Paros/T9040	17.9	6.9	15.5	12.3	9.8	9.6	16.4	6.7	9.4	26.5	8.5	3.5	7.5	12.8	4.3	-10.3	11.5
T9040/Paros	17.3	19.5	25.0	25.3	12.9	21.5	39.3	17.7	19.7	19.5	24.8	8.8	22.5	22.6	5.8	27.0	21.6
Saar	12.1	5.7	9.9	6.9	6.7	19.4	9.5	3.5	9.5	16.5	11.5	3.3	7.5	11.1	3.2	-18.8	14.4
Filin	12.7	4.8	5.6	12.8	14.9	10.8	11.5	6.1	11.1	5.5	8.0	2.4	6.5	13.5	1.5	-20.2	9.3
Milan	17.8	9.1	27.4	22.0	15.5	26.7	27.2	5.5	35.1	31.2	28.8	7.6	25.0	7.0	3.3	25.4	15.9
Pfau/Milan	11.3	9.9	12.6	7.6	13.7	10.4	13.6	3.8	17.4	14.5	17.8	3.4	16.0	18.6	5.5	-10.0	10.1
Bau/Milan -2	34.7	24.8	43.1	37.5	37.5	39.8	34.6	15.0	46.1	42.3	37.0	28.8	11.5	18.2	14.6	73.2	15.4
Dulus	14.5	10.2	32.7	19.9	22.7	22.2	28.2	10.7	25.2	32.4	17.5	7.4	15.6	17.9	2.8	22.8	33.5
Gondo -1	19.3	11.3	18.0	18.1	21.3	20.6	19.7	6.0	16.5	25.9	15.5	7.8	11.4	15.7	5.3	9.9	10.0
Catbird -2	25.5	13.7	17.6	25.8	20.3	34.6	33.6	10.6	31.9	NA	16.0	7.4	7.5	14.2	8.9	29.5	7.9
Croc_1/Ae.squarrosa (205)//Kauz	4.0	0.5	2.0	3.0	4.0	3.6	12.9	0.5	0.5	18.7	2.3	1.8	4.4	4.8	3.0	-38.2	8.4
Altar84/Ae.squarrosa(219)// 2*Seri	12.9	1.6	23.0	6.6	8.3	10.0	10.1	1.6	8.5	7.5	14.3	2.1	4.0	4.1	0.3	-23.2	8.6
Altar84/Ae.sq(219)//2*Seri/3/ Avle	2.2	1.0	2.1	2.0	1.5	0.5	4.0	1.0	1.0	3.7	1.8	1.0	2.5	2.0	1.4	-47.8	13.9
Kariega	44.7	29.8	58.1	69.2	55.0	55.0	44.5	53.5	55.1	58.2	53.0	28.9	59.4	58.4	19.3	144.4	36.4
Avocet YrA	55.5	76.3	74.7	76.0	72.9	79.3	79.7	76.3	75.0	73.8	70.0	54.0	68.3	53.5	41.2	221.0	42.8
NK93604	10.3	7.7	11.0	19.4	13.3	7.7	19.8	7.0	3.7	14.0	14.6	6.6	12.5	9.4	3.6	-12.9	34.3
CJ9306	38.6	49.5	68.2	64.9	58.7	59.8	59.8	67.9	66.4	57.0	53.0	38.6	50.0	40.0	14.8	157.8	46.3
CJ9403	71.5	44.6	73.1	69.8	76.2	79.1	63.5	67.4	74.1	85.4	61.7	NA	40.0	64.8	30.1	200.8	40.4
512-21	53.7	29.3	52.7	74.5	75.9	50.5	57.1	38.1	40.5	68.2	49.9	52.7	35.0	41.6	40.4	150.6	46.9
512-50	28.9	34.1	42.9	34.9	35.2	34.6	36.8	23.8	37.9	29.5	38.1	28.8	19.4	16.4	21.3	68.9	34.7
512-54	37.8	30.2	52.3	65.5	57.4	39.3	50.2	6.9	27.6	39.7	48.3	34.9	35.0	16.5	20.5	98.1	34.6

512-70	48.5	34.3	53.1	65.1	50.5	54.5	57.6	47.1	46.9	47.7	48.9	45.3	50.6	18.4	26.1	128.7	22.5
512-87	59.1	54.6	77.6	79.6	74.7	59.3	69.0	43.8	58.8	53.0	64.6	45.1	40.0	64.9	33.5	179.4	28.9
SHA3/CBRD	30.9	24.4	42.5	27.5	35.3	40.2	45.8	14.7	30.3	39.9	30.6	27.3	27.5	18.9	27.0	69.7	27.1
Soru #1	62.1	64.8	77.5	69.1	64.8	75.7	68.4	70.3	81.3	72.7	59.7	42.4	45.0	55.1	34.7	197.7	35.1
Sumai 3 (18.)	58.6	48.8	82.7	80.4	87.5	65.0	59.7	43.8	71.1	69.9	64.9	36.7	52.5	18.6	30.7	183.0	41.0
Nobeokabouzu (Mhazy)	24.7	19.6	37.2	40.8	33.0	34.9	35.2	25.0	19.1	32.4	25.0	17.4	12.5	10.4	18.3	51.7	37.8
Frontana (95)	24.4	12.8	32.5	29.3	35.4	31.0	27.8	23.3	29.6	39.9	29.3	18.7	20.0	18.3	6.7	51.6	39.8
Nanjing 7840 - Pl.4	NA	59.7	87.8	80.2	72.7	74.9	50.3	74.9	81.0	70.2	66.9	62.5	45.0	14.7	33.7	199.9	45.3
Ning 8343 - Pl.4	26.8	7.2	42.8	25.2	29.0	31.4	29.7	7.6	31.0	36.0	18.9	7.0	20.0	10.2	17.9	39.8	29.7
Vinjett	2.2	0.5	2.6	1.5	0.0	2.4	15.1	1.5	4.0	2.0	3.0	1.9	4.0	1.0	5.1	-43.2	5.7
DH20070	9.6	3.6	7.8	2.0	19.9	2.1	9.6	5.6	2.8	10.4	21.9	4.5	5.6	8.3	3.6	-25.2	15.5
DH20097	10.1	4.1	9.7	17.3	8.1	8.2	20.6	3.4	5.6	17.4	4.7	5.5	8.5	4.0	3.0	-19.3	32.6
GONDO	30.2	22.2	42.3	35.6	35.6	39.4	49.7	14.9	44.8	30.9	30.0	23.7	9.0	23.0	32.7	70.2	26.6
MILAN/SHA7	29.1	14.7	42.9	27.4	30.6	25.1	26.9	8.0	37.4	37.5	37.9	7.7	14.0	37.2	5.1	53.1	28.5
CBRD/KAUZ	33.3	20.2	27.6	29.8	27.8	29.5	28.0	14.3	29.6	37.5	19.6	9.8	13.5	29.2	11.4	43.1	16.5
R37/GHL121//KAL/BB/3/JUP/MUS/4/2*YMI #6/5/CBRD	23.2	9.8	38.1	36.0	29.9	35.3	32.0	11.2	24.7	NA	34.7	11.7	14.4	28.7	5.6	49.9	28.8
GUAM92//PSN/BOW	24.3	22.1	52.3	44.7	46.3	44.2	32.3	27.8	50.5	44.5	32.0	18.5	14.0	10.7	20.4	78.1	30.5
NG8675/CBRD	34.0	26.3	57.8	50.5	40.4	54.5	43.4	29.8	51.2	49.5	45.5	27.1	29.4	48.9	10.2	109.4	25.8
ALTAR 84/AE.SQUARROSA (224)//ESDA	24.8	6.8	12.8	22.0	20.8	15.3	31.6	4.3	14.4	25.5	16.2	8.8	14.4	14.9	8.8	10.4	16.5
BCN*2//CROC_1/AE.SQUARROSA (886)	30.4	20.5	43.4	40.4	31.0	29.7	34.6	29.9	45.3	54.7	40.2	17.5	22.5	36.4	14.7	78.9	26.5
MAYOOR//TK SN1081/ AE.SQUARROSA (222)	20.1	7.5	14.9	8.4	20.3	20.7	17.0	3.5	12.4	24.9	18.7	4.5	9.4	15.2	9.0	0.3	18.5

AC Somerset	66.1	59.4	15.0	8.2	5.5	4.5	12.7	69.0	16.4	18.2	10.1	6.1	4.5	3.1	5.3	19.7	23.7
Sport	8.4	2.2	10.2	7.7	6.1	4.0	18.6	5.3	7.7	17.0	5.3	3.6	6.0	2.0	7.6	-22.4	9.5
CD87	22.9	14.2	37.7	27.4	21.2	34.6	22.1	13.0	27.4	48.5	22.8	5.8	17.5	13.7	4.0	40.2	16.4
Chara	29.5	29.4	47.7	60.4	50.7	50.7	60.9	27.0	49.5	69.0	44.5	23.7	65.0	54.8	19.6	132.1	29.5
Kukri	18.3	12.0	22.8	7.4	12.5	20.1	21.3	10.7	14.8	24.2	15.9	8.9	NA	2.6	3.0	1.2	6.3
Naxos/2*Saar	8.1	3.8	2.9	2.5	2.0	4.6	6.3	0.0	1.0	3.7	3.5	2.0	1.4	2.0	0.5	-44.0	6.2
ONPMSYDER-05	12.0	5.4	17.8	11.9	7.8	17.2	14.8	19.2	14.9	25.7	9.1	5.2	20.0	16.5	2.1	-1.5	17.3
BAJASS-5	2.7	3.0	6.2	14.8	4.8	13.7	18.1	9.0	4.7	16.2	6.4	6.4	15.0	1.5	16.0	-19.6	17.0
NK00521	6.3	2.8	4.5	4.6	2.0	3.9	12.4	0.5	4.0	3.7	3.0	2.9	4.5	4.7	4.6	-38.7	10.0
NK01513	5.1	4.3	14.8	15.2	3.0	12.9	29.3	7.6	16.2	17.2	15.0	3.4	17.5	12.6	3.5	-6.8	25.3
Demonstrant	31.0	16.8	41.3	54.8	39.6	40.7	50.4	30.3	36.6	56.2	37.8	21.1	17.5	44.6	29.9	92.5	24.3
Krabat	16.5	4.8	19.7	31.9	19.5	19.3	22.0	7.7	11.5	23.7	23.5	9.4	15.0	16.0	6.4	13.1	16.8
GN03531	2.2	1.0	5.0	3.0	4.9	8.8	28.6	3.2	2.8	2.7	6.9	3.4	13.5	5.1	NA	-31.5	10.9
GN04537	22.1	21.4	32.9	37.4	19.1	29.7	35.2	21.6	27.5	63.5	29.3	16.1	25.0	23.1	12.8	60.0	25.0
GN05507	3.4	6.2	12.6	7.9	4.2	5.5	3.0	10.3	8.4	20.2	14.4	4.9	12.5	7.8	4.3	-16.4	10.2
Laban	1.0	0.5	1.4	0.5	0.0	1.0	2.5	1.0	3.5	2.5	2.3	1.7	5.5	1.5	1.7	-49.0	10.2
Breeding line 1	0.5	0.5	0.9	0.0	0.0	0.0	8.2	2.0	0.0	2.0	1.5	1.3	3.5	3.3	1.1	-49.1	5.7
Breeding line 2	19.5	9.7	20.3	30.6	13.2	19.9	22.1	12.3	15.9	14.9	28.5	11.3	12.5	6.7	7.1	9.9	8.4
GN03597	2.2	0.5	3.8	5.4	4.0	1.0	2.0	2.0	2.3	6.7	5.5	1.2	5.6	5.5	1.6	-42.5	2.9
GN04528	0.5	0.5	0.0	0.0	0.0	0.0	0.5	0.5	0.0	2.7	0.0	NA	1.6	1.0	0.0	-53.8	2.3
GN05580	1.7	1.6	2.7	1.5	1.5	1.0	3.4	0.0	1.0	5.2	3.8	1.7	2.0	4.4	2.3	-46.8	8.3

GN06557	3.0	1.1	0.9	2.5	1.5	0.5	2.0	2.0	2.8	3.7	1.8	2.9	5.5	13.3	0.7	-45.3	10.6
GN06573	0.5	1.0	0.0	0.5	1.0	0.0	3.0	1.5	0.0	1.5	1.8	1.0	2.5	1.5	0.0	-51.6	13.2
Breeding line 3	0.5	0.0	1.5	0.5	0.0	0.5	1.0	0.0	0.0	0.0	0.0	0.5	0.0	2.0	0.0	-53.7	5.2
Amulett	0.0	0.3	0.8	0.5	0.0	0.0	1.5	0.0	0.8	0.5	0.5	0.0	1.0	1.0	0.0	-53.6	10.5
Bombona	8.7	5.0	22.3	19.0	8.0	7.8	26.1	9.2	18.2	15.7	17.6	6.0	12.5	10.5	12.2	-0.1	13.6
QUARNA	21.7	11.6	37.3	29.6	16.2	22.3	28.3	22.2	18.8	37.0	25.3	8.9	12.5	14.1	7.7	33.0	22.5
GN03529	1.9	0.0	3.3	4.3	2.5	1.0	8.3	2.0	2.3	2.7	2.8	0.8	6.5	2.1	1.6	-43.9	18.0
Breeding line 4	11.9	4.1	27.7	19.7	9.2	19.6	40.5	3.8	18.3	20.2	25.5	4.0	15.0	12.2	17.9	13.9	34.9
GN04526	5.6	2.1	7.7	5.2	5.2	8.3	19.6	5.5	3.2	6.5	11.5	1.5	8.6	14.1	5.0	-27.6	26.2
J03	15.8	12.9	32.7	24.7	25.3	20.9	30.0	28.7	20.4	43.2	35.1	21.5	20.0	6.4	14.9	44.0	15.1
NK01565	10.4	2.1	14.7	20.8	10.2	13.8	22.4	4.4	3.6	16.0	11.3	3.1	11.5	5.6	7.3	-13.3	5.6
GN03503	17.1	6.9	12.1	23.9	11.1	17.0	24.7	8.3	14.5	11.5	19.8	3.8	9.5	7.5	4.7	-3.3	7.1
GN05551	7.1	4.4	7.5	4.2	5.7	10.4	16.8	4.4	4.0	13.4	8.9	3.0	15.6	9.9	4.9	-25.2	5.8
GN05589	6.7	3.5	10.9	8.3	9.9	15.4	23.5	2.0	5.1	24.7	14.8	8.7	6.5	1.5	15.8	-13.8	7.3
GN06578	0.5	0.0	2.1	0.0	0.5	0.0	10.0	0.5	1.0	2.0	1.8	4.0	4.4	1.0	3.1	-47.7	2.4
GN07581	0.0	1.0	1.0	0.0	1.5	0.0	3.2	1.6	0.0	2.7	0.5	0.5	10.0	2.2	0.3	-49.2	7.7
GN08504	1.7	1.1	2.7	1.5	2.0	3.0	7.6	2.4	2.3	3.7	2.3	3.3	6.5	3.2	0.0	-44.1	3.9
GN08531	1.0	1.1	1.7	2.0	2.0	1.4	4.6	1.9	1.0	2.7	3.5	2.9	2.4	0.5	0.2	-47.7	1.8
GN08533	1.7	0.0	3.7	1.5	1.0	0.5	3.7	0.0	1.0	8.2	2.0	3.7	2.5	2.4	2.6	-46.2	1.8
GN08534	14.5	5.5	23.0	28.4	10.9	18.2	40.8	10.8	15.4	39.5	18.2	15.0	12.5	11.8	13.0	22.3	13.2
GN08541	2.5	1.6	12.9	6.2	4.3	2.3	3.0	4.1	4.0	16.2	3.5	2.9	20.0	10.7	3.4	-30.3	4.7

GN08554	0.5	1.0	2.7	1.5	1.0	1.0	2.6	1.0	2.3	3.0	3.0	1.7	1.0	2.7	1.9	-48.6	2.3
GN08557	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.3	0.0	1.0	2.6	0.0	-54.3	2.0
GN08564	1.2	1.1	3.9	2.0	2.0	1.0	8.8	2.0	1.8	5.7	2.3	1.8	5.0	2.0	4.3	-44.3	2.4
GN08568	0.5	1.0	1.5	0.0	2.0	0.5	8.3	1.0	1.0	3.0	2.0	2.2	8.5	4.7	1.5	-45.0	3.2
GN08588	1.7	2.1	3.7	3.0	2.0	5.0	11.3	2.6	2.3	5.2	7.3	3.7	9.0	2.0	3.5	-38.9	3.6
GN08595	1.8	6.0	10.0	4.4	1.0	4.3	11.1	7.8	5.0	6.8	5.3	3.8	15.0	3.6	4.7	-32.3	12.0
GN08596	0.0	1.0	1.0	0.0	1.0	1.0	7.3	0.5	0.5	1.0	1.0	1.6	1.5	4.5	0.8	-50.0	16.1
GN08597	1.7	1.1	4.2	2.5	1.5	0.5	11.5	1.0	3.5	3.0	3.0	NA	4.0	6.2	4.2	-42.8	5.8
GN08647	1.2	0.5	2.3	2.5	0.5	1.0	11.2	0.5	2.3	8.2	2.3	0.5	0.6	1.5	4.6	-44.5	2.3
TJALVE/Purpur seed	15.8	13.1	22.5	25.4	29.8	20.0	30.2	19.5	25.8	31.5	27.5	10.1	29.4	19.0	6.6	32.1	15.5
Sabin	25.1	21.0	57.8	50.2	49.1	35.3	55.0	44.2	50.2	63.2	29.4	26.1	59.4	25.5	7.9	111.7	25.6
Breeding line 5	8.3	2.1	12.7	14.0	6.7	7.6	9.2	3.0	8.3	10.4	12.5	3.8	10.0	4.7	19.6	-20.1	8.2
Breeding line 6	0.5	0.0	1.0	0.0	0.0	0.0	0.5	0.0	0.0	1.5	0.0	0.0	1.0	0.0	0.0	-54.1	3.5
Breeding line 7	7.4	1.6	10.1	4.1	3.5	9.8	11.5	4.9	13.3	11.0	11.0	3.5	6.4	5.6	4.1	-25.1	8.5
Breeding line 8	1.0	0.5	1.0	0.0	0.0	0.5	10.3	0.0	0.9	2.5	2.0	0.5	5.6	4.2	3.4	-47.4	9.6
Breeding line 9	3.3	1.0	8.1	20.6	3.0	4.1	7.1	8.2	7.9	9.7	15.5	5.2	10.0	5.6	14.4	-22.9	22.6
Breeding line 10	5.8	2.5	18.2	14.5	2.5	9.9	25.4	1.1	11.6	10.4	25.4	6.8	13.5	13.6	13.1	-9.7	17.3
Granary	7.0	3.9	18.3	7.8	8.4	9.8	11.6	9.4	13.5	17.9	16.8	4.1	11.5	3.7	4.4	-14.9	13.0
Tom	15.8	10.8	25.2	30.1	19.8	19.8	28.2	6.9	20.5	38.2	29.8	7.4	14.0	29.3	6.4	28.5	20.0
RB07	36.0	28.8	67.9	50.4	38.6	50.5	49.4	37.5	51.9	53.5	47.2	27.7	70.0	26.1	16.4	121.2	37.3
C80.1/3*QT4522//2*ATTILA	18.8	17.4	22.9	30.3	30.3	28.5	22.3	3.4	31.9	16.0	28.8	11.8	25.0	3.5	9.2	30.3	23.9

