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Identification and validation of SNP markers for Fusarium head blight resistance in wheat

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Agriculture and horticulture

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Abstract

Fusarium graminearum is a fungal pathogen known to cause Fusarium head blight, and has greatly affected the yield and grain quality of Norwegian wheat. The most cost efficient way to reduce infection and severity of the disease is to develop new resistant cultivars. Fusarium resistance is a complex trait, caused by many medium to small effect genes. Genome wide association mapping can be a powerful tool to map these genes. In this thesis, we use marker from the 90K SNP array, along with phenotypic data from a core collection of 405 MASBASIS spring and winter wheat lines from 2013-2015. The population consists of lines from eight different subpopulation with different geographical origin and habitat. The traits that are being assessed are mainly fusarium head blight severity, deoxynivalenol content, and anther extrusion. Plant height and earliness are also being noted due to its close relationship to fusarium head blight infection. All traits showed significant markers around previously documented QTLs, indicating that the markers for undocumented QTLs that were discovered in this associating mapping might be significant to. Heritabilities for each trait were calculated using analysis of variance, which showed that observed variance resulting genetics were lower for FHB than for DON. This indicates that FHB is more affected by environmental effects and assessment errors. DON could therefore be considered a more accurate parameter than FHB, which shows in both the heritability and number of valid significant markers found. The goal of this thesis is to map the resistance QTLs of the Norwegian breeding material, and validate new QTLs that can be used marker assisted selection for the breeding company Graminor in Norway.

Thesis organization

This thesis focus on association mapping of quantitative trait loci for Fusarium head blight, and is separated into five chapters. Chapter 1 focus on literature on the topic, and materials and methodology. Chapter 2 focus on results from heritability testing, correlation between traits, and correlation between number for favorable genes and traits. Chapter 3 focus on the association mapping, and documenting the results, as well as discussing them. Chapter 4 focus on the validation test for significant markers. Chapter 5 focus on discussion, advantages and limitations of association mapping, and how genomic selection could be implemented in breeding.

Four appendixes are attached at the end of the paper, which include all significant marker from the association mapping, the entire validation test, and QQ-plots from the association mappings.

Abbreviations

FHB – *Fusarium* head blight

DON – Deoxynivalenol

DH – Days to heading

HD – Heading date

PH – Plant height

AE – Anther extrusion

FHB_reg – Regression for *Fusarium* head blight

DON_reg – Regression for deoxynivalenol

QTL – Quantitative trait loci

SNP – Single nucleotide polymorphism

GWAS – Genome-wide association study

MLM – Mixed linear model

Lsmeans – least squares means

SSR – Simple sequence repeat

Content

Chapter 1: General introduction and methodology

1.1. Literature review

1.1.1. Bread wheat

Wheat is one of the 3 most important staple crops in the world along with rice and maize. It was first cultivated around 10 000 years ago. Domestication of wheat, along with other crops, led to a drastic increase in food production. Which then led to community settlements, increase in population, and cultural evolution. From then until now, wheat has developed a large variation, resulting in over 25 000 different cultivars. Wheat has high yield, and is able to grow in many different environments, from 67°N in Norway, Finland and Russia to 45°S in Argentina. The main production regions are southern Russia, Ukraine, central USA and adjacent areas in Canada, northwestern Europe, north-central China, India, Argentina and south western Australia(Smartts & Simmonds, 1995).

The modern cultivars belong to the allohexaploid bread wheat *Triticum aestivum.* It contains 3 sets of diploid subgenomes, derived from 3 species in the Triticae tribe: *Triticum Urartu*(AA), an unknown close relative to *Aegilops speltoides*(BB), *and Ae. Tauschii*. The hypothesis is that the initial allopolyploidization involved A and B genomes, which formed the tetraploid emmer wheat(T. turgidum, AABB). Emmer then hybridized with the D genome and formed the modern bread wheat (*T. aestivum,* AABBDD)(Marcussen, 2014)