C80.1/3*QT4522//2*PASTOR	12.7	7.3	25.8	26.0	16.8	22.1	14.4	4.5	24.6	18.7	19.3	4.3	19.4	8.1	8.1	8.3	16.7
Møystad	21.0	14.6	17.7	29.4	22.0	13.8	30.8	14.0	5.2	27.0	19.9	10.9	25.0	6.4	4.8	14.6	31.5
Rollo	28.7	19.6	37.5	37.7	28.5	29.6	37.2	32.1	10.1	35.2	31.5	29.9	15.0	14.2	4.7	51.1	15.2
Norrøna	23.6	22.2	52.9	49.2	22.5	30.0	44.8	35.1	32.3	46.8	36.1	32.4	25.0	10.4	20.1	75.9	20.7
Fram II	17.8	19.9	42.1	18.8	17.7	22.6	39.9	24.2	29.7	33.2	30.9	12.7	30.0	9.8	22.8	47.4	17.3
Sumai #3-1 (12SRSN)	50.3	37.4	67.6	60.0	71.1	65.3	62.0	38.2	63.4	73.7	54.7	27.5	65.0	29.8	27.1	159.8	30.5
Mirakel	2.3	0.3	3.7	4.5	1.0	1.0	9.5	2.0	0.8	4.6	3.8	1.2	10.0	6.0	4.8	-41.4	5.2
Rabagast	2.5	2.1	5.4	8.8	1.5	2.5	7.8	1.3	2.3	8.5	6.1	2.9	4.0	2.6	2.5	-38.3	4.7
Seniorita	1.3	0.8	1.3	1.3	2.0	2.0	2.0	4.9	2.3	3.3	2.0	1.4	2.0	14.0	0.5	-45.1	2.8
GN07548	2.8	2.1	1.1	0.0	1.0	0.0	10.3	4.0	2.3	6.2	1.3	2.5	5.0	3.8	1.5	-44.8	4.5
GN07560	2.3	5.2	7.4	7.3	4.8	10.1	28.1	2.0	3.6	12.7	9.0	4.5	14.4	3.5	7.6	-22.8	6.1
GN07525	3.5	2.7	10.1	7.3	4.0	4.3	13.3	3.5	2.8	10.2	5.0	3.6	6.5	5.3	15.5	-31.1	5.3
GN08530	1.8	1.1	1.5	2.0	1.5	1.3	1.0	3.3	3.5	3.7	2.0	2.9	2.5	2.0	0.0	-47.7	3.6
GN09572	2.5	3.5	10.3	10.1	4.0	4.6	23.3	3.9	8.5	17.7	9.0	4.4	17.5	3.3	4.7	-21.3	7.6
GN08581	0.8	0.5	1.6	1.3	1.0	0.0	2.0	1.8	1.8	3.3	1.0	0.8	6.5	5.3	0.5	-48.3	2.6
GN10510	1.7	1.1	5.0	3.8	1.0	3.7	21.1	4.4	3.5	9.0	4.0	2.4	11.4	3.0	4.0	-34.3	5.6
Willy	3.3	1.5	7.5	7.9	8.7	7.7	20.9	4.6	5.0	6.4	4.3	2.9	12.5	8.1	4.7	-27.3	6.2
GN10524	2.3	2.1	5.8	6.4	1.0	7.2	9.0	1.4	2.8	13.2	5.8	8.3	1.4	7.0	NA	-35.1	3.2
Berlock	1.5	2.3	4.6	4.3	1.5	3.1	19.9	2.7	7.8	7.0	7.8	3.1	7.0	6.6	1.8	-33.7	4.3
Arabella	1.5	1.5	4.3	7.9	3.0	3.2	28.4	2.6	5.0	3.8	6.6	3.0	7.5	3.1	4.7	-31.3	4.8
Breeding line 11	4.7	0.5	4.7	NA	2.0	3.2	17.2	4.2	3.2	3.7	12.1	3.4	11.0	NA	5.5	-32.7	13.5

GN07580	1.3	1.0	0.5	0.0	0.0	0.0	0.0	1.5	0.0	2.5	0.8	1.0	1.0	6.0	0.0	-51.9	2.3
GN09584	0.0	0.0	0.0	0.0	0.0	0.0	3.0	0.0	0.0	1.0	0.0	0.5	2.0	1.5	0.0	-53.3	18.9
GN10512	1.0	0.0	0.0	0.0	0.0	1.0	27.3	0.0	0.5	2.0	1.0	NA	17.5	13.3	3.7	-37.2	20.7
Polkka	24.1	14.5	32.2	35.2	15.9	19.6	29.7	27.8	20.2	33.5	26.8	16.5	17.5	19.5	4.8	34.0	31.9
Avans	3.6	2.1	6.7	3.8	4.4	3.6	10.0	3.1	4.0	7.4	5.0	3.9	10.0	4.5	4.0	-35.2	10.3
BJY/COC//CLMS/GEN	32.0	45.1	57.3	54.6	60.1	44.9	52.1	33.8	45.8	57.0	45.4	27.4	50.6	51.9	22.7	128.3	49.2
HAHN/PRL//AUS1408	34.2	19.4	48.0	54.3	36.9	45.1	42.0	33.5	34.3	37.3	36.3	22.4	40.0	60.2	19.9	92.2	21.9
TUI/RL4137	49.0	30.0	68.1	54.7	50.2	56.0	40.2	36.4	54.4	54.2	47.6	23.8	50.0	29.9	26.9	126.4	32.8
T7347	NA	10.2	27.4	28.9	17.6	15.1	24.7	16.8	19.9	33.7	15.3	5.9	17.5	11.4	4.1	20.4	25.7
Reno	57.8	34.9	67.8	74.7	60.5	60.3	61.9	49.1	63.7	76.5	62.5	42.6	70.0	62.6	33.3	179.3	48.8
Bjarne/LW91W86	1.7	1.0	0.9	0.5	0.0	1.0	13.9	1.5	0.0	2.2	1.5	0.5	NA	1.5	0.0	-47.8	14.4
Anniina	NA	12.7	20.3	NA	11.3	13.9	12.4	6.5	9.9	NA	25.3	8.3	17.5	17.6	5.2	0.5	21.3
Aino	39.7	24.3	52.5	50.0	35.2	39.7	52.9	24.4	34.3	74.9	37.6	27.9	17.5	25.9	14.2	94.5	31.9
Kruunu	40.6	21.6	37.7	40.4	32.7	35.2	46.7	45.7	26.8	48.5	47.8	27.6	20.6	25.2	32.9	84.6	25.8
Marble	33.4	14.9	52.2	NA	35.1	40.3	32.5	16.7	35.0	NA	30.6	25.0	15.0	9.6	13.6	63.4	16.0
Wanamo	38.5	24.2	53.0	NA	30.3	35.1	31.1	28.4	34.9	NA	39.6	30.1	45.0	35.5	18.8	92.5	29.9
Wellamo	18.8	22.3	33.2	NA	34.3	36.6	50.2	20.9	35.9	NA	43.9	33.8	45.0	22.0	13.6	79.0	42.3
Scirocco	8.8	6.1	15.4	12.3	8.6	13.0	26.4	6.0	6.9	25.0	17.8	5.5	11.0	11.3	7.8	-4.8	15.9
Dragon	7.2	1.9	9.9	10.0	4.0	5.5	11.8	5.2	9.9	12.3	12.2	4.5	10.0	9.8	6.8	-23.6	12.6
Sirius	NA	11.9	27.5	24.0	22.8	20.2	29.7	10.6	22.0	17.3	25.2	5.5	12.5	45.6	2.4	24.8	14.6
Cadenza	NA	NA	NA	33.0	18.4	25.0	30.3	NA	NA	23.7	14.9	9.9	17.5	31.4	5.0	31.6	9.8

GN11591	2.3	2.4	NA	NA	2.0	2.0	4.0	3.4	NA	NA	7.8	3.6	9.0	2.8	5.1	-38.3	5.7
GN11569	5.3	2.9	NA	NA	7.0	15.3	25.9	8.4	NA	NA	14.6	7.0	8.0	8.6	3.6	-6.7	7.5
GN11572	1.0	1.4	NA	NA	1.5	1.3	10.4	1.5	NA	NA	2.5	1.8	10.0	2.7	5.4	-39.6	7.0
GN10607	0.5	1.4	NA	NA	2.0	1.0	5.1	1.5	NA	NA	3.3	3.5	2.5	3.2	2.4	-43.5	4.5
GN10613	2.3	2.4	NA	NA	3.5	3.1	19.1	1.0	NA	NA	4.7	5.5	7.5	2.0	3.0	-31.1	5.5
GN12639	8.8	0.5	NA	NA	4.3	5.0	15.6	4.9	NA	NA	5.6	3.6	5.6	5.4	2.3	-29.3	3.8
GN12640	8.8	0.5	NA	NA	8.1	5.0	7.3	4.9	NA	NA	17.3	4.4	10.0	13.2	2.3	-21.2	7.8
GN12700	NA	1.4	NA	NA	0.0	0.5	0.5	1.0	NA	NA	0.3	0.0	2.5	5.4	0.0	-49.1	2.5
GN12733	NA	2.4	NA	NA	5.4	4.4	12.8	1.0	NA	NA	3.3	3.0	1.4	2.8	4.9	-35.3	4.0
GN12699	NA	1.4	NA	NA	2.0	0.0	2.5	3.9	NA	NA	3.8	2.1	10.0	16.7	0.0	-36.8	4.9
Breeding line 11	0.5	1.4	NA	NA	NA	0.0	6.9	1.5	NA	NA	NA	1.0	3.0	1.5	2.5	-46.6	3.4
GN11505	0.0	1.4	NA	NA	0.5	0.0	0.5	0.5	NA	NA	1.3	NA	3.5	6.2	0.0	-48.5	4.0
GN11537	5.3	2.4	NA	NA	3.0	2.5	3.5	3.9	NA	NA	5.1	3.0	7.4	4.9	1.4	-38.0	5.4
GN11604	1.0	1.9	NA	NA	0.5	2.2	9.5	0.5	NA	NA	1.0	2.3	1.4	3.2	1.3	-44.9	6.9
GN11634	3.8	1.4	NA	NA	3.0	0.0	5.0	0.0	NA	NA	5.6	1.9	9.0	10.8	2.5	-38.8	8.2
Breeding line 12	NA	0.5	NA	NA	NA	5.5	34.7	3.9	NA	NA	NA	4.6	10.0	3.5	4.4	-14.4	7.5
Breeding line 13	NA	1.9	NA	NA	NA	7.5	21.0	1.0	NA	NA	NA	2.7	9.4	3.5	9.8	-21.2	4.9
Breeding line 14	NA	2.9	NA	NA	NA	1.6	23.0	3.9	NA	NA	NA	2.8	5.0	3.9	3.7	-23.2	4.0
Breeding line 15	NA	2.9	NA	NA	NA	2.7	11.7	2.0	NA	NA	NA	4.3	4.5	9.5	2.7	-33.1	4.6
GN12722	NA	0.5	NA	NA	0.5	0.0	1.5	1.5	NA	NA	2.5	1.0	7.5	7.1	1.3	-45.0	5.4
GN11527	1.0	1.9	NA	NA	2.0	1.0	3.5	0.0	NA	NA	2.8	2.2	5.0	1.0	4.0	-44.6	3.6

GN11551	1.0	1.9	NA	NA	2.5	5.4	13.1	1.5	NA	NA	6.7	4.2	15.0	10.4	1.4	-29.4	6.0
GN10680	0.5	0.5	NA	NA	1.0	3.0	2.5	1.5	NA	NA	2.3	1.8	9.0	3.7	3.4	-43.7	5.3
GN11516	1.0	0.5	NA	NA	5.5	4.9	8.3	0.5	NA	NA	4.8	3.1	11.0	2.0	2.3	-34.7	4.3
GN10547	1.8	1.9	NA	NA	4.2	4.3	9.1	3.4	NA	NA	9.8	5.5	15.0	10.1	2.5	-27.9	10.1
GN10603	1.0	1.4	NA	NA	0.5	0.0	4.0	1.5	NA	NA	2.3	1.6	3.5	1.5	0.3	-46.8	3.4
GN11574	0.0	0.5	NA	NA	4.2	10.2	36.9	1.0	NA	NA	1.3	1.4	0.0	8.9	8.0	-23.6	5.0
GN11646	2.3	1.9	NA	NA	2.0	3.7	11.7	3.4	NA	NA	4.0	1.7	2.5	1.5	2.1	-39.5	3.2
GN12606	1.8	3.4	NA	NA	3.0	3.8	13.8	1.0	NA	NA	4.5	2.1	9.4	2.0	1.5	-35.3	5.2
GN12625	0.0	1.9	NA	NA	0.5	0.5	0.5	0.5	NA	NA	0.5	0.0	1.5	2.0	0.0	-51.3	4.5
GN12628	2.8	2.4	NA	NA	4.0	6.2	11.6	1.5	NA	NA	5.3	4.5	4.5	2.0	3.2	-35.5	9.4
GN12634	2.8	1.9	NA	NA	3.0	4.4	12.1	3.9	NA	NA	5.3	2.8	10.0	2.6	3.5	-33.4	5.2
GN12635	4.3	1.9	NA	NA	4.0	4.0	19.0	3.9	NA	NA	7.8	3.9	7.5	7.6	3.6	-27.9	10.6
GN12641	2.8	1.9	NA	NA	7.8	4.6	11.4	9.4	NA	NA	11.1	3.1	14.4	11.8	8.3	-21.2	5.7
GN04603	12.3	3.4	14.8	NA	15.8	22.9	35.6	9.4	17.0	NA	18.6	13.5	25.0	12.9	13.5	20.5	8.7
GN11592	1.0	1.4	3.4	NA	0.5	2.4	4.6	0.0	2.0	NA	5.9	3.0	11.5	2.0	3.3	-41.9	2.8
GN11514	1.0	2.4	3.1	NA	2.0	4.5	5.7	0.0	0.0	NA	2.5	2.7	7.5	1.5	4.7	-42.1	2.1
GN12750	NA	1.4	0.5	NA	0.0	0.0	0.5	0.0	0.5	NA	1.3	0.5	1.0	3.5	0.8	-50.6	0.9
GN12626	0.0	1.9	0.0	NA	0.0	0.0	1.0	3.4	0.0	NA	1.0	0.3	0.0	1.0	0.0	-51.1	1.4
GN12656	NA	1.9	0.0	NA	0.0	0.0	0.0	2.0	0.0	NA	0.8	0.9	4.0	4.1	0.0	-49.7	2.1
GN12658	NA	1.4	0.5	NA	0.5	1.0	3.0	0.0	0.0	NA	1.8	0.8	5.0	3.8	0.9	-47.6	5.1
GN13542	NA	NA	0.0	NA	0.5	0.0	2.0	NA	1.2	NA	2.5	0.7	6.0	3.9	0.5	-48.6	3.4

GN13576	NA	NA	1.5	NA	0.5	1.0	7.3	NA	0.5	NA	2.0	1.0	2.5	3.1	1.2	-46.0	9.7
GN13577	NA	NA	3.1	NA	NA	2.0	9.6	NA	1.2	NA	NA	3.2	2.5	1.0	2.2	-43.0	4.6
Mandaryna	5.3	1.9	17.3	NA	NA	9.4	38.4	1.5	14.5	NA	NA	8.7	22.5	3.2	12.8	-2.1	9.2
Breeding line 16	NA	0.5	3.1	NA	NA	0.5	7.2	1.0	3.0	NA	NA	1.6	5.0	1.0	2.0	-44.2	7.2
Breeding line 17	NA	1.4	22.3	NA	NA	9.5	22.1	8.4	17.0	NA	NA	4.6	11.0	6.7	13.8	-1.7	5.0
Breeding line 18	NA	1.4	14.8	NA	NA	4.9	26.2	3.9	9.5	NA	NA	3.3	35.0	3.9	8.2	-1.0	5.9
GN12727	NA	1.4	0.0	NA	0.0	0.0	0.0	1.0	1.0	NA	1.0	0.0	2.5	1.0	0.0	-51.0	1.6
GN12721	NA	1.9	1.0	NA	1.5	1.0	2.0	1.5	1.2	NA	1.8	0.7	6.0	9.2	0.0	-44.8	4.5
GN13614	NA	NA	1.5	NA	0.5	0.0	2.5	NA	1.0	NA	1.8	1.2	0.6	5.1	0.5	-49.2	3.4
GN13615	NA	NA	0.0	NA	0.5	0.0	4.0	NA	1.0	NA	1.3	0.5	2.5	3.7	1.1	-49.4	5.4
Breeding line 19	NA	NA	3.6	NA	NA	1.3	10.1	NA	1.0	NA	NA	1.4	12.5	7.3	3.1	-37.3	4.6
Breeding line 20	NA	NA	14.8	NA	NA	5.5	14.9	NA	8.5	NA	NA	7.0	17.5	10.5	19.6	-10.4	6.1
Breeding line 21	NA	NA	5.1	NA	NA	4.3	6.5	NA	3.5	NA	NA	1.2	22.5	5.8	1.8	-31.8	7.2
GN11641	2.3	1.9	3.1	NA	1.5	6.7	10.8	2.0	1.2	NA	2.5	3.2	7.6	4.1	1.7	-38.5	3.0
GN12607	1.8	1.9	4.1	NA	3.0	3.3	14.4	1.5	2.2	NA	2.5	1.4	5.0	4.1	4.1	-38.1	2.5
GN13528	NA	NA	0.0	NA	0.0	0.0	0.5	NA	0.0	NA	0.0	0.0	2.0	0.0	0.0	-53.5	2.2
GN12681	NA	2.4	12.3	NA	1.5	1.6	1.0	4.9	4.5	NA	2.8	1.7	13.5	4.9	0.0	-36.1	3.5
GN12697	NA	1.4	8.3	NA	0.5	0.0	12.8	7.9	4.5	NA	3.5	3.8	9.0	23.9	1.0	-29.1	4.8
GN12759	NA	1.4	1.5	NA	0.0	2.5	1.5	2.0	2.2	NA	1.5	1.0	6.5	2.8	0.5	-45.9	2.0
GN12701	NA	1.4	0.0	NA	0.5	0.0	0.0	0.5	0.0	NA	0.3	0.5	1.5	4.7	0.0	-50.9	1.6
GN13505	NA	NA	1.0	NA	1.0	1.0	0.5	NA	1.2	NA	1.3	0.5	9.4	1.0	0.5	-47.4	1.6