1.1.2. Fusarium head blight

Fusarium is a genus in the phylum ascomycetes, and is also the collective name for the asexual stage of many fungi species. The genus includes pathogens known to cause diseases in a large variety of plant species, including wheat, barley, oat, maize and others grasses (Schamle III & Bergstrom, 2003). There are several symptoms to Fusarium pathogens, and include head blight, root rot, crown rot, foot rots and seedling blight (Brodal, 2012). Above ground symptoms like head blight is promoted by humid conditions, whilst below ground symptoms like root rot is promoted by dry conditions. In Norway the climate is usually warm and humid in late summer, early autumn. Which means Fusarium head blight is the main problem in cereal crops. Fusarium has been present in cereal crops for many decades, but has become a problem since the early 1990s. The reason for this outbreak is considered a combination of low resistance in existing cultivars, climate change with more rainfall and humid conditions in late summer, and the global adaptation of reduced tillage systems. The

reason reduced tillage is an important factor is that the main source of the primary inoculum is from plant residues.

Fusarium head blight causes major yield and economical damage in cereal crops, by reducing seed germination, causing floret sterility, reducing seed filling(Figure 2), and producing mycotoxins. The symptoms can be observed as premature bleaching of one or more spiklets(Figure 1). If the tissue is killed in the middle of the head, the grains above that point will not fill at all. In epidemics, for instance in the United States, regional yield losses has been reported up to 30 %. In addition to the yield loss, the quality loss due to mycotoxins severely affects the amount of edible product for humans, which in turn affects to economical income.

Figure 1: Shows two infected wheat heads. One on the left is completely infected, while the one on the right has one infected spiklet. (Foto: Jansen, 2015)

Figure 2: Shows difference in grain filling in resistant cultivars Sumai 3 and Mirakel(on the left) and susceptible cultivars Avocet YrA and Vinjett(On the right).

1.1.2.1. Life cycle

The pathogen survives winter on plant residues as perithecia, and mycelium. These can survive in the soil for several years. The primary inoculum comes from either airborne spores of the perithecia, or splash dispersed conidia spores. These infects the spiklets of the plant between head emergence and harvest. Warm and moist conditons then facilitates spore germination and invasion of spike tissue. After mycelium grow in the head, asexual conidia spores can continue the spread downwards and upwards in the plant by rain dispersal(Brodal, 2012). Despite this, Fusarium is considered a monocyclic disease, because perithecia does not have the time to grow and spread for a new cycle before harvest.

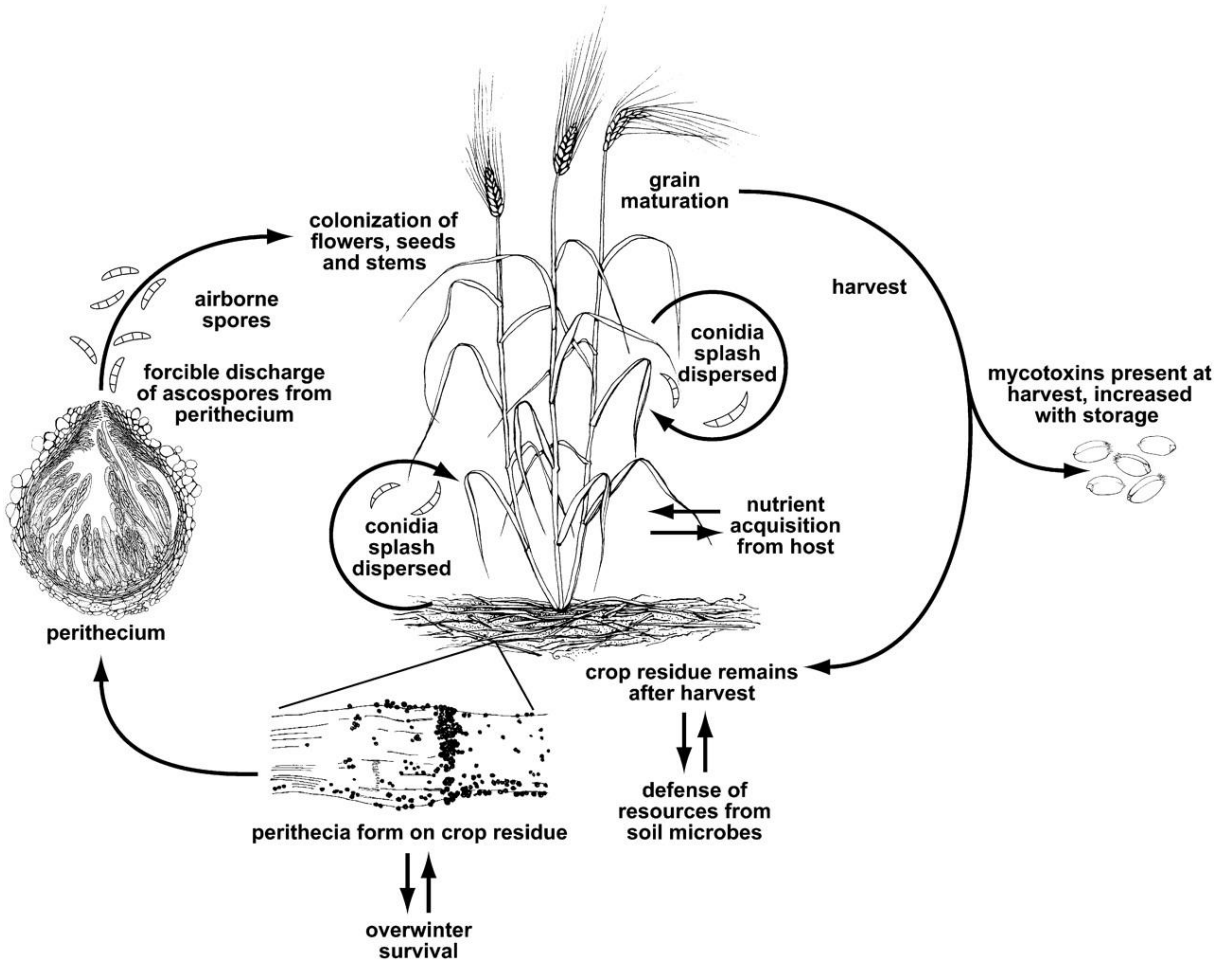

Figure 3: Life cycle of Fusarium graminerarum (teleomorph stage: Gibberella zeae). (Trail, 2009)

1.1.3. Fusarium resistance

Fusarium resistance is first separated into two categories, active and passive mechanisms. The active mechanisms are separated into type 1-5, and include resistance to primary infection, spread of infection, mycotoxin production, kernel infection and tolerance (Mesterhazy, 1995). The breeding programs focus on reducing infection, since this will in turn reduce mycotoxin levels, and reduce yield loss.

Table 1: Different types of Fusarium resistance and their description

Types	Description
I	Resistance to infection
II	Resistance to fungal spread
III	Resistance to accumulation of mycotoxins
IV	Resistance to kernel infection
V	Tolerance

The passive mechanisms include earliness, plant height and anther extrusion. If the plant flower early, it will most likely avoid the most intense infection period. Taller plants are

farther away from the splash dispersed conidia spores that comes from plant debris on the ground. Anther extrusion is the plants ability to release its anthers during flowering. Poor anther extrusion makes the anthers get stuck in between the awns. This gives the pathogen easies access to the flower, and a good growth medium on the anthers themselves.

1.1.4. Known resistance loci

1.1.4.1. Fhb1 on 3BS

This QTL contributes to type 1, 2 and 3 resistance, and explains 15-60% of the phenotypic variance(Lu, 2011). The source of the gene is Sumai 3, and is present in the breeding line CJ9306. The QTL was fine mapped by Cuthbert et. al in 2006(Cuthbert et al., 2006), and will be cloned in 2016 by Rawat et al. Rawat et al., 2016)

1.1.4.2. Fhb2 on 6BS

This QTL mainly contributes with type 2 resistance (Lu, 2011). The source of the gene is Sumai 3, but QTL from the same cluster has been found in other sources as well, like Wangshuibai, Ning8026, Ning 894037, Swiss wheat Arina, US Patton and French Apache. Closely linked markers were found by Cuthbert et. al in 2007 by point and spray inoculation (Cuthbert et al., 2007).