GN13509	NA	NA	0.5	NA	1.5	0.0	4.0	NA	1.2	NA	3.3	0.8	1.6	2.0	0.0	-47.4	1.0
GN13516	NA	NA	0.5	NA	0.0	0.5	0.5	NA	0.5	NA	2.3	2.5	11.0	1.0	0.5	-48.1	1.7
GN13523	NA	NA	0.0	NA	0.0	0.0	1.5	NA	1.0	NA	0.0	0.5	1.5	0.5	0.0	-52.5	2.6
GN12741	NA	1.9	0.5	2.0	1.0	0.5	0.0	0.5	0.0	1.5	1.0	0.5	0.0	2.9	0.0	-51.7	2.3
GN13633	NA	NA	0.0	NA	0.0	0.0	1.0	NA	0.0	NA	0.0	0.0	2.6	2.0	0.0	-52.5	3.9
GN13641	NA	NA	0.5	NA	0.5	0.0	2.5	NA	0.5	NA	0.0	0.0	1.5	2.0	0.5	-51.5	4.3
GN11644	2.8	1.9	5.1	8.7	2.5	9.2	31.2	7.4	7.0	11.6	9.4	2.9	10.0	8.1	5.9	-22.3	5.5
GN12630	2.8	2.4	3.6	10.2	4.3	4.7	21.1	3.4	3.5	14.1	7.8	6.3	12.0	2.9	5.0	-27.2	7.0
GN10677	0.5	0.5	0.0	1.0	0.5	0.0	5.2	0.0	0.5	2.0	2.3	1.4	5.5	1.5	0.5	-50.0	2.2
GN11542	2.8	1.9	1.5	9.5	2.0	2.6	13.0	1.0	2.5	15.0	5.6	3.8	6.5	1.5	1.4	-36.5	3.9
GN12687	NA	1.9	4.6	4.0	3.0	7.5	7.2	4.9	9.5	9.1	4.8	3.6	9.0	6.5	2.7	-32.9	3.5
GN12770	NA	2.9	4.1	14.8	6.9	11.8	15.1	1.0	5.5	10.1	7.9	1.7	6.5	9.1	3.5	-25.7	5.6
GN13578	NA	NA	3.1	1.5	1.5	3.1	5.0	NA	1.2	7.1	3.3	2.7	5.5	3.8	2.7	-44.1	3.0
GN12645	NA	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.3	0.0	2.5	0.5	0.5	-54.1	1.2
GN13521	NA	NA	0.0	0.0	0.0	0.0	1.5	NA	0.0	0.0	1.5	NA	8.0	3.5	0.0	-52.2	4.6
GN12767	NA	2.4	14.8	15.5	6.3	4.5	7.9	3.9	4.5	11.6	9.7	2.7	6.5	6.3	1.3	-26.0	3.7
GN13560	NA	NA	5.1	7.7	4.0	5.0	14.4	NA	3.5	6.6	9.7	2.6	14.0	4.3	12.0	-29.0	3.9
GN14502	NA	NA	NA	0.5	1.0	0.5	2.0	NA	NA	2.0	1.5	0.8	2.0	2.5	0.5	-51.7	1.4
GN14512	NA	NA	NA	4.0	2.5	8.5	5.2	NA	NA	4.8	6.2	3.7	8.0	5.6	2.6	-36.7	3.4
GN14547	NA	NA	NA	0.5	0.5	0.5	0.5	NA	NA	0.5	1.0	0.3	2.5	1.5	0.0	-54.1	1.0
GN14634	NA	NA	NA	0.5	0.0	0.0	0.0	NA	NA	5.0	1.3	0.5	4.0	5.1	0.5	-50.8	6.7

GN14636	NA	NA	NA	4.0	5.5	2.5	4.0	NA	NA	10.0	3.5	3.9	10.0	8.1	1.0	-36.9	5.8
GN14649	NA	NA	NA	5.0	3.5	5.0	17.6	NA	NA	8.1	3.5	3.7	5.5	4.0	3.2	-33.2	5.3
Caress	0.0	1.9	0.5	0.5	0.0	0.5	21.8	0.5	1.2	2.0	1.3	0.0	1.0	3.7	6.9	-45.3	5.7
GN10637	5.3	1.9	9.8	20.2	6.0	12.6	28.0	3.4	2.5	10.1	8.8	4.9	7.5	2.0	4.8	-19.5	3.4
Breeding line 22	NA	NA	1.5	3.0	4.8	4.1	10.4	NA	2.2	6.3	5.3	3.4	5.0	5.2	3.1	-39.0	8.9
Breeding line 23	NA	NA	4.1	2.0	0.5	1.0	9.2	NA	2.2	6.3	2.0	1.6	2.0	3.7	3.5	-44.4	3.4
Breeding line 24	NA	NA	10.8	16.3	21.0	11.4	24.1	NA	9.5	21.8	15.2	10.4	20.0	6.9	10.9	0.8	12.9
GN13618	NA	NA	0.5	0.5	0.0	0.5	3.0	NA	1.0	1.5	0.0	0.0	4.0	4.3	0.0	-51.8	3.4
Breeding line 25	NA	NA	12.3	27.3	4.2	9.3	15.1	NA	12.0	26.8	4.8	3.0	6.0	2.0	1.6	-14.1	7.5
Breeding line 26	NA	NA	6.1	18.3	3.5	4.7	18.7	NA	3.5	16.8	9.1	3.1	3.5	4.7	10.2	-23.8	4.1
Breeding line 27	NA	NA	14.8	30.5	9.8	20.0	14.9	NA	17.0	29.3	21.0	7.2	12.5	12.5	4.0	10.4	12.9
Breeding line 28	NA	NA	NA	3.0	0.5	1.0	6.4	NA	NA	9.3	3.0	1.1	9.5	1.5	2.1	-42.5	3.0
Breeding line 29	NA	NA	NA	3.5	0.5	1.0	18.9	NA	NA	6.8	6.5	1.9	21.0	5.6	3.5	-31.4	7.1
Breeding line 30	NA	NA	NA	1.5	0.0	3.3	12.5	NA	NA	1.5	2.3	1.7	2.5	0.5	3.3	-45.6	1.4
Breeding line 31	NA	NA	NA	17.7	9.2	8.8	17.2	NA	NA	21.8	6.4	3.0	17.5	5.8	7.2	-10.0	7.5
GN13616	NA	NA	0.5	0.5	1.0	0.5	0.5	NA	0.5	0.0	0.5	0.3	0.5	1.1	0.5	-54.1	1.9
GN14539	NA	NA	NA	5.0	2.0	3.3	15.6	NA	NA	5.8	5.2	2.8	6.5	3.9	7.4	-35.0	6.6
GN14540	NA	NA	NA	5.0	3.0	3.0	7.7	NA	NA	11.8	5.0	2.6	10.0	5.1	3.6	-34.8	3.9
GN14544	NA	NA	NA	3.5	1.5	2.2	11.7	NA	NA	2.5	2.0	3.0	3.0	7.5	2.4	-42.7	4.0
GN14583	NA	NA	NA	5.8	2.0	3.9	10.0	NA	NA	6.8	6.5	2.1	8.6	9.2	2.9	-34.6	3.2
GN12637	10.3	1.9	4.6	17.7	12.2	9.7	22.9	6.9	4.5	11.8	17.5	7.1	11.0	7.7	1.5	-14.8	5.4

GN12737	NA	1.4	0.5	0.5	0.5	0.5	1.5	1.0	0.0	1.5	1.3	0.8	1.5	1.8	0.3	-51.8	1.0
GN12760	NA	0.0	1.0	1.0	0.0	1.4	3.0	1.5	1.2	5.8	1.8	1.2	9.0	1.5	0.0	-47.4	3.6
GN12661	NA	2.4	3.1	3.5	1.5	0.0	5.2	3.4	4.5	17.3	0.8	1.0	8.6	11.6	1.5	-37.8	3.2
GN14529	NA	NA	NA	1.5	0.5	0.0	3.0	NA	NA	2.5	2.8	0.3	2.0	5.5	0.6	-50.2	2.2
GN14530	NA	NA	NA	0.0	0.0	0.0	0.0	NA	NA	1.5	0.8	0.3	6.5	11.9	0.5	-50.5	2.1
GN13527	NA	NA	6.1	13.8	4.0	7.6	15.1	NA	2.5	21.8	9.7	10.1	25.0	9.1	3.1	-17.0	7.1
GN12764	NA	1.4	0.0	0.0	0.5	0.0	0.0	0.0	0.0	1.0	0.8	0.5	1.0	2.9	0.0	-53.2	8.1
GN13519	NA	NA	0.0	0.5	0.0	0.5	1.0	NA	0.0	1.0	0.3	0.5	3.0	2.0	0.5	-53.6	4.3
GN13606	NA	NA	0.5	8.3	1.5	2.7	9.2	NA	0.5	4.8	2.3	4.1	5.0	1.6	2.2	-42.3	4.6
GN13626	NA	NA	8.3	7.5	2.0	4.4	23.4	NA	5.5	7.8	10.7	3.1	14.4	3.0	2.6	-26.4	4.6
GN12615	16.3	2.4	19.8	27.7	22.0	19.6	19.2	6.9	14.5	16.8	18.8	3.6	15.0	23.0	8.1	8.6	7.7
GN13553	NA	NA	9.8	12.7	4.3	1.0	17.5	NA	2.5	9.3	7.6	1.3	15.0	5.5	1.3	-28.5	3.4
GN14522	NA	NA	NA	2.0	0.0	0.5	10.6	NA	NA	2.0	3.0	1.4	2.5	2.0	1.5	-47.1	0.9
GN13595	NA	NA	3.1	1.5	0.0	1.0	3.5	NA	1.2	2.0	1.3	0.5	10.0	1.0	0.5	-48.1	1.3
GN13596	NA	NA	0.5	1.0	0.5	0.5	0.0	NA	0.0	0.0	0.8	1.7	2.5	2.7	0.0	-53.1	3.5
GN12650	NA	1.9	NA	0.0	0.0	0.0	0.5	1.5	NA	1.5	2.0	0.3	10.0	3.9	0.5	-49.0	3.9
GN14506	NA	NA	NA	3.0	0.0	1.0	10.4	NA	NA	3.0	3.3	2.2	5.5	1.5	2.9	-44.7	17.2
GN14511	NA	NA	NA	1.5	1.0	0.5	8.1	NA	NA	1.0	2.0	1.4	4.5	1.0	2.9	-48.5	16.6
GN14515	NA	NA	NA	9.8	6.1	10.0	39.2	NA	NA	9.1	9.8	NA	14.0	4.0	5.5	-6.3	16.6
GN14516	NA	NA	NA	10.8	3.0	5.8	20.3	NA	NA	5.6	7.3	2.6	6.5	3.7	5.6	-28.7	21.2
EMB16/CBRD//CBRD	NA	NA	NA	NA	36.0	55.0	38.5	NA	NA	NA	42.9	25.9	25.0	8.8	19.8	84.7	26.8

N894037	NA	NA	NA	NA	63.9	64.6	68.1	NA	NA	NA	55.8	24.9	19.4	46.4	28.8	147.9	30.6
SHA5/WEAVER//80456/YANGMAI 5	NA	NA	NA	NA	17.5	19.9	20.1	NA	NA	NA	16.9	8.0	8.0	13.2	6.1	5.8	22.7
VERDE/3/BCN//DOY1/AE.SQUARROSA (447)	NA	NA	NA	NA	31.9	29.3	30.3	NA	NA	NA	28.3	18.6	50.0	17.8	20.4	63.2	27.8
80456/YANGMAI 5//SHA5/WEAVER/3/PRINIA	NA	NA	NA	NA	59.0	39.8	52.5	NA	NA	NA	49.8	26.1	30.0	40.7	24.6	121.9	33.7
NG8675/CBRD//SHA5/WEAVER	NA	NA	NA	NA	22.1	34.8	32.1	NA	NA	NA	32.0	8.6	19.4	32.7	7.1	46.6	28.8
TRAP#1/BOW//TAIGU DERIVATIVE	NA	NA	NA	NA	17.5	25.0	25.8	NA	NA	NA	27.4	5.7	9.4	22.2	15.0	24.6	21.8
IVAN/6/SABUF/5/BCN/4/RABI//GS/CRA/3/AE.SQUARROSA (190)	NA	NA	NA	NA	39.6	40.4	42.4	NA	NA	NA	36.4	25.1	29.4	22.8	25.4	92.8	27.6
GAMENYA	NA	NA	NA	NA	49.6	49.5	31.4	NA	NA	NA	33.0	20.0	22.5	47.4	24.4	92.6	16.7
WHEAR/2*KRONSTAD F2004	NA	NA	NA	NA	25.9	29.2	25.7	NA	NA	NA	29.8	18.6	20.0	14.1	8.2	39.0	18.1
T.DICOCCON PI94625/AE.SQUARROSA (372)//TUI/CLMS/3/2*PASTOR/4/EXCALIBUR	NA	NA	NA	NA	28.9	20.0	14.9	NA	NA	NA	28.4	15.1	NA	26.8	8.5	32.4	16.3

Table 2 Winter MASBASIS lines with lsmeans for disease severity in each environment, PC1 and over all environments.

Name	**Vb14**	**Vb15**	**1-Vb16**	**2_Vb16**	**Vb17**	**Vb18**	**Vb19**	**PC1**	**All Env.**
Bjørke	13.2	11.4	18.4	33.7	18.3	10.0	29.1	32.9	19.2
Folke	4.5	4.8	6.4	7.3	7.1	7.7	7.8	-5.7	6.5
Mjølner	3.4	5.2	7.2	12.5	5.8	1.6	6.5	-4.5	6.0
Magnifik	2.8	2.7	7.5	10.7	8.4	3.0	12.6	-2.4	6.8
Olivin	4.6	6.4	5.8	9.9	14.9	8.2	18.7	3.8	9.8
Finans	25.8	14.6	14.1	56.7	33.2	8.6	27.0	54.5	25.7
NK03029	4.3	2.2	1.4	5.0	3.6	5.1	3.5	-13.0	3.6
RE714	9.9	3.8	9.1	42.7	6.5	8.3	10.4	20.3	13.0
Massey	6.7	3.0	5.0	7.2	4.8	3.1	8.8	-7.2	5.5
Fenman	4.4	1.6	2.9	4.1	4.7	0.7	3.9	-13.5	3.2
Soissons	4.5	1.5	4.6	7.9	6.4	4.6	11.3	-5.8	5.8
Arina	15.4	6.4	7.8	19.0	16.3	12.9	20.0	15.3	14.0
LW91W89	3.5	3.1	1.5	2.9	3.3	5.9	33.4	-1.2	7.7
Bersee	2.2	2.8	8.0	16.1	5.4	4.6	8.1	-1.7	6.7
Apollo	1.1	10.3	23.3	27.8	23.2	10.9	25.4	27.2	17.4
Spark	15.4	12.6	19.8	36.5	19.9	5.6	26.5	34.6	19.5
Vlasta	4.8	3.2	2.6	7.7	5.0	1.9	6.9	-9.2	4.6
Senat	6.7	3.8	7.6	15.2	9.8	8.6	12.4	3.3	9.2
Solist	6.0	3.0	4.3	7.2	6.8	5.5	12.6	-4.8	6.5
Ambition	5.9	1.3	6.8	21.3	6.8	7.6	27.7	11.6	11.1
Jenga	14.8	4.9	11.1	19.5	13.2	12.9	22.5	16.2	14.1
Senta	23.8	6.6	20.1	22.0	8.4	8.9	18.4	19.5	15.5
Mironovskaja 808	4.8	3.9	8.6	8.8	8.3	3.8	10.1	-3.4	6.9
Siria	3.5	2.2	3.9	7.9	3.3	2.8	11.2	-7.8	5.0
Regina	25.3	12.0	26.5	35.2	16.6	23.9	18.0	37.1	22.5
GN04035	1.8	2.7	2.8	1.3	4.8	2.1	5.0	-15.1	2.9
GN04034	1.1	1.5	0.9	2.0	2.3	5.0	0.8	-17.9	1.9
GN05012	1.6	1.7	1.4	2.3	2.8	2.1	2.8	-16.8	2.1
GN05013	6.6	3.6	6.6	18.2	7.1	2.5	13.0	3.0	8.2
V1004	12.0	7.1	4.7	14.8	10.1	8.1	14.8	5.4	10.2
V9001	3.8	5.8	6.8	8.3	5.0	6.8	7.9	-5.8	6.3
TARSO	3.7	1.2	2.5	6.2	3.2	2.7	4.6	-12.4	3.4
Kamerat	2.1	2.1	5.3	7.5	1.7	4.6	4.7	-11.1	4.0
Rida	11.9	8.8	13.4	21.6	8.1	6.8	27.1	17.4	14.0
Trond	5.0	11.4	15.2	19.6	16.5	20.3	19.9	17.6	15.4
Sigyn II	2.1	2.8	3.9	6.7	3.6	5.0	4.1	-11.4	4.0
REDCOAT	18.5	9.2	19.9	24.4	23.2	12.6	26.9	29.7	19.2
Skagen	4.1	2.3	3.0	10.9	7.2	6.6	5.0	-6.6	5.6
Plutos	16.4	5.1	8.0	19.4	11.8	12.8	18.0	13.2	13.1
Akratos	4.2	2.5	6.7	10.4	6.6	8.6	8.0	-4.1	6.7

Jantarka	3.1	1.2	2.7	5.1	3.6	8.1	4.5	-12.1	4.0
Akteur	1.7	2.4	1.8	4.8	3.5	4.3	5.3	-13.1	3.4
Breeding line 0	0.1	1.1	0.0	0.0	0.4	4.6	3.1	-19.5	1.3
Ellvis	20.1	12.2	12.7	20.2	29.8	19.5	29.0	30.2	20.5
GN08004	3.1	2.2	2.1	3.5	2.7	2.3	4.3	-14.6	2.9
Frontal	7.0	2.7	7.4	10.9	9.3	6.4	19.0	2.7	9.0
Kalle	6.1	12.9	23.0	22.6	11.6	6.0	18.0	17.5	14.3
Portal	13.5	8.3	8.3	21.7	20.0	11.8	25.2	20.4	15.5
Rudolf	3.3	7.4	3.5	5.1	3.8	4.2	3.5	-11.6	4.4
Kosack	5.0	2.6	6.3	7.8	4.8	7.3	6.2	-7.3	5.7
Granitt	2.8	3.9	5.8	10.3	11.6	0.9	9.1	-3.8	6.3
Kuban	0.3	0.8	1.3	9.7	1.5	5.9	4.3	-11.8	3.4
USG3209	7.4	4.8	9.3	8.3	5.7	5.8	6.2	-4.9	6.8
Stava	NA	NA	1.6	0.7	1.4	1.8	1.2	-19.5	0.2
NK03030	NA	NA	4.0	8.5	4.8	5.3	6.3	-8.2	4.7
GN04041	NA	NA	1.8	1.9	2.0	2.3	1.5	-18.1	0.8
20121	NA	NA	12.3	34.3	10.2	8.4	17.3	22.3	15.4
20126	NA	NA	13.4	9.8	8.6	14.0	11.9	2.5	10.4
20128	NA	NA	8.2	8.8	4.8	10.5	9.5	-3.7	7.3
20130	NA	NA	5.3	5.3	4.9	10.6	7.6	-8.2	5.6
20146	NA	NA	13.4	19.3	11.9	9.2	15.1	11.4	12.7
20228	NA	NA	2.7	4.1	4.2	3.8	5.3	-12.9	2.9
Kanzler	18.8	26.4	36.5	59.5	29.9	18.9	45.0	72.9	33.6
Breeding line1	13.9	3.0	3.0	9.1	3.5	13.4	2.5	-5.9	6.9
KWS-Ozon	0.0	0.0	0.8	0.8	1.4	2.3	5.5	-18.1	1.5
Breeding line2	0.5	1.0	0.4	1.1	3.9	3.2	3.0	-17.7	1.9
Breeding line3	4.4	6.8	5.6	6.3	6.8	2.7	16.5	-3.4	7.0
Breeding line4	0.3	1.0	1.8	1.9	3.4	5.1	5.2	-15.7	2.7
Breeding line5	NA	4.0	5.9	19.2	9.9	11.6	26.1	13.0	12.5
Prierier	9.9	3.0	4.8	18.2	8.3	15.6	6.0	3.0	9.4
Sarmund	0.5	1.0	1.8	3.8	2.2	4.4	4.5	-15.2	2.6
Breeding line6	NA	1.0	3.1	5.1	3.5	2.7	4.1	-13.3	2.9
Breeding line7	NA	1.0	1.9	9.0	4.1	16.2	7.9	-6.3	6.4
Agil	4.7	2.0	6.5	8.6	7.6	12.5	11.2	-2.8	7.6
Breeding line8	NA	0.0	0.0	0.0	1.3	5.6	3.6	-18.8	1.4
Breeding line9	4.2	3.0	6.7	15.6	7.6	6.5	14.8	2.3	8.3
Breeding line10	3.9	3.0	2.6	8.5	5.2	2.8	6.3	-9.0	4.6
Breeding line11	0.0	4.0	2.8	4.0	4.3	1.2	3.5	-14.5	2.8
GN11018	0.0	1.0	1.1	0.9	1.4	7.8	7.0	-16.0	2.7
GN13023	2.7	2.0	4.3	4.1	5.1	2.5	5.1	-12.4	3.7
Ceylon	NA	4.3	9.7	16.7	10.0	10.1	9.0	4.2	9.7
Mariboss	4.2	0.5	4.3	7.2	3.3	5.0	13.7	-6.7	5.5
Torp	NA	NA	1.6	5.2	2.8	16.8	22.9	-1.6	8.8
Ritmo	NA	NA	9.9	37.2	16.3	16.4	19.0	28.6	18.7

KWS Magic	NA	NA	2.4	2.4	2.1	2.4	19.8	-8.2	4.7
BAYP4535 (W01217.4 Me/De)	NA	NA	2.5	14.8	3.0	6.0	9.8	-2.9	6.1
Julius	NA	NA	2.8	8.3	6.2	7.0	8.9	-6.6	5.5
Potenzial	NA	NA	3.3	10.8	5.7	7.2	6.9	-5.8	5.7
Format	NA	NA	5.9	10.3	5.2	18.9	10.6	-0.9	9.1
FIRL3565(Amigos)	NA	NA	3.1	4.6	5.9	5.5	12.4	-7.9	5.2
Bussard	NA	NA	8.5	21.2	11.8	14.6	17.8	13.5	13.7
Event	NA	NA	1.1	0.5	1.0	3.3	8.3	-16.1	1.7
SvP72017	NA	NA	NA	NA	8.5	1.8	5.6	-10.1	4.4
Alchemy	NA	NA	5.2	7.5	5.2	2.6	5.4	-9.3	4.1
Brompton	NA	NA	10.0	17.7	13.2	10.2	12.5	8.4	11.6
Claire	NA	NA	11.6	20.7	23.5	6.6	26.3	21.6	16.6
Hereward	NA	NA	10.7	16.5	14.8	7.4	18.9	11.1	12.6
Rialto	NA	NA	6.1	16.2	5.9	5.2	13.2	2.1	8.2
Robigus	NA	NA	2.9	7.7	4.5	3.6	17.9	-3.8	6.2
Xi19	NA	NA	4.1	6.0	6.1	9.8	9.6	-6.9	6.0
Matrix	0.3	NA	1.8	1.3	2.9	7.2	9.7	-13.7	3.3
Arktis	0.3	NA	1.4	1.8	2.6	2.2	0.4	-18.9	0.8
Breeding line12	NA	0.5	0.0	0.0	1.6	3.2	2.0	-19.8	0.9

Table 3 Interesting and significant markers in spring wheat supported with chromosome location, physical position (bp), -log10 (p-value) for all environments

Marker	Chr.	Phys.Pos	Vb 12	Vb 13	Vb 14	Vb 15	Vb 16	Vb 17	Vb 19	St 13	St 14	St 15	St 16	St 17	St 18	St 19	Sa 18	Hs 19
AX-94551566	1A	NA	1.02	1.74	1.32	1.70	3.18	1.51	1.54	1.25	1.25	1.02	2.23	1.67	1.46	0.99	1.06	1.09
AX-94955419	1A	2,978,831	2.65	2.69	2.65	1.93	3.29	3.85	2.44	2.58	2.39	2.61	2.74	4.27	0.45	1.48	1.37	2.89
AX-94838936	1A	9,357,669	3.13	2.32	3.77	2.95	2.71	1.47	1.50	1.34	3.70	1.95	1.93	0.70	1.00	1.45	2.12	2.21
AX-94565449	2A	3,259,160	1.95	1.64	4.17	2.39	2.98	3.02	2.27	2.22	3.37	3.10	3.31	1.57	1.93	2.01	1.88	2.21
AX-95188522	2A	NA	1.81	1.66	5.28	2.82	1.45	3.78	5.15	2.37	3.84	3.44	4.79	1.94	2.32	3.06	0.61	3.06
AX-95238660	2A	515,452,422	2.59	4.35	3.30	3.23	3.70	2.75	3.30	3.30	2.14	4.26	3.66	4.65	1.55	2.58	1.78	4.75
AX-94397387	2A	515,945,795	2.22	3.59	2.25	2.01	3.23	1.76	2.55	1.92	1.39	2.53	2.37	3.85	1.12	1.60	0.90	3.48
AX-94509071	2A	516,396,000	2.21	3.56	2.14	2.45	1.99	1.63	1.95	2.76	1.26	3.22	1.61	2.57	0.93	1.77	0.87	2.55
AX-95630172	2A	517,399,128	0.95	1.59	2.31	2.68	2.25	1.49	1.95	1.18	0.99	3.42	1.73	2.41	1.16	1.73	0.81	2.32
AX-94742698	2A	520,308,995	2.39	3.44	2.12	2.73	2.14	1.58	2.11	2.62	1.17	3.33	1.83	2.10	0.88	1.71	1.00	2.50
AX-94789549	2A	520,990,823	0.95	1.59	2.31	2.68	2.25	1.49	1.95	1.18	0.99	3.42	1.73	2.41	1.16	1.73	0.81	2.32
AX-94493722	2A	522,515,722	1.50	2.55	2.93	3.23	2.76	2.22	2.63	1.98	1.69	4.05	2.29	3.15	1.53	2.36	1.30	3.12
AX-94396940	2A	524,331,716	2.22	3.63	2.28	2.54	2.06	1.69	2.03	2.83	1.34	3.31	1.71	2.64	0.96	1.84	0.88	2.64
AX-95018590	2A	NA	1.64	2.38	2.63	3.44	2.79	2.05	2.69	1.76	1.44	4.17	2.37	2.53	1.49	2.20	1.42	2.91
AX-94801027	2A	NA	2.40	3.59	2.40	2.81	0.99	2.29	1.28	3.33	1.90	3.30	1.34	2.46	0.61	1.30	0.39	1.70
AX-94514944	2A	605,000,772	2.57	1.08	0.90	1.21	3.84	1.26	0.45	2.05	1.26	1.21	1.00	1.07	1.74	1.23	0.72	1.51
AX-94480083	2A	605,634,830	3.19	2.26	1.13	1.08	2.97	1.64	0.81	3.43	2.91	0.41	1.52	1.60	3.22	1.43	0.78	2.87
AX-95160643	2A	NA	1.92	2.04	2.36	2.60	5.01	2.85	1.49	3.95	3.27	0.97	2.63	3.61	3.97	2.99	1.58	3.14
AX-94963427	2A	NA	2.14	1.46	2.97	2.54	1.21	3.18	1.69	3.27	1.71	2.91	2.01	1.14	1.86	1.34	0.86	0.79

AX-95102130	2A	739,308,962	2.56	4.91	2.48	2.13	2.44	3.72	1.52	5.30	3.07	1.74	1.59	1.54	1.03	1.99	2.34	2.13
AX-94481517	2A	NA	1.08	0.28	1.79	2.36	1.74	2.26	2.18	0.57	0.67	3.28	2.68	0.89	2.44	2.10	0.76	1.80
AX-94802107	2A	757,948,239	1.03	2.83	3.02	2.23	3.67	3.69	3.26	3.50	2.41	2.07	2.27	3.02	1.53	3.24	1.71	2.49
AX-94517549	2B	9,016,421	0.40	0.88	2.61	1.85	1.72	1.69	2.47	1.28	1.65	3.27	2.80	2.09	1.55	2.50	2.30	1.35
AX-95112632	2B	9,120,910	1.26	2.74	3.55	2.45	2.18	3.30	1.87	2.94	3.06	3.04	3.76	2.11	2.35	2.89	1.24	2.07
AX-95194336	2B	9,890,064	3.12	2.92	4.29	3.20	2.45	3.46	3.31	3.30	3.71	3.32	3.82	2.54	1.99	2.67	1.94	2.69
AX-95201364	2B	NA	1.82	2.12	2.64	1.51	1.75	1.91	2.03	2.07	2.63	1.29	1.77	2.69	1.81	0.90	1.53	1.85
AX-95173587	2B	12,076,575	0.47	0.44	2.78	1.62	1.65	2.01	1.40	1.53	2.22	2.53	3.29	1.25	1.81	1.60	1.27	1.74
AX-94489937	2B	17,394,536	1.03	1.18	1.87	1.53	1.21	2.33	3.31	2.05	1.21	1.67	2.67	1.28	1.38	1.79	0.80	1.64
AX-95017965	2B	19,070,596	2.22	2.15	3.73	3.64	3.13	4.44	4.94	2.69	4.05	3.86	4.62	3.32	2.04	2.61	1.79	3.77
AX-94520248	2B	NA	1.56	1.64	2.69	2.21	1.77	3.28	4.67	2.61	1.94	2.96	2.98	2.07	2.01	2.01	0.72	1.86
AX-95087040	2B	NA	1.75	1.42	2.42	1.69	1.50	2.75	3.34	2.57	1.87	1.88	3.26	1.46	1.40	2.80	1.00	2.62
AX-95147784	2B	26,564,120	1.74	2.59	2.83	2.86	1.54	2.39	2.21	2.48	2.79	2.24	2.24	2.44	1.49	2.79	0.93	2.33
AX-95652890	2B	26,581,493	1.43	2.10	3.34	3.23	1.18	1.87	2.26	2.00	2.99	2.20	2.30	2.09	1.43	1.52	0.80	2.01
AX-94508950	2B	26,581,682	2.12	2.45	3.19	3.00	1.80	2.76	2.68	2.42	2.71	2.35	3.07	2.81	2.05	1.88	1.05	2.37
AX-94483531	2B	26,986,944	2.12	2.29	3.02	2.90	1.93	3.45	2.89	2.00	2.26	2.84	3.23	3.12	2.13	2.31	1.43	2.63
AX-94547080	2B	30,321,933	1.22	1.18	1.79	2.78	2.13	1.87	3.09	0.72	2.38	1.99	1.24	2.11	1.09	0.87	0.44	2.65
AX-94480585	3A	7,653,799	3.13	2.25	1.37	1.24	1.13	0.72	0.48	1.32	0.89	0.32	1.06	1.54	0.45	0.36	0.08	1.48
AX-94555538	3A	8,325,662	5.67	3.39	3.18	4.34	3.40	2.57	2.92	2.70	3.90	2.37	2.53	2.50	3.07	1.78	2.19	3.34
AX-95232198	3A	9,603,484	3.25	1.95	1.75	1.72	2.05	1.50	1.17	1.27	1.95	0.85	1.50	1.34	1.19	0.43	1.93	2.02
AX-94461092	3A	12,494,352	3.03	1.27	1.98	2.31	2.71	2.28	1.15	1.60	1.91	0.90	2.28	2.33	2.43	0.50	0.86	2.40

AX-94706753	3A	16,467,149	3.27	2.11	1.23	1.13	1.76	1.08	1.05	1.22	1.12	0.26	1.78	0.76	0.31	1.30	1.27	1.69
AX-94567981	3A	NA	1.81	0.95	0.49	0.39	0.76	1.64	1.53	0.77	1.00	1.52	1.18	0.49	0.29	2.34	3.43	1.34
AX-94675268	3A	NA	3.03	1.58	1.07	1.35	1.36	0.93	0.93	0.85	1.15	0.59	1.11	0.95	0.66	0.34	1.36	1.51
AX-94932563	3A	NA	3.39	2.43	0.99	1.34	1.46	1.20	1.20	1.63	0.92	0.72	1.33	0.83	0.40	1.21	0.84	1.71
AX-94446053	3A	67,908,995	1.61	0.95	1.69	2.19	2.92	2.74	3.64	0.82	1.87	1.68	2.58	1.93	5.16	2.83	2.35	1.18
AX-94468868	3A	69,665,200	1.66	1.31	2.22	2.15	2.47	3.38	3.59	1.26	2.99	1.72	2.40	2.44	4.57	2.66	1.00	0.81
AX-94441567	3A	NA	1.63	1.29	2.05	2.49	2.93	2.87	3.74	1.22	2.79	2.24	2.20	1.94	5.90	2.60	2.88	0.88
AX-94636432	3A	NA	1.58	0.81	1.60	2.45	2.71	2.76	3.89	0.73	1.92	1.91	2.51	1.67	5.30	3.12	2.38	1.27
AX-94652031	3A	NA	1.63	1.29	2.21	2.15	2.46	3.27	3.50	1.23	2.97	1.70	2.33	2.37	4.55	2.55	0.99	0.79
AX-94796463	3A	NA	1.57	0.86	1.45	2.22	2.71	2.60	3.77	0.75	1.76	1.80	2.31	1.67	5.15	2.91	2.33	1.23
AX-95095284	3A	NA	1.52	1.25	2.06	2.49	2.87	2.75	3.46	1.20	2.81	2.23	2.08	1.89	5.81	2.49	2.71	0.83
AX-95116004	3A	NA	0.77	0.52	1.21	1.18	1.71	1.38	1.56	0.57	1.75	0.71	1.82	0.75	3.47	1.10	3.00	0.08
AX-94580039	3A	NA	1.03	2.34	2.38	2.43	2.21	1.79	2.58	1.51	2.08	1.14	3.37	3.53	3.02	1.45	2.40	2.48
AX-94623333	3A	621,834,060	2.96	3.83	2.89	2.81	2.59	4.07	4.24	3.87	4.97	3.03	2.25	3.09	3.08	5.85	2.28	3.64
AX-94422954	3A	623,038,503	2.65	2.11	1.70	1.36	1.15	2.68	2.38	2.47	3.15	1.61	1.11	1.46	1.32	3.50	1.39	2.35
AX-94772403	3B	NA	1.39	2.16	2.30	2.65	3.18	3.10	2.07	1.73	1.94	2.38	2.82	3.15	0.70	1.99	0.95	3.11
AX-95197805	3B	NA	1.39	2.07	3.00	3.24	3.13	3.60	2.21	2.23	2.54	3.01	2.80	3.00	0.73	2.23	1.04	3.13
AX-94570899	3B	46,282,133	1.79	2.21	4.07	3.11	2.46	3.01	1.86	1.87	3.64	3.65	3.00	2.04	3.04	2.54	5.16	2.42
AX-95245849	3B	51,814,203	1.90	0.95	2.35	3.84	2.98	2.82	2.52	0.59	1.30	2.42	3.72	1.92	2.40	1.68	1.69	1.51
AX-94644783	3B	NA	1.90	2.45	4.13	2.97	2.46	3.07	1.87	2.14	3.73	3.50	2.89	2.16	3.30	2.56	4.90	2.48
AX-94681037	3B	556,273,564	1.21	2.24	2.44	1.62	2.62	3.22	2.11	3.47	2.17	2.23	3.17	1.98	1.43	1.51	0.84	1.84