1.1.4.3. Fhb3

This QTL was identified introgression lines between the alien species Leymus racemosus and bread wheat. It is mainly a type 2 resistance gene, and is located on chromosome 7. (Lu, 2011)

1.1.4.4. Fhb4

This QTL is located on chromosome 4B and explains 17,5% of the phenotypic variance. It mainly contribute to type 1 resistance, and comes from the resistance source Wangshuibai. The gene has been fine mapped to an interval of 1,7 cM (Lu, 2011.

1.1.4.5. Fhb5

This QTL is located on chromosome 5A and explains 27% of the phenotypic variance. It mainly contribute to type 1 resistance, and comes from the resistance source Wangshuibai. The gene has been fine mapped to an interval of 0,3 cM (Lu, 2011).

1.1.4.6. Meta QTLs

Liu et al. used meta-analysis in 2009 to review 249 mapped FHB resistance QTL in 46 unique line from 45 different experiments (Liu et al, 2009). Results from individual studies were combined to estimate the confidence interval (CI) of QTLs that were then projected onto 2

different consensus maps made song et al. in 2005, and Somers et al. in 2004. QTL positions were then compared to identify overlapping areas. 209 of the 249 QTL were successfully onto the consensus map. The remaining 40 lacked markers in common with either map, and therefore assessed. 130 of the 209 QTL affects type 2 resistance, 32 affects type 1, 25 affects type 3, and 22 affects type 4 resistance. All chromosomes contain more than 1 QTL. Of the reported QTLs, 48% comes from Asian sources, while only 14% comes from north and south American sources. Asian sources are the only ones that reports QTLs on chromosome 2D and 5D, while European sources are the only ones that reports QTLs on chromosome 4A, 6A, 3D and 6D. The 209 QTLs were classified into 43 different clusters. These clusters were almost evenly distributed on the 3 genomes, 15 on A, 15 on B and 13 on D. But the B genome has more QTLs identified (100) than the A genome (65) and D genome (45). Table 2 shows the confirmed and unique QTLs from this meta-analysis, the type of resistance they contribute to, and their source. Results from the association mapping will be compared to these QTLs to see if we have overlapping areas.

Table 2: confirmed and unique QTL for FHB resistance in wheat based on a meta-analysis of 46 lines in 45 different studies from 2001 to 2009(Liu et al. 2009)

Chromosome locations	Type of resistance	Source of resistance
Confirmed QTL		
3A	II	Frontana
5A	I, II, III	Sumai 3
5A	I	Wangshuibai
7A	II	Wangshuibai
1B	II	Wangshuibai
3BS	I, II, III, IV	Sumai 3
3BS	II	Wangshuibai
3BSc	II	Wangshuibai
5B	II	Wangshuibai
6BS	I, II, IV	Sumai 3
6B	II	Arina
2DL	II	Sumai 3
Unique QTL		
1A	II	Wangshuibai
2A	III	NK93604
2A	IV	Wangshuibai
3A	I	Wangshuibai
5AL	II	Renan
7A	II	Frontana
1B	I, II	Cansas, Arina
2B	I	Goldfield
5B	I, I, II	Cansas, Wangshuibai, Arina
7B	I, I, II	Cansas, Goldfield, CJ9306
1D	I, II, II, IV	Ritmo, Apache, Pirat, DH181
3D	I, II	Cansas, Arina
5D	II	Chokwang

6D	II, II, II	Arina, Renan, Romanus
7D	IV	Wangshuibai

1.1.5. CJ9306

In Norway, one of the sources breeders use for fusarium resistance is the inbred line Changjiang 9306(CJ9306). CJ9306 is derived from the Chinese cultivar Sumai 3, and show better type 2 resistance, as well as good agronomical traits. The line was created through multiple parent crossing, and recurrent selection combined using the dominant male sterile gene *Ta1(Jiang et al., 2006)*.

Jiang et al. performed in 2007 a QTL analysis of CJ9306, by using single floret inoculation in greenhouses, and measuring the percentage of scabby spiklets 25 days after inoculation (Jiang et al., 2007A). They verified the gene *fhb1* on chromosome 3BS, which explained 30.7% of the phenotypic variation. Another major QTL were verified on 2DL, which explained 9.9 – 28.4% of the phenotypic variation. Three other markers on chromosomes 5AS, 2BL and 1BC were validated and were able to reduce the percentage of scabby kernels by 10.3, 13.2 and 11.4 percent respectively. Another QTL study by Jiang et al. was done in 2007 were they measured DON accumulation instead of infection spread (Jiang et al., 2007B). This study validated the major QTLs on 3BS and 5AS, and also detected two new QTL on 2DL and 1AS. 3BS and 2DL explained 23 and 20 % respectively of the phenotypic variation, while 1AS and 5AS explained separately 4-6 %.

1.1.6. Norwegian cultivars

In the Norwegian material, there has been generally small variations in DON values. But cultivars with high DON values can easily be found outside the market cultivars. Field trials has been done at Vollebekk research station in Norway from 2007 – 2015. Figure 4 and 5 was made based on data from Lillemo et al. in 2013, and data from my own field trial. Figure 5 shows variations at some of the cultivars in the different field trials (Lillemo et al., 2013). This also shows that in 2009, the variation is lost. This was due to very high infection pressure. Figure 4 shows that the Norwegian breeding programs has clearly improved Fusarium resistance in the Norwegian cultivars (Lillemo et al., 2013. This is especially clear in the 3 newest cultivars Senorita, Mirakel and Krabat. The Chinese material shows the potential that the Norwegian programs are working towards. The breeders use the line CJ9306 among others to improve the Norwegian material to the standards of Sumai 3. The challenge is to incorporate the resistant genes, while keeping resistance to other disease as well as high

yield and quality. Right now, a combination of markers and phenotypic selection is being used.