AX-94583481	3B	NA	1.87	0.99	1.73	1.73	1.50	1.37	1.63	1.43	1.65	1.04	2.52	1.26	0.29	1.15	3.32	0.39
AX-95072927	3B	NA	1.95	1.01	1.88	1.50	1.56	1.45	1.48	1.30	1.73	0.95	2.54	1.38	0.38	1.35	3.38	0.50
AX-95216285	3B	NA	0.36	1.35	1.37	1.00	1.29	1.28	1.21	1.80	1.34	0.61	1.72	1.27	0.93	1.32	3.04	0.40
AX-94779453	3B	NA	2.07	1.04	1.85	1.91	1.35	1.20	1.64	1.56	1.77	1.11	2.42	1.11	0.28	0.98	3.30	0.33
AX-94636050	4B	642,628,555	0.73	1.99	2.16	1.75	3.50	3.40	1.53	3.07	1.64	1.16	3.49	1.99	2.70	2.01	1.77	1.51
AX-94719086	4D	40,156,250	1.30	2.77	3.05	2.32	3.70	3.54	1.94	2.56	2.75	2.46	1.85	3.13	0.89	3.58	2.73	2.10
AX-94728173	4D	NA	1.69	1.45	3.11	3.39	2.05	2.82	1.90	2.31	2.04	3.26	1.58	1.64	0.57	0.90	2.92	1.38
AX-94773648	4D	NA	1.63	1.40	2.99	3.30	1.99	2.69	1.79	2.27	1.99	3.09	1.47	1.54	0.49	0.82	2.86	1.35
AX-95257633	4D	NA	1.63	1.49	2.94	3.20	2.05	2.68	1.77	2.20	1.89	2.97	1.45	1.62	0.53	0.88	2.83	1.40
AX-95018258	5A	700,665,613	3.08	2.82	3.37	3.35	4.98	5.29	2.61	3.51	4.78	4.59	2.47	3.80	1.42	3.27	1.88	4.64
AX-94525543	5A	702,750,297	3.04	3.52	3.42	2.76	5.43	4.89	2.56	3.00	3.92	3.63	3.17	3.24	2.81	3.86	2.66	3.53
AX-95223659	5A	706,240,239	0.59	0.38	0.92	1.71	3.16	1.30	1.26	0.37	1.47	0.79	1.78	1.57	2.69	2.34	2.33	1.88
AX-95077733	5A	706,274,335	0.05	0.34	0.12	0.41	0.89	0.28	0.94	0.56	0.22	0.14	0.63	0.53	1.40	1.42	0.71	0.32
AX-95231592	5A	708,165,048	1.06	1.25	1.30	1.34	3.86	1.50	1.39	0.22	1.71	0.31	2.47	2.97	2.03	1.70	1.55	2.14
AX-94492644	5A	NA	0.71	0.68	1.10	1.45	3.11	1.08	1.15	0.22	1.17	0.40	1.62	1.93	1.98	1.26	1.92	1.79
AX-94771047	5A	NA	2.60	4.44	3.32	2.05	2.84	4.36	2.76	3.18	3.43	3.26	2.34	2.19	2.04	2.60	1.51	1.68
AX-95117188	5A	NA	0.34	0.46	0.92	2.51	2.01	1.56	1.56	0.10	1.52	3.16	1.14	1.33	0.46	1.58	0.46	0.88
AX-94892575	5A	NA	0.25	0.24	1.14	1.12	1.33	1.51	1.48	0.56	1.36	2.04	1.47	1.67	3.41	1.68	0.44	1.32
AX-94575407	5A	NA	2.89	2.20	1.56	1.32	1.19	1.29	0.58	3.23	2.27	1.17	1.26	0.67	0.98	1.43	2.38	0.85
AX-95201760	5A	428,671,127	2.62	3.30	4.56	2.09	2.16	3.64	3.22	3.36	5.61	4.04	2.72	2.23	3.33	4.78	1.06	2.58
AX-94643574	5A	602,915,718	1.20	1.28	1.14	1.92	3.93	3.66	3.37	0.98	1.63	1.72	3.26	1.58	2.74	3.22	3.73	3.93

AX-95211290	5A	606,985,567	3.40	2.95	1.88	1.08	1.70	1.90	1.76	0.85	1.84	1.27	1.88	1.80	2.11	2.77	0.40	2.40
AX-94520697	6A	608,500,190	1.88	1.37	2.26	1.60	1.07	2.02	1.14	2.28	3.72	2.72	1.64	0.55	0.47	1.35	2.26	0.88
AX-94384372	6A	609,032,563	3.16	1.79	4.36	1.76	1.64	2.41	1.76	1.95	4.51	3.47	2.27	1.27	1.91	2.82	1.01	2.06
AX-95124661	6A	609,377,249	1.02	1.41	1.83	2.07	1.62	2.06	2.28	2.00	3.03	2.16	2.14	1.30	1.35	2.59	2.06	1.95
AX-94424805	6B	622,730,026	1.78	1.01	2.87	3.18	3.86	1.98	1.79	1.79	2.79	2.00	3.30	3.01	2.36	2.20	2.87	3.89
AX-95629643	6B	631,740,534	2.15	0.96	2.35	3.27	2.97	2.36	1.97	0.98	2.07	2.36	3.26	2.16	1.19	1.33	2.72	3.07
AX-94411826	6B	NA	1.75	0.67	1.08	1.18	2.22	1.91	1.30	1.29	1.05	1.16	1.49	1.52	1.43	1.78	0.79	4.36
AX-95017886	6B	NA	1.49	0.54	0.96	0.83	2.24	1.79	1.20	1.18	0.95	0.82	1.27	1.47	1.41	1.59	0.54	4.02
AX-95157887	6B	NA	1.73	0.67	1.05	1.16	2.21	1.89	1.28	1.29	1.03	1.13	1.47	1.51	1.42	1.76	0.79	4.34
AX-95195965	6B	NA	2.05	1.02	1.26	1.40	1.89	2.35	1.46	2.15	1.50	1.11	1.53	1.82	1.23	1.82	0.54	4.75
AX-95121488	6B	NA	1.98	0.97	0.43	0.29	1.02	0.81	0.56	1.53	0.32	0.48	0.49	0.47	0.37	1.01	0.14	3.12
AX-94843008	7B	626,239,342	1.99	2.78	1.91	1.53	2.34	1.77	2.10	2.57	1.38	1.24	1.95	2.76	3.06	1.80	1.08	1.88
AX-95156242	7B	637,589,373	1.87	1.90	2.99	2.84	4.08	5.06	1.97	2.00	2.35	1.94	3.31	5.63	3.45	5.16	1.16	3.41
AX-95146286	7B	NA	3.15	2.01	2.22	2.13	2.71	3.08	1.68	2.73	1.97	1.48	1.59	2.13	2.68	3.12	1.93	1.87
AX-95011176	7B	NA	1.38	3.31	0.82	1.07	1.01	1.89	1.39	4.19	0.72	0.43	1.36	1.40	1.42	0.68	0.57	0.71
AX-95074996	7B	NA	1.19	2.56	0.69	1.50	1.12	2.14	1.40	3.57	0.53	0.62	1.37	1.23	1.42	0.63	0.78	1.17
AX-95171526	7B	NA	1.99	2.78	1.91	1.53	2.35	1.76	2.10	2.57	1.38	1.24	1.95	2.75	3.06	1.80	1.08	1.88
AX-94616771	7B	654,951,795	1.09	1.50	1.05	1.29	1.45	2.27	1.62	1.90	2.71	1.38	2.65	2.49	1.85	1.52	1.06	2.05
AX-95154008	7B	655,019,195	2.23	2.87	1.91	1.84	2.08	2.88	2.42	2.75	3.11	2.48	3.55	3.27	3.09	3.10	2.38	2.36
AX-94859831	7B	709,514,961	0.59	1.22	0.05	0.04	0.18	0.09	0.83	0.89	0.19	0.05	0.45	0.35	0.97	0.26	0.56	0.43
AX-95217260	7B	713,360,201	1.68	0.87	3.20	3.34	2.60	2.77	4.34	1.43	3.08	3.73	2.97	2.90	5.28	1.75	2.15	4.14

AX-94435697	7D	55,072,941	2.01	3.49	3.09	3.07	3.59	5.53	2.47	4.03	3.60	3.68	2.14	4.32	2.17	2.28	0.98	3.49
Terp_Syn	Unassigned	NA	1.56	1.76	2.13	3.12	5.24	2.21	2.36	2.32	2.28	1.13	2.90	4.52	3.46	3.63	1.65	3.63

Table 4 interesting and significant markers in spring wheat supported with chromosome location, physical position (bp), – log10 (p-value) for each location over years, different time periods, PC1 and PC2.

Marker	Chr.	Phys.Pos.	Vb	Staur	all env.	12-13-14	15-16	17-18-19	PC1	PC2
AX-94551566	1A	NA	2.50	1.75	1.08	1.61	2.50	1.72	2.23	0.19
AX-94955419	1A	2,978,831	3.22	2.70	2.34	2.51	3.45	2.75	3.18	0.37
AX-94838936	1A	9,357,669	2.16	1.47	0.41	3.43	2.00	1.83	1.93	0.09
AX-94565449	2A	3,259,160	3.46	3.08	3.04	3.41	3.61	2.66	3.27	0.14
AX-95188522	2A	NA	3.66	3.57	2.84	3.42	3.20	3.19	3.48	1.48
AX-95238660	2A	515,452,422	4.08	3.42	2.38	3.22	3.88	3.38	3.97	0.57
AX-94397387	2A	515,945,795	3.07	2.26	1.85	2.12	2.67	2.28	2.79	0.68
AX-94509071	2A	516,396,000	2.37	1.98	1.68	2.40	2.07	1.90	2.22	0.78
AX-95630172	2A	517,399,128	2.03	1.95	1.40	1.44	2.21	1.88	1.97	0.33
AX-94742698	2A	520,308,995	2.47	1.94	1.56	2.36	2.25	1.90	2.27	0.71
AX-94789549	2A	520,990,823	2.03	1.95	1.40	1.44	2.21	1.88	1.97	0.33
AX-94493722	2A	522,515,722	2.74	2.67	1.83	2.20	2.83	2.64	2.73	0.17
AX-94396940	2A	524,331,716	2.47	2.06	1.65	2.51	2.15	1.96	2.31	0.76
AX-95018590	2A	NA	2.67	2.50	1.75	1.93	2.91	2.52	2.63	0.24
AX-94801027	2A	NA	1.78	1.70	1.40	2.88	1.63	1.50	1.73	0.70
AX-94514944	2A	605,000,772	1.79	1.99	2.01	1.72	2.19	1.39	2.05	1.25
AX-94480083	2A	605,634,830	1.87	2.47	1.59	2.98	1.81	2.00	2.27	0.79
AX-95160643	2A	NA	3.36	3.62	2.10	3.56	3.23	3.42	3.62	0.15
AX-94963427	2A	NA	2.52	2.11	2.09	3.03	2.57	1.93	2.49	0.13
AX-95102130	2A	739,308,962	3.27	2.22	1.47	4.77	2.03	2.51	3.05	3.96
AX-94481517	2A	NA	2.05	2.40	2.90	1.02	3.09	2.07	2.12	1.28
AX-94802107	2A	757,948,239	4.07	3.25	3.01	3.36	3.45	3.33	3.79	0.14
AX-94517549	2B	9,016,421	1.85	2.34	2.13	1.50	2.63	2.39	2.14	1.15
AX-95112632	2B	9,120,910	2.83	3.55	1.23	3.16	3.46	2.73	3.24	0.13
AX-95194336	2B	9,890,064	3.52	2.99	2.75	3.73	3.53	3.11	3.31	0.07
AX-95201364	2B	NA	2.57	2.32	2.82	3.06	1.98	2.37	2.53	0.07
AX-95173587	2B	12,076,575	1.46	2.23	1.82	1.62	2.49	1.69	1.84	0.67
AX-94489937	2B	17,394,536	2.53	2.12	1.52	1.99	2.36	2.21	2.39	0.99
AX-95017965	2B	19,070,596	4.80	3.92	2.10	3.62	4.23	3.94	4.33	0.47
AX-94520248	2B	NA	3.72	2.99	2.07	2.88	3.42	2.96	3.43	1.08
AX-95087040	2B	NA	2.52	2.52	2.39	2.28	2.55	2.55	2.62	0.82
AX-95147784	2B	26,564,120	2.23	2.84	3.30	3.19	2.33	2.52	2.44	0.16
AX-95652890	2B	26,581,493	1.98	2.23	2.96	2.86	1.91	2.05	2.05	0.23
AX-94508950	2B	26,581,682	2.70	2.98	4.09	3.27	2.84	2.74	2.84	0.28
AX-94483531	2B	26,986,944	3.25	3.45	3.94	2.87	3.02	3.14	3.33	0.24
AX-94547080	2B	30,321,933	2.32	1.70	1.21	1.49	1.91	1.99	1.95	0.77
AX-94480585	3A	7,653,799	1.32	0.76	0.34	1.93	1.02	0.76	1.12	1.35
AX-94555538	3A	8,325,662	3.68	2.98	1.10	4.00	3.24	3.29	3.45	0.19
AX-95232198	3A	9,603,484	1.89	1.32	0.19	2.05	1.82	1.59	1.82	0.37

AX-94461092	3A	12,494,352	2.49	1.91	0.65	1.95	2.38	1.99	2.41	0.12
AX-94706753	3A	16,467,149	1.31	0.94	1.47	1.60	1.34	1.20	1.23	0.52
AX-94567981	3A	NA	0.98	1.39	1.11	0.76	1.06	1.72	1.18	0.08
AX-94675268	3A	NA	1.30	0.93	0.09	1.41	1.37	1.14	1.27	0.18
AX-94932563	3A	NA	1.40	1.05	1.52	1.59	1.28	1.21	1.36	0.74
AX-94446053	3A	67,908,995	2.91	3.41	2.80	1.75	2.63	3.81	2.94	3.97
AX-94468868	3A	69,665,200	3.22	3.55	1.49	2.48	2.39	3.41	3.07	2.56
AX-94441567	3A	NA	3.24	3.55	2.16	2.40	2.72	3.87	3.16	3.39
AX-94636432	3A	NA	2.94	3.52	2.80	1.68	2.59	3.88	2.97	4.46
AX-94652031	3A	NA	3.16	3.47	1.45	2.43	2.34	3.35	3.00	2.54
AX-94796463	3A	NA	2.74	3.29	2.63	1.50	2.40	3.75	2.79	4.38
AX-95095284	3A	NA	3.10	3.42	1.99	2.38	2.56	3.71	3.02	3.21
AX-95116004	3A	NA	1.53	1.83	0.84	1.32	1.52	2.01	1.61	2.02
AX-94580039	3A	NA	2.24	2.47	3.51	2.54	2.77	2.87	2.46	0.58
AX-94623333	3A	621,834,060	4.01	4.46	2.65	4.15	2.78	4.67	4.15	0.13
AX-94422954	3A	623,038,503	2.40	2.43	1.50	2.61	1.36	2.62	2.35	0.43
AX-94772403	3B	NA	3.37	2.76	0.98	2.76	3.46	2.50	3.08	0.25
AX-95197805	3B	NA	3.69	2.98	1.12	3.00	3.70	2.67	3.43	0.23
AX-94570899	3B	46,282,133	2.64	3.10	0.79	3.04	2.69	3.36	3.02	0.04
AX-95245849	3B	51,814,203	3.27	3.07	2.07	1.39	3.86	2.82	3.28	1.14
AX-94644783	3B	NA	2.69	3.15	0.80	3.22	2.63	3.42	3.08	0.01
AX-94681037	3B	556,273,564	3.12	2.69	1.98	2.85	3.37	2.26	3.00	0.54
AX-94583481	3B	NA	2.02	1.57	1.91	1.81	2.44	1.50	1.94	0.56
AX-95072927	3B	NA	2.00	1.65	1.63	1.85	2.34	1.60	1.97	0.51
AX-95216285	3B	NA	1.53	1.53	1.22	1.56	1.69	1.66	1.72	0.11
AX-94779453	3B	NA	1.87	1.42	1.85	1.93	2.28	1.40	1.79	0.50
AX-94636050	4B	642,628,555	2.85	2.69	1.21	2.25	3.04	2.80	3.10	0.24
AX-94719086	4D	40,156,250	3.23	2.62	1.48	2.96	2.27	3.24	3.12	0.30
AX-94728173	4D	NA	2.71	1.72	0.83	2.87	2.22	2.15	2.50	0.56
AX-94773648	4D	NA	2.59	1.59	0.74	2.79	2.08	2.03	2.37	0.65
AX-95257633	4D	NA	2.57	1.62	0.69	2.73	2.06	2.07	2.37	0.59
AX-95018258	5A	700,665,613	4.72	3.71	3.68	4.45	4.24	3.82	4.53	1.27
AX-94525543	5A	702,750,297	4.78	4.21	2.98	4.08	4.09	4.31	4.74	0.41
AX-95223659	5A	706,240,239	1.28	1.86	1.15	0.72	1.47	2.38	1.55	1.76
AX-95077733	5A	706,274,335	0.58	0.75	0.96	0.05	0.50	1.07	0.53	3.22
AX-95231592	5A	708,165,048	2.10	1.81	1.58	1.13	2.33	2.24	2.03	0.25
AX-94492644	5A	NA	1.40	1.41	1.12	0.71	1.70	1.92	1.43	1.18
AX-94771047	5A	NA	3.98	3.10	1.74	4.08	2.86	3.14	3.70	0.54
AX-95117188	5A	NA	1.81	1.65	2.42	0.72	1.89	1.35	1.60	0.10
AX-94892575	5A	NA	1.27	2.29	0.79	0.81	1.66	1.94	1.72	2.61
AX-94575407	5A	NA	1.39	1.55	0.42	2.73	1.38	1.52	1.62	0.90
AX-95201760	6A	428,671,127	3.33	4.37	1.61	5.04	2.82	3.41	3.66	0.22
AX-94643574	6A	602,915,718	3.50	2.97	3.90	1.32	3.41	4.07	3.51	1.04
AX-95211290	6A	606,985,567	2.22	2.33	1.60	2.57	1.66	2.10	2.06	0.34

AX-94520697	6A	608,500,190	1.71	1.40	0.35	3.05	1.60	1.34	1.77	1.27
AX-94384372	6A	609,032,563	2.25	2.93	1.45	4.15	2.18	2.15	2.52	0.05
AX-95124661	6A	609,377,249	1.95	2.19	0.69	2.36	1.98	2.30	2.13	0.24
AX-94424805	6B	622,730,026	3.30	2.96	1.87	3.05	3.40	3.11	3.31	0.01
AX-95629643	6B	631,740,534	3.18	2.28	2.32	2.29	3.36	2.51	2.92	0.02
AX-94411826	6B	NA	1.67	1.68	2.05	1.26	1.91	2.07	1.78	0.39
AX-95017886	6B	NA	1.49	1.45	1.99	1.21	1.66	1.89	1.57	0.32
AX-95157887	6B	NA	1.64	1.66	2.03	1.23	1.89	2.05	1.76	0.38
AX-95195965	6B	NA	1.91	1.73	1.36	1.70	1.91	2.16	1.95	0.01
AX-95121488	6B	NA	0.89	0.62	1.77	1.11	0.80	0.85	0.87	0.75
AX-94843008	7B	626,239,342	2.47	2.23	1.75	2.47	2.22	2.36	2.35	0.12
AX-95156242	7B	637,589,373	3.86	4.75	4.02	2.98	3.83	4.20	4.16	0.10
AX-95146286	7B	NA	2.78	2.86	2.32	2.61	2.15	3.00	2.82	0.16
AX-95011176	7B	NA	1.98	1.07	1.35	2.12	1.28	1.43	1.59	1.66
AX-95074996	7B	NA	2.02	1.11	1.97	1.80	1.59	1.59	1.66	1.10
AX-95171526	7B	NA	2.47	2.23	1.75	2.48	2.23	2.36	2.34	0.12
AX-94616771	7B	654,951,795	1.73	2.74	3.39	2.17	2.06	2.21	2.19	0.19
AX-95154008	7B	655,019,195	2.57	3.95	3.52	3.15	2.95	3.50	3.30	0.03
AX-94859831	7B	709,514,961	0.24	0.27	0.43	0.18	0.33	0.57	0.26	3.56
AX-95217260	7B	713,360,201	3.40	3.52	3.26	2.77	3.16	4.03	3.52	2.88
AX-94435697	7D	55,072,941	4.15	3.67	2.01	4.37	3.43	3.58	3.91	1.24
Terp_Syn	unassigned	NA	3.34	3.20	2.38	2.64	3.59	3.48	3.29	0.20

Table 5 Interesting and significant markers in winter wheat supported with cM position (Allen et al., 2017), physical position (bp), -log10 (p-value) for all environments separately, over all environments, PC1 and PC2

Marker	Chr.	cM	Physical position.	Vb14	Vb15	1-Vb16	2-Vb16	Vb17	Vb18	Vb19	all env.	PC-1	PC-2
AX-94526630	1A	74	42,550,052	2.68	2.09	2.42	3.62	1.84	3.12	2.09	3.06	3.28	0.63
AX-94395420	1A	89	NA	0.41	1.11	3.51	1.53	2.47	0.18	1.84	1.88	1.90	0.33
AX-94972660	1A	89	566,477,994	1.07	1.64	3.10	2.93	2.19	0.42	1.48	2.43	2.55	0.60
AX-95150580	1A	89	566,478,081	1.07	1.64	3.10	2.93	2.19	0.42	1.48	2.43	2.55	0.60
AX-94469723	1B	26	512,870,104	0.91	0.87	0.82	0.42	1.52	3.03	0.18	1.02	0.80	0.10
AX-94692952	1B	26	512,879,110	0.91	0.87	0.82	0.42	1.52	3.03	0.18	1.02	0.80	0.10
AX-94780679	1B	107	660,100,902	2.01	0.98	1.82	1.56	1.61	3.21	1.47	2.07	1.82	0.03
AX-94513670	1D	0	NA	1.64	2.06	3.48	2.60	2.01	0.02	1.38	2.11	2.27	0.65
AX-94519856	1D	0	NA	1.29	1.73	3.33	2.71	2.09	0.01	1.38	2.28	2.46	0.61
AX-94734276	2A	2	30,550,326	1.36	2.21	3.15	3.04	1.83	0.28	1.60	2.77	2.78	0.72
AX-95209305	2A	83	92,314,333	1.06	1.29	1.57	3.17	1.20	0.85	0.69	2.16	2.37	1.85
AX-94667578	2D	107	69,504,737	1.30	2.25	3.04	0.99	1.55	0.42	1.38	1.54	1.42	0.22
AX-94884342	2D	107	NA	1.74	2.57	3.88	1.36	2.02	0.59	2.06	2.08	1.96	0.38
AX-95652891	2D	107	181,596,843	1.29	2.24	3.02	1.00	1.55	0.38	1.37	1.54	1.42	0.21
AX-94543041	2D	136	60,790,460	1.17	4.17	2.83	0.36	0.32	1.22	0.91	1.09	0.92	0.37
AX-94387409	2D	161	70,523,081	1.30	2.25	3.04	0.99	1.55	0.42	1.38	1.54	1.42	0.22
AX-94448812	2D	161	NA	1.29	2.24	3.02	1.00	1.55	0.38	1.37	1.54	1.42	0.21
AX-94452929	2D	161	68,734,043	1.25	2.21	3.03	0.96	1.56	0.46	1.36	1.50	1.38	0.23
AX-94482907	2D	161	68,733,890	1.29	2.24	3.02	1.00	1.55	0.38	1.37	1.54	1.42	0.21
AX-94497996	2D	161	70,951,376	1.63	2.83	3.44	1.15	1.94	0.49	1.66	1.92	1.77	0.29
AX-94511393	2D	161	66,764,490	1.30	2.25	3.04	0.99	1.55	0.42	1.38	1.54	1.42	0.22
AX-94513876	2D	161	68,733,980	1.30	2.25	3.04	0.99	1.55	0.42	1.38	1.54	1.42	0.22
AX-94515662	2D	161	NA	1.36	2.31	3.11	1.07	1.62	0.56	1.52	1.63	1.51	0.26
AX-94520851	2D	161	64,981,268	1.28	2.27	3.31	1.64	1.95	0.49	2.03	2.13	2.10	0.18
AX-94592813	2D	161	67,557,233	1.30	2.25	3.04	0.99	1.55	0.42	1.38	1.54	1.42	0.22
AX-94635765	2D	161	NA	1.23	2.26	3.04	0.95	1.52	0.36	1.33	1.50	1.38	0.22
AX-94644814	2D	161	65,537,025	1.30	2.25	3.28	1.61	1.82	0.38	1.96	2.06	2.04	0.15
AX-94655116	2D	161	67,225,124	1.30	2.25	3.04	0.99	1.55	0.42	1.38	1.54	1.42	0.22
AX-94686759	2D	161	NA	1.40	2.35	3.02	0.90	1.61	0.54	1.48	1.55	1.40	0.36

AX-94704355	2D	161	64,190,373	1.30	2.25	3.04	0.99	1.55	0.42	1.38	1.54	1.42	0.22
AX-94731207	2D	161	NA	1.29	2.24	3.02	1.00	1.55	0.38	1.37	1.54	1.42	0.21
AX-94794336	2D	161	67,552,856	1.30	2.25	3.04	0.99	1.55	0.42	1.38	1.54	1.42	0.22
AX-94847111	2D	161	65,266,660	1.30	2.25	3.06	1.00	1.56	0.44	1.37	1.55	1.43	0.21
AX-94855228	2D	161	294,476,254	1.35	2.28	3.34	1.83	1.84	0.39	1.96	2.15	2.17	0.05
AX-94877462	2D	161	65,638,251	1.29	2.24	3.02	1.00	1.55	0.38	1.37	1.54	1.42	0.21
AX-94918359	2D	161	NA	1.30	2.25	3.09	1.04	1.66	0.35	1.41	1.55	1.44	0.21
AX-94923294	2D	161	70,634,052	1.30	2.25	3.04	0.99	1.55	0.42	1.38	1.54	1.42	0.22
AX-94966893	2D	161	NA	1.36	2.31	3.11	1.07	1.62	0.56	1.52	1.63	1.51	0.26
AX-94988703	2D	161	67,441,352	1.30	2.25	3.04	0.99	1.55	0.42	1.38	1.54	1.42	0.22
AX-95093372	2D	161	70,633,953	1.30	2.25	3.04	0.99	1.55	0.42	1.38	1.54	1.42	0.22
AX-95097352	2D	161	65,638,467	1.30	2.25	3.04	0.99	1.55	0.42	1.38	1.54	1.42	0.22
AX-95139529	2D	161	67,968,962	1.27	2.21	3.04	1.01	1.53	0.40	1.36	1.52	1.41	0.19
AX-95153839	2D	161	NA	1.30	2.25	3.04	0.99	1.55	0.42	1.38	1.54	1.42	0.22
AX-95176461	2D	161	NA	1.18	2.04	3.08	0.93	1.67	0.44	1.28	1.46	1.30	0.23
AX-95254619	2D	161	69,251,649	1.30	2.25	3.04	0.99	1.55	0.42	1.38	1.54	1.42	0.22
AX-95629820	2D	161	65,265,143	1.30	2.25	3.00	0.93	1.51	0.40	1.36	1.48	1.36	0.24
AX-95629830	2D	161	67,233,723	1.25	2.24	3.01	1.05	1.56	0.37	1.37	1.56	1.46	0.17
AX-95631062	2D	161	71,208,586	1.30	2.25	3.04	0.99	1.55	0.42	1.38	1.54	1.42	0.22
AX-94652021	3B	176	775,562,023	3.34	3.05	2.09	2.17	3.12	1.94	1.96	3.17	3.03	0.01
AX-94563379	3B	245	817,414,366	2.70	3.03	1.81	2.25	2.15	0.44	1.46	2.32	2.47	0.32
AX-94981476	4A	187	688,099,427	2.20	3.10	2.36	2.57	2.08	0.38	2.00	2.68	2.78	0.18
AX-94563149	5A	29	5,298,324	2.13	0.64	0.96	0.35	1.48	4.23	0.65	1.37	1.01	0.35
AX-94400860	5A	79	473,312,398	1.43	1.19	1.99	1.77	1.65	3.04	2.91	2.74	2.52	0.83
AX-94691627	5A	79	NA	2.74	2.85	3.00	2.34	2.32	2.95	2.74	3.45	3.23	0.23
AX-94966165	5A	79	475,268,568	2.63	2.72	3.18	2.52	3.09	3.26	3.12	3.92	3.61	0.36
AX-94450199	5A	83	488,410,411	1.37	0.94	0.77	0.45	3.66	0.59	1.04	1.34	1.17	0.76
AX-94552728	5B	102	458,053,044	1.85	3.31	1.73	1.91	3.08	1.08	1.81	2.31	2.26	0.14
AX-94816812	5B	102	458,147,251	1.85	3.31	1.73	1.91	3.08	1.08	1.81	2.31	2.26	0.14
AX-95077961	5B	102	458,052,944	1.85	3.31	1.73	1.91	3.08	1.08	1.81	2.31	2.26	0.14
AX-95227700	5B	102	458,052,843	1.85	3.31	1.73	1.91	3.08	1.08	1.81	2.31	2.26	0.14
AX-95679618	5B	102	458,150,676	1.85	3.31	1.73	1.91	3.08	1.08	1.81	2.31	2.26	0.14

AX-94471685	6A	101	446,301,699	1.21	3.11	1.65	1.41	1.35	0.49	1.00	1.55	1.51	0.12
AX-94688926	6A	102	454,939,671	1.92	5.10	4.02	2.95	2.16	2.21	1.73	3.30	3.12	0.41
AX-95254635	6A	102	454,939,755	1.89	5.04	4.02	2.95	2.15	2.18	1.72	3.29	3.12	0.42
AX-94920804	6B	130	705,315,409	2.73	2.33	1.72	2.68	3.21	1.62	1.22	2.71	2.76	0.64
AX-94615671	6D	84	326,538,778	0.63	0.97	1.38	2.15	1.23	0.61	3.00	1.73	2.02	0.55
AX-94699453	6D	84	327,981,887	0.57	1.38	1.98	2.87	1.20	1.65	3.60	2.59	2.79	0.44
AX-94890346	7A	26	NA	2.80	2.27	1.72	3.65	2.93	0.67	2.64	3.18	3.46	0.33
AX-94513729	7A	30	78,430,148	3.46	2.74	2.17	2.52	3.45	0.84	3.00	3.01	3.26	0.37
AX-94586475	7A	30	NA	2.95	3.14	2.04	2.14	3.36	0.77	2.79	3.12	3.17	0.41
AX-94395845	7A	33	28,444,123	2.04	1.50	1.57	3.84	1.64	1.18	2.59	2.72	3.14	0.45
AX-94752160	7A	38	33,870,742	2.65	3.29	3.11	3.08	2.07	1.40	1.56	2.95	3.04	0.74
AX-94879825	7B	97	643,295,990	1.78	1.61	2.39	2.08	1.68	1.48	3.10	2.47	2.57	0.62
AX-94412216	7D	18	44,524,105	2.42	1.93	1.40	3.44	2.55	0.45	2.29	2.83	3.13	0.41

Table 6 Allele stacking Table for studied QTL in all spring wheat cultivars/lines, powdery mildew lsmeans over all spring environments and sum number of resistant alleles for all studied QTL in each line. (T/A are computed letters and do not refer to nucleotide allele, N marker is not valid in this line).

Name	PM-Lsmeans	AX-95238660	AX-95017965	AX-94623333	AX-94525543	AX-94643574	AX-95156242	AX-94435697	Nr of QTL
Resistant allele		**A**	**A**	**T**	**T**	**A**	**A**	**A**	
Croc_1/Ae.squarrosa (205)//Kauz	8.4	A	T	T	T	A	A	A	6
Altar84/Ae.squarrosa(219)// 2*Seri	8.6	A	T	T	T	A	A	A	6
Altar84/Ae.sq(219)//2*Seri/3/ Avle	13.9	A	A	T	T	A	A	A	7
512-21	46.9	T	T	T	A	A	T	A	3
512-50	34.7	A	T	T	T	A	A	A	6
512-54	34.6	T	N	T	T	A	A	A	5
512-70	22.5	A	T	T	T	A	T	A	5
512-87	28.9	T	T	T	T	A	A	A	5
80456/YANGMAI 5//SHA5/WEAVER/3/PRINIA	33.7	T	T	T	A	T	A	T	2
AC Somerset	23.7	T	T	A	T	A	A	A	4
Aino	31.9	T	T	T	T	A	A	T	4
Anniina	21.3	A	T	T	T	A	A	A	6
Avans	10.3	A	T	T	T	A	A	A	6
Avle	14.3	A	T	T	T	A	A	A	6
Avocet YrA	42.8	A	T	A	T	T	T	T	2
BAJASS-5	17.0	A	T	T	T	A	A	A	6
BJY/COC//CLMS/GEN	49.2	A	T	T	T	T	A	A	5
Bau/Milan -2	15.4	A	T	A	T	A	A	T	4
Bastian	17.2	A	T	N	T	A	A	A	5
Berserk	20.2	A	A	T	T	A	A	A	7
Bjarne/LW91W86	14.4	T	T	T	T	A	A	A	5
Bjarne	20.8	A	T	T	T	A	A	A	6
Bombona	13.6	A	T	T	T	A	A	A	6
Brakar	29.8	T	T	T	T	A	A	A	5
C80.1/3*QT4522//2*ATTILA	23.9	A	T	T	T	T	A	A	5
C80.1/3*QT4522//2*PASTOR	16.7	A	T	T	T	A	A	T	5
CD87	16.4	A	T	T	T	T	T	A	4
Arabella	4.8	A	T	T	T	A	A	A	6
CJ9306	46.3	A	N	A	A	A	A	A	4
CJ9403	40.4	A	T	A	A	A	A	T	3
Cadenza	9.8	A	T	T	T	A	A	A	6
Catbird -2	7.9	A	N	A	A	T	A	T	2
Chara	29.5	A	T	A	T	T	T	A	3
Paros/T9040	11.5	A	A	T	T	A	A	T	6
Paros/NK93602	14.9	A	T	T	T	A	A	A	6
T9040/Paros	21.6	A	T	T	T	A	A	A	6
Mandaryna	9.2	A	T	T	T	A	A	N	5
DH20070	15.5	A	T	T	T	A	A	A	6

DH20097	32.6	A	N	T	T	A	A	A	6
DH 49-18 Bastian/Adder	25.4	A	T	T	T	A	T	A	5
Dragon	12.6	A	T	T	T	A	A	A	6
Dulus	33.5	A	A	T	T	A	A	A	7
EMB16/CBRD//CBRD	26.8	A	T	A	A	T	T	T	1
Filin	9.3	A	T	T	T	A	T	A	5
Fram II	17.3	T	T	T	T	T	A	A	4
Frontana (95)	39.8	A	T	T	T	T	A	A	5
GAMENYA	16.7	A	T	T	T	T	T	A	4
GN03503	7.1	A	T	T	T	T	A	A	5
Krabat	16.8	A	T	T	T	A	A	A	6
GN03529	18.0	A	T	T	T	T	A	A	5
GN03531	10.9	A	T	T	T	A	A	A	6
GN03597	2.9	A	T	T	T	T	A	A	5
GN04526	26.2	A	T	T	T	T	A	A	5
GN04528	2.3	A	A	T	T	A	A	A	7
GN04537	25.0	A	T	T	T	A	A	A	6
GN04603	8.7	A	T	T	T	A	A	N	5
GN05507	10.2	A	T	T	T	A	A	N	5
GN05551	5.8	A	T	T	T	A	A	A	6
Laban	10.2	A	T	T	T	A	A	A	6
GN05580	8.3	A	T	T	T	A	A	A	6
GN05589	7.3	A	T	T	T	A	A	A	6
GN06557	10.6	A	A	T	T	A	A	A	7
GN06573	13.2	A	A	T	T	A	A	A	7
GN06578	2.4	A	T	T	T	A	A	A	6
Mirakel	5.2	A	T	T	T	A	A	A	6
Rabagast	4.7	A	T	T	T	A	A	A	6
GN07525	5.3	A	T	T	T	A	A	A	6
GN07548	4.5	A	A	T	T	A	A	A	7
GN07560	6.1	A	T	T	T	A	A	A	6
Seniorita	2.8	A	A	T	T	A	A	A	7
GN07580	2.3	A	A	T	T	A	A	A	7
GN07581	7.7	A	N	T	T	A	A	A	6
GN08504	3.9	A	T	T	T	A	A	A	6
GN08530	3.6	A	A	T	T	A	A	A	7
GN08531	1.8	A	T	T	T	A	A	A	6
GN08533	1.8	A	T	T	T	A	A	N	5
GN08534	13.2	A	T	T	T	A	A	N	5
GN08541	4.7	A	T	T	T	A	A	A	6
GN08554	2.3	A	T	T	T	A	A	A	6
GN08557	2.0	A	A	T	A	A	A	A	6
GN08564	2.4	A	T	T	T	A	A	A	6
GN08568	3.2	A	T	T	T	A	A	A	6