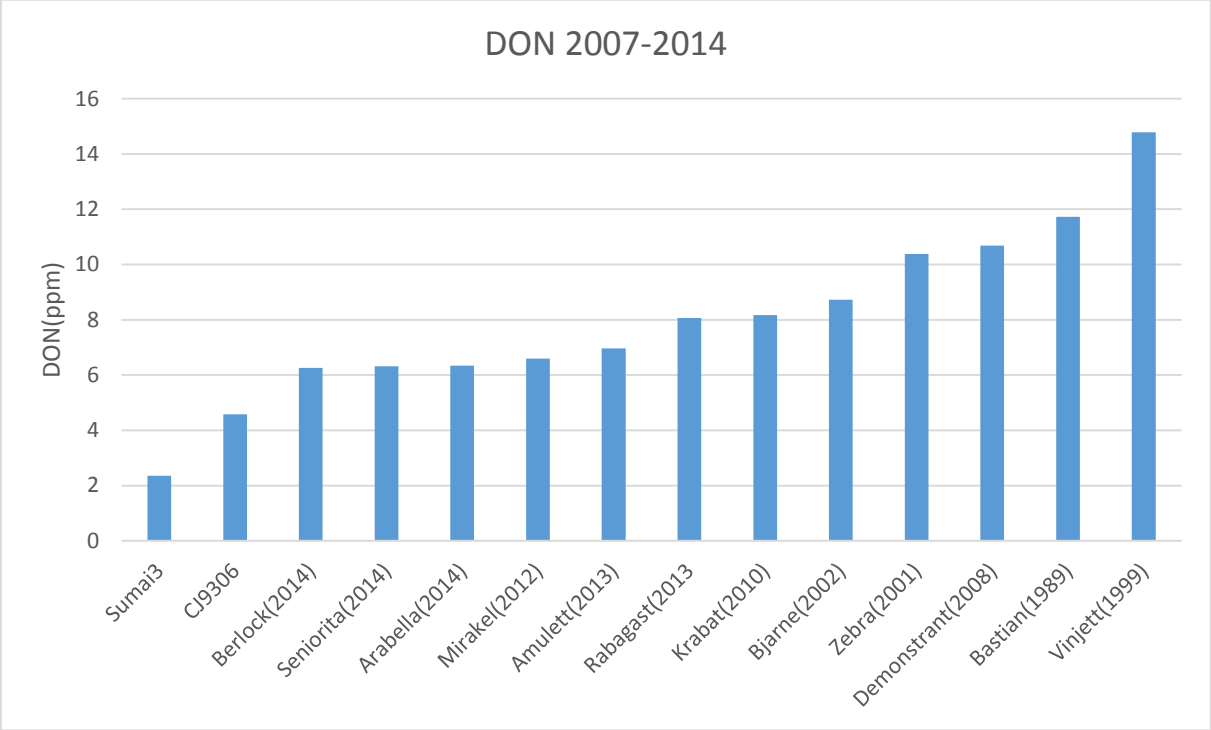

Figure 4: Varitation in DON values, based on mean values from field trials at Vollebekk, and Staur reasearch stations from 2007 – 2014. (Lillemo et al., 2013)