GN08581	2.6	A	A	T	T	A	A	A	7
GN08588	3.6	A	T	T	T	A	A	A	6
GN08595	12.0	A	T	T	T	A	A	A	6
GN08596	16.1	A	T	T	T	A	A	A	6
GN08597	5.8	A	T	T	T	A	A	A	6
GN08647	2.3	A	T	T	T	A	A	A	6
GN09572	7.6	A	T	T	T	A	A	A	6
GN09584	18.9	A	A	T	T	A	A	A	7
GN10510	5.6	A	T	T	T	A	A	A	6
GN10512	20.7	A	A	T	T	A	A	A	7
Willy	6.2	A	T	T	T	A	A	A	6
GN10524	3.2	A	T	T	T	A	A	A	6
GN10547	10.1	A	T	T	T	A	A	A	6
GN10603	3.4	A	T	T	T	A	A	A	6
GN10607	4.5	A	T	T	T	A	A	A	6
GN10613	5.5	A	T	T	T	A	A	A	6
GN10637	3.4	A	T	T	T	A	A	A	6
GN10677	2.2	A	A	T	T	A	A	A	7
GN10680	5.3	A	A	T	T	A	A	A	7
GN11505	4.0	T	A	T	T	A	A	A	6
GN11514	2.1	A	T	T	T	A	A	A	6
GN11516	4.3	A	T	T	T	A	A	A	6
GN11527	3.6	A	T	T	T	A	A	N	5
GN11537	5.4	A	T	T	T	A	A	A	6
GN11542	3.9	A	T	T	T	A	A	A	6
GN11551	6.0	T	A	T	T	A	A	A	6
GN11569	7.5	A	T	T	T	A	A	A	6
GN11574	5.0	T	T	A	T	T	A	A	3
GN11591	5.7	A	T	T	T	A	A	A	6
GN11592	2.8	A	T	T	T	A	A	A	6
GN11604	6.9	A	T	T	T	A	A	N	5
GN11634	8.2	A	T	T	T	T	A	A	5
GN11641	3.0	A	T	T	T	A	A	A	6
GN11644	5.5	A	T	T	T	T	A	A	5
GN11646	3.2	A	T	T	T	A	A	A	6
GN12606	5.2	A	T	T	T	A	A	A	6
GN12607	2.5	A	T	T	T	A	A	A	6
GN12615	7.7	A	T	T	T	T	A	A	5
GN12625	4.5	A	T	T	T	A	A	N	5
GN12626	1.4	A	T	T	T	A	A	N	5
GN12628	9.4	A	T	T	T	A	A	A	6
GN12630	7.0	A	T	T	T	A	A	A	6
GN12634	5.2	A	T	T	T	A	A	A	6
GN12635	10.6	A	T	T	T	A	A	A	6

GN12637	5.4	A	N	T	T	A	A	A	6
GN12639	3.8	A	T	T	T	A	A	A	6
GN12640	7.8	A	T	T	T	A	A	A	6
GN12641	5.7	A	T	T	T	A	A	A	6
GN12645	1.2	A	A	T	T	A	A	A	7
GN12650	3.9	A	A	T	T	A	A	A	7
GN12656	2.1	A	A	T	T	A	A	A	7
GN12658	5.1	A	T	T	T	A	A	A	6
GN12661	3.2	A	A	T	T	A	A	A	7
GN12681	3.5	A	A	T	T	A	A	A	7
GN12687	3.5	A	A	T	T	A	A	A	7
GN12697	4.8	A	A	T	T	A	A	A	7
GN12699	4.9	A	A	T	T	A	A	A	7
GN12700	2.5	A	A	T	T	A	A	A	7
GN12701	1.6	A	A	T	T	A	A	A	7
GN12721	4.5	A	A	T	T	A	A	A	7
GN12722	5.4	A	A	T	T	A	A	A	7
GN12727	1.6	A	A	T	T	A	A	A	7
GN12733	4.0	A	T	T	T	A	A	A	6
GN12737	1.0	A	T	T	T	A	A	A	6
GN12741	2.3	A	A	T	T	A	A	A	7
GN12750	0.9	A	T	T	T	A	A	A	6
GN12759	2.0	A	A	T	T	A	A	A	7
GN12760	3.6	A	A	T	T	A	A	A	7
GN12764	8.1	A	A	T	T	A	A	A	7
GN12767	3.7	A	T	T	T	A	A	A	6
GN12770	5.6	A	A	T	T	A	A	A	7
GN13505	1.6	A	A	T	T	A	A	A	7
GN13509	1.0	A	T	T	T	A	A	A	6
GN13516	1.7	A	A	T	T	T	A	A	6
GN13519	4.3	A	T	T	T	A	A	A	6
GN13521	4.6	A	A	T	T	A	A	A	7
GN13523	2.6	A	A	T	T	A	A	N	6
GN13527	7.1	A	T	T	T	A	A	A	6
GN13528	2.2	A	T	T	T	A	A	A	6
GN13542	3.4	A	T	T	T	A	A	A	6
GN13553	3.4	A	T	T	T	A	A	A	6
GN13560	3.9	A	T	T	T	A	A	A	6
GN13576	9.7	A	T	T	T	A	A	A	6
GN13577	4.6	A	T	T	T	A	A	A	6
GN13578	3.0	A	T	T	T	A	A	A	6
GN13595	1.3	A	A	T	T	A	A	A	7
GN13596	3.5	A	T	T	T	T	A	A	5
GN13606	4.6	A	N	T	T	A	A	A	6

GN13614	3.4	T	T	T	T	A	A	A	5
GN13615	5.4	T	T	T	T	A	A	A	5
GN13616	1.9	A	T	T	T	A	A	A	6
GN13618	3.4	A	T	T	T	A	A	A	6
GN13626	4.6	A	T	T	T	A	A	A	6
GN13633	3.9	A	A	T	T	A	A	A	7
GN13641	4.3	A	A	T	T	A	A	A	7
GN14502	1.4	A	A	T	T	A	A	A	7
GN14506	17.2	A	T	T	T	A	A	A	6
GN14511	16.6	A	T	T	T	A	A	A	6
GN14512	3.4	A	T	T	T	A	A	A	6
GN14515	16.6	A	A	T	T	A	A	A	7
GN14516	21.2	A	T	T	T	A	A	A	6
GN14522	0.9	A	T	T	T	A	A	A	6
GN14529	2.2	A	T	T	T	A	A	A	6
GN14530	2.1	A	A	T	T	A	A	A	7
GN14539	6.6	A	T	T	T	A	A	A	6
GN14540	3.9	A	T	T	T	A	A	A	6
GN14544	4.0	A	T	T	T	A	A	A	6
GN14547	1.0	A	A	T	T	A	A	A	7
GN14583	3.2	A	T	T	T	T	A	A	5
GN14634	6.7	A	A	T	T	A	A	A	7
GN14636	5.8	A	A	T	T	A	A	A	7
GN14649	5.3	A	A	T	T	A	A	A	7
Gondo -1	10.0	A	T	T	T	A	A	T	5
Granary	13.0	A	T	T	T	A	A	A	6
HAHN/PRL//AUS1408	21.9	A	T	T	T	T	A	A	5
IVAN/6/SABUF/5/BCN/4/RABI//GS/CRA/3/AE.SQUA RROSA (190)	27.6	A	T	A	A	T	A	A	3
J03	15.1	T	T	T	T	T	A	A	4
Kariega	36.4	A	T	A	T	T	T	A	3
Kruunu	25.8	A	T	T	T	A	A	T	5
Kukri	6.3	A	T	T	T	A	A	A	6
MS 273-150	32.1	T	T	T	T	T	A	A	4
Marble	16.0	A	T	T	T	A	A	A	6
Milan	15.9	A	T	T	T	A	A	A	6
Møystad	31.5	N	T	T	T	T	A	A	4
N894037	30.6	A	T	A	A	A	A	A	4
NG8675/CBRD//SHA5/WEAVER	28.8	A	T	T	A	T	A	T	3
NK00521	10.0	A	T	T	T	A	A	N	5
NK01513	25.3	A	T	T	T	A	A	A	6
NK01565	5.6	A	T	T	T	A	A	A	6
Demonstrant	24.3	A	T	T	T	A	A	A	6
NK93602 (1995)	23.9	T	T	T	T	A	A	A	5
NK93604	34.3	A	T	T	T	A	A	A	6

Nanjing 7840 - Pl.4	45.3	A	T	A	A	A	T	T	2
Naxos/2*Saar	6.2	A	A	T	T	A	A	A	7
Naxos (x3)	24.2	A	A	T	T	A	T	N	5
Ning 8343 - Pl.4	29.7	A	N	A	A	A	T	A	3
Nobeokabouzu (Mhazy)	37.8	N	A	T	T	A	T	A	5
Norrøna	20.7	T	T	T	T	A	A	A	5
ONPMSYDER-05	17.3	A	T	T	T	A	A	T	5
GONDO	26.6	A	T	A	T	A	A	T	4
MILAN/SHA7	28.5	A	T	A	T	A	T	A	4
CBRD/KAUZ	16.5	A	T	T	A	T	A	T	3
GUAM92//PSN/BOW	30.5	A	T	T	A	A	T	T	3
NG8675/CBRD	25.8	A	T	A	A	A	T	T	2
ALTAR 84/AE.SQUARROSA (224)//ESDA	16.5	A	T	T	T	A	A	A	6
BCN*2//CROC_1/AE.SQUARROSA (886)	26.5	A	T	T	T	T	A	A	5
MAYOOR//TK SN1081/ AE.SQUARROSA (222)	18.5	A	T	T	T	T	A	A	5
Breeding line 24	12.9	A	T	T	T	A	A	A	6
Paros	14.4	T	A	T	T	A	A	N	5
Pfau/Milan	10.1	T	T	T	T	A	A	A	5
Polkka	31.9	A	T	T	T	A	A	A	6
QUARNA	22.5	A	A	T	T	A	A	A	7
RB07	37.3	A	T	T	T	A	T	T	4
Reno	48.8	T	N	T	T	T	A	N	3
Rollo	15.2	T	T	T	T	A	A	A	5
Runar	32.3	T	T	T	T	A	A	A	5
Breeding line 31	7.5	A	A	A	T	A	A	A	6
Breeding line 30	1.4	A	A	T	T	A	A	A	7
SHA3/CBRD	27.1	A	T	A	A	A	T	T	2
SHA5/WEAVER//80456/YANGMAI 5	22.7	A	T	T	A	A	A	T	4
Breeding line 11	3.4	A	T	T	T	A	A	A	6
Caress	5.7	A	T	T	T	T	A	A	5
Breeding line 25	7.5	A	T	T	T	A	A	A	6
Breeding line 12	7.5	A	T	T	T	A	A	A	6
Breeding line 13	4.9	A	T	T	T	A	A	A	6
Breeding line 16	7.2	A	T	T	T	A	A	N	5
Breeding line 14	4.0	A	T	T	T	A	A	A	6
Breeding line 15	4.6	A	T	T	T	A	A	N	5
Breeding line 17	5.0	A	T	T	T	T	A	N	4
Breeding line 22	8.9	A	T	T	T	T	A	A	5
Breeding line 23	3.4	A	A	T	T	A	A	A	7
Breeding line 18	5.9	A	T	T	T	A	A	A	6
Breeding line 28	3.0	A	T	T	T	A	A	A	6
Breeding line 29	7.1	A	T	T	T	A	A	A	6
Breeding line 26	4.1	A	T	T	T	A	A	A	6
Breeding line 20	6.1	A	T	T	T	T	A	A	5

Breeding line 21	7.2	A	T	T	T	A	A	A	6
Breeding line 27	12.9	A	T	T	T	A	A	A	6
Breeding line 5	8.2	A	T	T	T	A	A	A	6
Breeding line 6	3.5	A	T	T	T	A	A	A	6
Breeding line 1	5.7	A	T	T	T	A	A	A	6
Breeding line 4	34.9	A	T	T	T	A	A	A	6
Breeding line 2	8.4	A	T	T	T	A	A	A	6
Breeding line 3	5.2	A	A	T	T	A	A	N	6
Amulett	10.5	A	T	T	T	A	A	A	6
Breeding line 7	8.5	A	T	T	T	A	A	N	5
Breeding line 8	9.6	A	T	T	T	A	A	A	6
Berlock	4.3	A	T	T	T	A	A	A	6
Breeding line 9	22.6	A	T	T	T	A	A	A	6
Breeding line 10	17.3	A	T	T	T	A	A	A	6
Breeding line 11	13.5	A	T	T	T	A	A	A	6
Soru #1	35.1	T	T	A	A	A	T	A	2
Saar	14.4	A	T	T	T	A	A	A	6
Sabin	25.6	A	T	A	T	A	A	A	5
Scirocco	15.9	A	A	T	T	A	A	A	7
Sirius	14.6	A	T	T	T	A	A	A	6
Sport	9.5	A	T	T	T	A	A	A	6
Sumai 3 (18.)	41.0	T	T	A	A	A	T	A	2
T10014	37.3	T	T	T	T	T	A	T	3
T2038	22.9	A	T	T	T	A	A	A	6
T7347	25.7	A	T	T	T	A	A	A	6
T9040 (1995)	21.4	A	A	T	T	A	A	T	6
T9040	11.7	A	T	T	T	A	A	A	6
TJALVE/Purpur seed	15.5	A	T	T	A	A	A	T	4
TUI/RL4137	32.8	A	T	T	T	A	A	A	6
T.DICOCCON PI94625/AE.SQUARROSA (372)//TUI/CLMS/3/2*PASTOR/4/EXCALIBUR	16.3	A	T	T	T	A	A	T	5
Tjalve	26.1	A	T	T	A	A	A	A	5
Tom	20.0	A	T	A	T	A	N	A	4
VERDE/3/BCN//DOY1/AE.SQUARROSA (447)	27.8	A	T	A	T	A	A	A	5
Vinjett	5.7	A	T	T	T	A	A	A	6
WHEAR/2*KRONSTAD F2004	18.1	A	T	T	T	A	A	A	6
Wanamo	29.9	A	T	T	T	A	A	A	6
Wellamo	42.3	A	T	T	T	A	A	N	5
Zebra	13.9	A	T	T	T	T	A	A	5

Table 7 Allele stacking Table for studied QTL in all winter wheat cultivars/lines, powdery mildew lsmeans over all winter environments and sum number of resistant alleles in each line. (T/A are computed letters and do not refer to nucleotide allele, N means the marker is not valid in this line).

Name	PM-lsmeans	AX.94526630	AX.94652021	AX.94966165	AX.94688926	AX.94890346	AX.94395845	AX.94412216	Nr of resistant alleles
Resistant alleles		**A**	**A**	**T**	**A**	**T**	**T**	**A**	
Breeding line6	2.9	A	A	T	A	T	T	A	7
Breeding line7	6.4	T	A	A	A	T	T	A	5
Breeding line3	7.0	A	T	A	A	T	T	A	5
20121	15.4	A	A	A	A	T	T	A	6
20126	10.4	A	A	A	A	T	T	A	6
20128	7.3	A	A	N	A	T	T	A	6
20130	5.6	A	A	A	A	T	T	A	6
20146	12.7	A	A	T	A	T	T	A	7
20228	2.9	A	A	T	T	T	T	A	6
KWS Magic	4.7	A	A	T	A	T	T	A	7
Agil	7.6	A	A	A	A	T	A	A	5
Akratos	6.7	A	A	T	A	T	T	A	7
Akteur	3.4	A	T	A	A	T	T	A	5
Alchemy	4.1	A	A	T	A	T	T	A	7
Ambition	11.1	A	A	T	A	T	T	A	7
Apollo	17.4	A	A	A	T	T	T	A	5
Arina	14.0	A	T	A	A	A	T	T	3
Arktis	0.8	A	T	A	A	T	T	A	5
BAYP4535 (W01217.4 Me/De)	6.1	A	A	T	A	T	A	A	6
Bersee	6.7	A	A	A	A	T	T	A	6
Bjørke	19.2	A	A	A	T	T	T	A	5
Brompton	11.6	A	A	T	A	T	T	A	7
Bussard	13.7	A	T	A	T	T	T	A	4
Ceylon	9.7	A	A	T	A	T	T	A	7
Claire	16.6	A	A	A	A	T	T	A	6
Breeding line2	1.9	A	A	T	A	T	T	A	7
Breeding line5	12.5	T	T	A	A	T	A	N	2
Jantarka	4.0	A	A	T	A	T	T	A	7
Ellvis	20.5	A	T	A	A	T	T	A	5
Event	1.7	A	A	T	A	T	T	A	7
FIRL3565(Amigos)	5.2	A	T	T	A	T	T	A	6
Fenman	3.2	A	A	T	A	T	T	A	7
Finans	25.7	T	T	A	T	A	A	T	0
Folke	6.5	A	A	A	A	T	T	A	6
Format	9.1	A	T	A	A	T	T	A	5
Frontal	9.0	A	A	A	A	T	T	A	6
GN04034	1.9	A	T	T	A	T	T	A	6
GN04035	2.9	A	A	T	A	T	T	A	7
GN04041	0.8	A	T	T	A	T	T	A	6

GN05012	2.1	A	A	A	A	T	T	A	6
GN05013	8.2	A	A	T	A	T	T	A	7
GN08004	2.9	A	A	T	A	T	T	A	7
GN11018	2.7	A	A	T	A	T	T	A	7
GN13023	3.7	A	A	T	A	T	T	A	7
Breeding line9	8.3	T	A	A	A	T	T	A	5
Breeding line10	4.6	A	T	T	A	T	T	T	5
Breeding line11	2.8	A	A	T	A	T	T	A	7
Breeding line12	0.9	A	A	T	A	T	T	A	7
Granitt	6.3	A	A	T	A	T	T	A	7
Breeding line	1.3	A	A	T	A	T	T	A	7
Breeding line8	1.4	A	A	T	A	T	T	A	7
Hereward	12.6	A	T	T	A	T	T	A	6
Ritmo	18.7	A	A	T	A	T	T	A	7
Jenga	14.1	A	A	T	A	T	A	A	6
Julius	5.5	A	A	T	A	T	T	A	7
KWS-Ozon	1.5	A	A	T	A	T	T	A	7
Kalle	14.3	A	A	A	T	T	T	A	5
Kamerat	4.0	A	T	T	A	T	T	A	6
Kanzler	33.6	T	T	A	T	A	A	T	0
Kosack	5.7	A	A	A	A	T	T	A	6
Kuban	3.4	A	A	T	A	T	T	A	7
LW91W89	7.7	A	A	T	A	T	T	A	7
Magnifik	6.8	A	A	A	A	T	T	A	6
Mariboss	5.5	T	A	A	A	T	A	A	4
Massey	5.5	A	A	T	A	T	T	A	7
Matrix	3.3	A	A	T	A	T	T	A	7
Mironovskaja 808	6.9	A	T	T	A	A	T	T	4
Mjølner	6.0	A	A	A	A	T	T	A	6
NK03029	3.6	A	A	T	A	A	T	T	5
NK03030	4.7	A	A	T	A	A	T	T	5
Olivin	9.8	A	A	T	A	T	T	A	7
Plutos	13.1	A	T	A	A	T	A	A	4
Portal	15.5	A	T	A	A	T	T	A	5
Potenzial	5.7	T	A	A	A	T	T	A	5
Prierier	9.4	T	A	A	A	T	T	A	5
RE714	13.0	A	A	T	A	A	A	T	4
REDCOAT	19.2	A	A	A	A	A	T	T	4
Regina	22.5	T	T	A	T	T	T	A	3
Rialto	8.2	A	A	T	A	T	T	A	7
Rida	14.0	A	A	A	T	A	T	T	3
Robigus	6.2	A	A	A	A	T	T	A	6
Rudolf	4.4	A	A	A	T	T	T	A	5
Breeding line4	2.7	A	A	T	T	T	T	A	6

Breeding line1	6.9	A	A	T	A	T	T	A	7
Sarmund	2.6	A	A	A	A	T	T	A	6
Senat	9.2	A	A	T	A	T	T	A	7
Senta	15.5	A	T	A	A	T	T	A	5
Sigyn II	4.0	A	A	A	A	T	T	A	6
Siria	5.0	A	A	A	A	T	A	A	5
Skagen	5.6	A	A	T	A	T	T	A	7
Soissons	5.8	A	A	T	A	T	T	A	7
Solist	6.5	A	A	T	A	T	T	A	7
Spark	19.5	A	A	A	T	T	T	A	5
Stava	0.2	A	A	A	A	T	T	A	6
SvP72017	4.4	A	A	T	A	T	T	A	7
TARSO	3.4	A	A	T	A	T	T	A	7
Torp	8.8	A	A	T	A	T	T	A	7
Trond	15.4	A	A	A	T	T	T	A	5
USG3209	6.8	A	A	T	A	T	T	A	7
V1004	10.2	A	A	A	A	A	T	T	4
V9001	6.3	A	A	A	A	T	T	A	7
Vlasta	4.6	A	A	T	A	T	T	A	7
Xi19	6.0	A	A	A	T	N	T	A	4

Table 8 Dataset for haplotypes analysing on 5AL chromosome for all spring wheat cultivars/lines, powdery mildew lsmeans over all spring environments. (T/A are computed letters and do not refer to nucleotide allele, N means the marker is not valid in this line).

Name	PM-lsmeans	AX-95018258	AX-94525543	AX-94771047
Croc_1/Ae.squarrosa (205)//Kauz	8.4	T	T	A
Altar84/Ae.squarrosa(219)// 2*Seri	8.6	T	T	A
Altar84/Ae.sq(219)//2*Seri/3/ Avle	13.9	T	T	A
512-21	46.9	A	A	N
512-50	34.7	T	T	A
512-54	34.6	T	T	A
512-70	22.5	T	T	A
512-87	28.9	T	T	A
80456/YANGMAI 5//SHA5/WEAVER/3/PRINIA	33.7	A	A	N
AC Somerset	23.7	T	T	A
Aino	31.9	T	T	A
Anniina	21.3	T	T	A
Avans	10.3	T	T	A
Avle	14.3	T	T	A
Avocet YrA	42.8	T	T	A
BAJASS-5	17.0	T	T	N
BJY/COC//CLMS/GEN	49.2	T	T	A
Bau/Milan -2	15.4	T	T	A
Bastian	17.2	T	T	A
Berserk	20.2	T	T	A
Bjarne/LW91W86	14.4	T	T	A
Bjarne	20.8	T	T	A
Bombona	13.6	T	T	A
Brakar	29.8	T	T	A
C80.1/3*QT4522//2*ATTILA	23.9	T	T	N
C80.1/3*QT4522//2*PASTOR	16.7	T	T	A
CD87	16.4	T	T	A
Arabella	4.8	T	T	A
CJ9306	46.3	A	A	N
CJ9403	40.4	A	A	T
Cadenza	9.8	T	T	A
Catbird -2	7.9	A	A	T
Chara	29.5	T	T	N
Paros/T9040	11.5	T	T	A
Paros/NK93602	14.9	T	T	A
T9040/Paros	21.6	T	T	A
Mandaryna	9.2	T	T	A
DH20070	15.5	T	T	A
DH20097	32.6	T	T	T
DH 49-18 Bastian/Adder	25.4	T	T	A
Dragon	12.6	T	T	A

Dulus	33.5	T	T	A
EMB16/CBRD//CBRD	26.8	A	A	N
Filin	9.3	T	T	A
Fram II	17.3	T	T	A
Frontana (95)	39.8	T	T	A
GAMENYA	16.7	T	T	A
GN03503	7.1	T	T	A
Krabat	16.8	T	T	A
GN03529	18.0	T	T	A
GN03531	10.9	T	T	A
GN03597	2.9	T	T	A
GN04526	26.2	T	T	A
GN04528	2.3	T	T	A
GN04537	25.0	T	T	A
GN04603	8.7	T	T	A
GN05507	10.2	T	T	A
GN05551	5.8	T	T	A
Laban	10.2	T	T	A
GN05580	8.3	T	T	A
GN05589	7.3	T	T	A
GN06557	10.6	T	T	A
GN06573	13.2	T	T	A
GN06578	2.4	T	T	A
Mirakel	5.2	T	T	A
Rabagast	4.7	T	T	A
GN07525	5.3	T	T	A
GN07548	4.5	T	T	A
GN07560	6.1	T	T	A
Seniorita	2.8	T	T	A
GN07580	2.3	T	T	A
GN07581	7.7	T	T	A
GN08504	3.9	T	T	A
GN08530	3.6	T	T	A
GN08531	1.8	T	T	A
GN08533	1.8	T	T	A
GN08534	13.2	T	T	A
GN08541	4.7	T	T	A
GN08554	2.3	T	T	A
GN08557	2.0	T	A	N
GN08564	2.4	T	T	A
GN08568	3.2	T	T	A
GN08581	2.6	T	T	A
GN08588	3.6	T	T	A
GN08595	12.0	T	T	A

GN08596	16.1	T	T	A
GN08597	5.8	T	T	A
GN08647	2.3	T	T	A
GN09572	7.6	T	T	A
GN09584	18.9	T	T	A
GN10510	5.6	T	T	A
GN10512	20.7	T	T	A
Willy	6.2	T	T	A
GN10524	3.2	T	T	A
GN10547	10.1	T	T	A
GN10603	3.4	T	T	A
GN10607	4.5	T	T	A
GN10613	5.5	T	T	A
GN10637	3.4	T	T	A
GN10677	2.2	T	T	A
GN10680	5.3	T	T	A
GN11505	4.0	T	T	A
GN11514	2.1	T	T	A
GN11516	4.3	T	T	A
GN11527	3.6	T	T	A
GN11537	5.4	T	T	A
GN11542	3.9	T	T	A
GN11551	6.0	T	T	A
GN11569	7.5	T	T	A
GN11574	5.0	T	T	A
GN11591	5.7	T	T	A
GN11592	2.8	T	T	A
GN11604	6.9	T	T	N
GN11634	8.2	T	T	A
GN11641	3.0	T	T	A
GN11644	5.5	T	T	A
GN11646	3.2	T	T	A
GN12606	5.2	T	T	A
GN12607	2.5	T	T	A
GN12615	7.7	T	T	A
GN12625	4.5	T	T	A
GN12626	1.4	T	T	A
GN12628	9.4	T	T	A
GN12630	7.0	T	T	A
GN12634	5.2	T	T	A
GN12635	10.6	T	T	A
GN12637	5.4	T	T	A
GN12639	3.8	T	T	A
GN12640	7.8	T	T	A

GN12641	5.7	T	T	A
GN12645	1.2	T	T	A
GN12650	3.9	T	T	A
GN12656	2.1	T	T	A
GN12658	5.1	T	T	A
GN12661	3.2	T	T	A
GN12681	3.5	T	T	A
GN12687	3.5	T	T	A
GN12697	4.8	T	T	A
GN12699	4.9	N	T	A
GN12700	2.5	T	T	A
GN12701	1.6	T	T	A
GN12721	4.5	T	T	A
GN12722	5.4	T	T	A
GN12727	1.6	T	T	A
GN12733	4.0	T	T	A
GN12737	1.0	T	T	A
GN12741	2.3	T	T	A
GN12750	0.9	T	T	A
GN12759	2.0	T	T	A
GN12760	3.6	T	T	N
GN12764	8.1	T	T	A
GN12767	3.7	T	T	A
GN12770	5.6	T	T	A
GN13505	1.6	T	T	A
GN13509	1.0	T	T	A
GN13516	1.7	T	T	A
GN13519	4.3	T	T	A
GN13521	4.6	T	T	A
GN13523	2.6	T	T	A
GN13527	7.1	T	T	A
GN13528	2.2	T	T	A
GN13542	3.4	T	T	A
GN13553	3.4	T	T	A
GN13560	3.9	T	T	A
GN13576	9.7	T	T	A
GN13577	4.6	T	T	A
GN13578	3.0	T	T	A
GN13595	1.3	T	T	A
GN13596	3.5	T	T	N
GN13606	4.6	T	T	A
GN13614	3.4	T	T	A
GN13615	5.4	T	T	A
GN13616	1.9	T	T	A

GN13618	3.4	T	T	A
GN13626	4.6	T	T	A
GN13633	3.9	T	T	A
GN13641	4.3	T	T	A
GN14502	1.4	T	T	N
GN14506	17.2	T	T	A
GN14511	16.6	T	T	A
GN14512	3.4	T	T	A
GN14515	16.6	T	T	A
GN14516	21.2	T	T	A
GN14522	0.9	T	T	A
GN14529	2.2	T	T	A
GN14530	2.1	T	T	A
GN14539	6.6	T	T	A
GN14540	3.9	T	T	A
GN14544	4.0	T	T	A
GN14547	1.0	T	T	A
GN14583	3.2	T	T	N
GN14634	6.7	T	T	A
GN14636	5.8	T	T	A
GN14649	5.3	T	T	A
Gondo -1	10.0	T	T	A
Granary	13.0	T	T	A
HAHN/PRL//AUS1408	21.9	T	T	A
IVAN/6/SABUF/5/BCN/4/RABI//GS/CRA/3/AE.SQUARROSA (190)	27.6	A	A	T
J03	15.1	T	T	A
Kariega	36.4	T	T	A
Kruunu	25.8	T	T	A
Kukri	6.3	T	T	T
MS 273-150	32.1	T	T	A
Marble	16.0	T	T	A
Milan	15.9	T	T	A
Møystad	31.5	T	T	A
N894037	30.6	A	A	T
NG8675/CBRD//SHA5/WEAVER	28.8	A	A	T
NK00521	10.0	T	T	N
NK01513	25.3	T	T	A
NK01565	5.6	T	T	A
Demonstrant	24.3	T	T	A
NK93602 (1995)	23.9	T	T	A
NK93604	34.3	T	T	A
Nanjing 7840 - Pl.4	45.3	A	A	T
Naxos/2*Saar	6.2	T	T	A
Naxos (x3)	24.2	T	T	A

Ning 8343 - Pl.4	29.7	A	A	N
Nobeokabouzu (Mhazy)	37.8	T	T	A
Norrøna	20.7	T	T	A
ONPMSYDER-05	17.3	T	T	A
GONDO	26.6	T	T	A
MILAN/SHA7	28.5	T	T	A
CBRD/KAUZ	16.5	A	A	T
GUAM92//PSN/BOW	30.5	A	A	T
NG8675/CBRD	25.8	A	A	T
ALTAR 84/AE.SQUARROSA (224)//ESDA	16.5	T	T	A
BCN*2//CROC_1/AE.SQUARROSA (886)	26.5	T	T	A
MAYOOR//TK SN1081/ AE.SQUARROSA (222)	18.5	T	T	A
Breeding line 24	12.9	T	T	A
Paros	14.4	T	T	A
Pfau/Milan	10.1	T	T	A
Polkka	31.9	T	T	A
QUARNA	22.5	T	T	A
RB07	37.3	T	T	A
Reno	48.8	T	T	A
Rollo	15.2	T	T	A
Runar	32.3	T	T	A
Breeding line 31	7.5	T	T	A
Breeding line 30	1.4	T	T	A
SHA3/CBRD	27.1	A	A	T
SHA5/WEAVER//80456/YANGMAI 5	22.7	A	A	T
Breeding line 11	3.4	T	T	A
Caress	5.7	T	T	A
Breeding line 25	7.5	T	T	A
Breeding line 12	7.5	T	T	A
Breeding line 13	4.9	T	T	A
Breeding line 16	7.2	T	T	A
Breeding line 14	4.0	T	T	A
Breeding line 15	4.6	T	T	A
Breeding line 17	5.0	T	T	A
Breeding line 22	8.9	T	T	N
Breeding line 23	3.4	T	T	A
Breeding line 18	5.9	T	T	A
Breeding line 28	3.0	T	T	A
Breeding line 29	7.1	T	T	A
Breeding line 26	4.1	T	T	A
Breeding line 20	6.1	T	T	A
Breeding line 21	7.2	T	T	A
Breeding line 27	12.9	T	T	A
Breeding line 5	8.2	T	T	A

Breeding line 6	3.5	T	T	A
Breeding line 1	5.7	T	T	A
Breeding line 4	34.9	T	T	A
Breeding line 2	8.4	T	T	A
Breeding line 3	5.2	T	T	A
Amulett	10.5	T	T	A
Breeding line 7	8.5	T	T	A
Breeding line 8	9.6	T	T	A
Berlock	4.3	T	T	A
Breeding line 9	22.6	T	T	A
Breeding line 10	17.3	T	T	A
Breeding line 11	13.5	T	T	A
Soru #1	35.1	A	A	T
Saar	14.4	T	T	A
Sabin	25.6	T	T	A
Scirocco	15.9	T	T	N
Sirius	14.6	T	T	A
Sport	9.5	T	T	A
Sumai 3 (18.)	41.0	A	A	N
T10014	37.3	T	T	A
T2038	22.9	T	T	A
T7347	25.7	T	T	A
T9040 (1995)	21.4	T	T	A
T9040	11.7	T	T	A
TJALVE/Purpur seed	15.5	T	A	T
TUI/RL4137	32.8	T	T	A
T.DICOCCON PI94625/AE.SQUARROSA (372)//TUI/CLMS/3/2*PASTOR/4/EXCALIBUR	16.3	T	T	A
Tjalve	26.1	T	A	T
Tom	20.0	T	T	A
VERDE/3/BCN//DOY1/AE.SQUARROSA (447)	27.8	T	T	A
Vinjett	5.7	T	T	A
WHEAR/2*KRONSTAD F2004	18.1	T	T	A
Wanamo	29.9	T	T	A
Wellamo	42.3	T	T	A
Zebra	13.9	T	T	A

Table 9 Dataset for haplotypes analysing on 5AL chromosome for all winter wheat cultivars/lines, powdery mildew lsmeans over all winter environments. (T/A are computed letters and do not refer to nucleotide allele, N means the marker is not valid in this line and W refer to heterozygosity which had been removed from all results).

Name	PM-lsmeans	AX.94691627	AX.94966165	AX.94400860
Breeding line6	2.9	T	T	A
Breeding line7	6.4	A	A	A
Breeding line3	7.0	N	A	A
20121	15.4	A	A	A
20126	10.4	A	A	A
20128	7.3	A	N	W
20130	5.6	A	A	A
20146	12.7	T	T	T
20228	2.9	T	T	T
KWS Magic	4.7	T	T	A
Agil	7.6	N	A	A
Akratos	6.7	T	T	A
Akteur	3.4	A	A	A
Alchemy	4.1	T	T	T
Ambition	11.1	T	T	A
Apollo	17.4	A	A	A
Arina	14.0	A	A	A
Arktis	0.8	A	A	A
BAYP4535 (W01217.4 Me/De)	6.1	T	T	A
Bersee	6.7	A	A	A
Bjørke	19.2	A	A	A
Brompton	11.6	T	T	T
Bussard	13.7	N	A	A
Ceylon	9.7	T	T	A
Claire	16.6	N	A	A
Breeding line2	1.9	T	T	T
Breeding line5	12.5	A	A	A
Jantarka	4.0	T	T	A
Ellvis	20.5	A	A	A
Event	1.7	T	T	T
FIRL3565(Amigos)	5.2	T	T	T
Fenman	3.2	T	T	T
Finans	25.7	A	A	A
Folke	6.5	A	A	A
Format	9.1	A	A	A
Frontal	9.0	A	A	A
GN04034	1.9	T	T	A
GN04035	2.9	T	T	A
GN04041	0.8	T	T	T
GN05012	2.1	A	A	A
GN05013	8.2	T	T	A

GN08004	2.9	T	T	T
GN11018	2.7	T	T	A
GN13023	3.7	T	T	T
Breeding line9	8.3	A	A	A
Breeding line10	4.6	T	T	T
Breeding line11	2.8	T	T	T
Breeding line12	0.9	T	T	T
Granitt	6.3	T	T	T
Breeding line	1.3	T	T	T
Breeding line8	1.4	T	T	T
Hereward	12.6	T	T	T
Ritmo	18.7	T	T	A
Jenga	14.1	T	T	A
Julius	5.5	T	T	T
KWS-Ozon	1.5	T	T	A
Kalle	14.3	A	A	A
Kamerat	4.0	T	T	T
Kanzler	33.6	A	A	A
Kosack	5.7	A	A	A
Kuban	3.4	T	T	T
LW91W89	7.7	T	T	A
Magnifik	6.8	A	A	A
Mariboss	5.5	A	A	A
Massey	5.5	T	T	T
Matrix	3.3	T	T	T
Mironovskaja 808	6.9	T	T	T
Mjølner	6.0	A	A	A
NK03029	3.6	T	T	T
NK03030	4.7	T	T	T
Olivin	9.8	T	T	T
Plutos	13.1	A	A	A
Portal	15.5	A	A	A
Potenzial	5.7	A	A	A
Prierier	9.4	N	A	A
RE714	13.0	T	T	T
REDCOAT	19.2	A	A	A
Regina	22.5	A	A	A
Rialto	8.2	T	T	T
Rida	14.0	A	A	A
Robigus	6.2	A	A	A
Rudolf	4.4	A	A	A
Breeding line4	2.7	T	T	A
Breeding line1	6.9	T	T	T
Sarmund	2.6	A	A	A

Senat	9.2	T	T	A
Senta	15.5	A	A	A
Sigyn II	4.0	A	A	A
Siria	5.0	A	A	A
Skagen	5.6	T	T	T
Soissons	5.8	T	T	A
Solist	6.5	T	T	A
Spark	19.5	A	A	A
Stava	0.2	A	A	A
SvP72017	4.4	T	T	T
TARSO	3.4	T	T	T
Torp	8.8	T	T	A
Trond	15.4	A	A	A
USG3209	6.8	T	T	T
V1004	10.2	A	A	A
V9001	6.3	A	A	A
Vlasta	4.6	T	T	A
Xi19	6.0	A	A	A

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