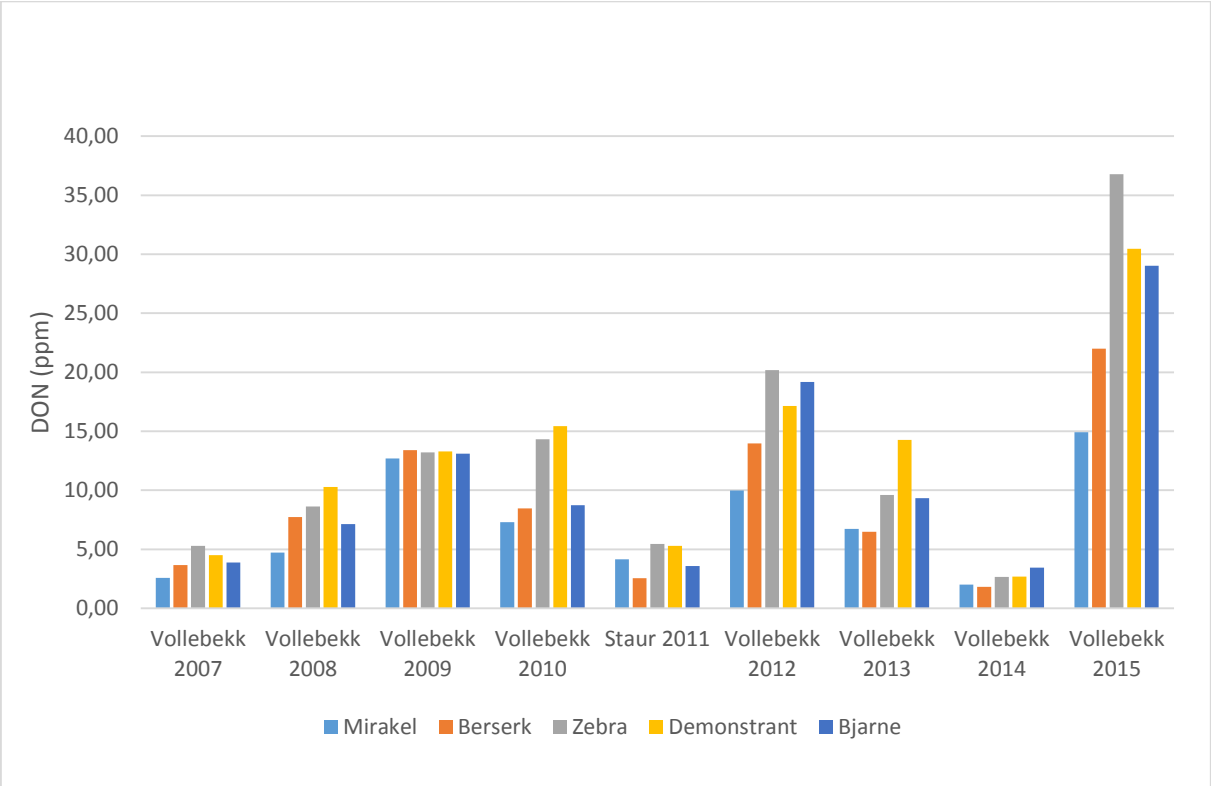

Figure 5: Variations in DON values between representative cultivars in field trials at Vollebekk, and Staur research stations, from 2007 – 2015. (Lillemo et al., 2013)

1.2. Aim of the study

The objective of this study is to identify the most important QTL for Fusarium resistance in the Norwegian spring and winter wheat lines, using genotype data from the 90K SNP assay and phenotypic data for DH, PH, AE, FHB and DON. Systematic testing of wheat lines from 2007 has revealed differences in resistance, and in 2014 Stine Cecilie Kjellvik Jansen used these data in an association mapping. By adding data from 2015, and using data previous years the association panel was tested (2013 and 2014), another AM will be done, with more high quality data. The most significant markers from this AM will be genotyped on the new breeding lines, and validated. The validated markers could then be used in marker assisted selection by the breeding company Graminor in Norway.

1.3. Materials and methods

1.3.1. Spawn inoculation

In the field, the plants are infected by spawn infection. This method involves spreading fusarium infected oat grains in the field, which provide a natural and even infection pressure. 4 different isolates are used, 2 from the veterinary institute, and 2 from NIBIO (figure 6). They are named 23, 77, 140/08 and 28/08. The isolates are produced on PDA, which is then mixed with 1g oat flour and 100 ml ionized water (figure 7). 14 culture vials are put on a shaking machine for 7 days in room temperature. After that, each culture is mixed in bag of 2 kg oat grains, closed with cotton tops to allow air in, and contain the infection (figure 8). The grains are stored for 3 weeks at room temperature until sufficient mycelium is produced. After which the bags are transferred to trolleys in the greenhouse for another 3 weeks (figure 9), where they are being irrigated daily with water to stimulate development of peritechia.

Figure 6: Grain spawn isolates prepared for cultivation.(Jansen, 2015)

Figure 7: Vials containing oat flour (on the left) mixed with ionized water and cultivated for 7 days. (right)(Jansen, 2015)

Figure 8: Infected oat kernels stored for 3 weeks (left) with mycelium produced (right)(Jansen, 2015)

Figure 9: Two of the four isolates on trolleys with daily irrigation. (Jansen, 2015)

In the growing season, the infected oat seeds are scattered in the field with a density of 10 g/m^2. In 2014, the seeds were scattered with a density of 5 g/m^2. The soil should be moist before the grain dispersal in order to give optimal conditions for peritechia production and spread in the field. The time of infection should be at the second or third registered node, or Zadoks 32-33.

1.3.2. Field trials

The fusarium field at Vollebekk in 2015 is setup as an alpha-lattice with 40 columns and 12 rows separated into 2 replications. Within each rep there are 24 blocks with 10 lines in each. This setup is meant to correct for any differences in growth conditions in the field. Figure 10 shows how the field trial looked in 2014, with sprinkler that mist irrigates the field every night to ensure good growing conditions for the pathogen.

Figure 10: Fusarium field trial at Vollebekk 2014 (Jansen, 2015).

FHB data was collected by visual scoring at early yellowing stage, or Zadoks 80. The scoring was done by field technician Cecilie Yri, and myself were we scored one replication each. The scoring was done by grabbing 10 random heads in the field, counting the number of spiklets on 5 heads and multiply by 2. Then the number of infected spiklets were counted and divided by the total number of spiklets. This was done 2 times on each field square.

Days to heading and plant height is also registered in the fusarium testing field, while anther extrusion is scored in another field trial. Anther extrusion is scored by visual assessment, with a score between 0 and 9, where 0 is no anther extrusion, and 9 is full anther extrusion.

1.3.3. Statistics

The results from the field trials were used to calculate the least squared means (lsmeans), in order to correct for any differences in local field conditions like sun, topography, edge effect etc. The calculation was done in the statistical software SAS, by using a package called PROC MIXED. Line, Column, Row, Rep and Block nested in Rep is used as factors when calculating the lsmeans. The lsmeans for FHB and DON is then used in a regression along with DH and PH, in order to correct the phenotypic data for earliness and plant height, which have shown to have a large effect on fusarium head blight severity. For phenotype data over years, a package in SAS called POC GLM to find the lsmeans.

In the mixed linear model (MLM), which is run in the statistical software TASSEL, the lsmeans for each trait is used along with the residuals from the regression with PH and DH. A hapmap file with genotype data for each SNP marker in the MASBASIS lines is added to the MLM. A kinship model is made based on this genotype data, and together with the population structure, is used to correct the MLM for relationship between lines. The population structure included eight subpopulations, from Norway, Sweden, Europe, China and CIMMYT in spring wheat, and Norway, Europe and CIMMYT in winter wheat (Jansen, 2015).

1.3.4. Heritability

Heritability for each trait in 2015 and over years were calculated using one-way analysis of variance, and the following formulas:

$H = \sigma^2G / \sigma^2p$

$H = \sigma^2G / \sigma^2G + (\sigma^2e/r)$

$MSe = \sigma^2e$

$MSL = r\ \sigma^2G + \sigma^2e$

σ^2G = genetic variance

σ^2p = phenotypic variance

σ^2e = environmental variance

r = number of reps and number of years

The random factor for each year included line, rep and block nested in rep. For analysis of variance, year and line was used as random factors on lsmeans data, since these data has already been corrected for differences in the field like rep and block.

1.3.5. Correlations between traits

Correlations between traits were calculated using Minitab version 17, by including lsmeans data for traits are associated. The results are shown in a scatterplot with an R^2 value that describes the degree the traits are associated with each other. These correlations explains why we correct the MLM for traits that are associated with each other like PH and FHB.

1.3.6. Correlations between number of QTLs and trait

This correlation was calculated in Minitab version 17. First, the significant markers from the association mapping for each trait were studied. Markers for the same QTL were grouped together to find the total number for significant QTLs. The marker with the highest minor allele frequency from each QTL were selected. In the hapmap file with the genotype data, all lines were analyzed for each marker, and given a score of 1 for each favorable allele, and 0 for unfavorable allele. By adding the scores together, we find the number of QTLs from our association mapping each line in the population has. By grouping the lines together by the number of favorable alleles, and comparing the groups with their phenotypic values, we get a boxplot as seen in figure 15-17. This shows how the lines with a favorable composition of alleles tend to have better resistance for FHB and DON, and higher AE.

Chapter 2: Heritability and correlations

2.1. Heritability

Heritability is a statistical parameter used to estimate how much variation in a phenotypic trait in a population is due to genetic variation among individuals. The broad sense heritability include all sources of genetic variation, including additive effects, dominance, epistasis, and maternal and paternal effects. In contrast, narrow sense heritability only include the additive effects. However, both parameters include the environmental effect, and measurement errors on the phenotypic variation. Therefore, it is important to remember that heritability is only valid at that particular site, at that particular time. The importance of heritability is to estimate the response to selection. If the heritability is high, then selecting individuals with desired traits is worthwhile. If heritability is low, then perhaps environment has too much effect on the phenotype, so it would be better to try to optimize environmental conditions and measurement methods.

2.1.1.Spring wheat 2015

Figure 11 shows that spring wheat data from 2015 is close to normal distributed. DON and PH show a slightly right skewed distribution, and AE have a couple of high peaks to the right and left of the middle.

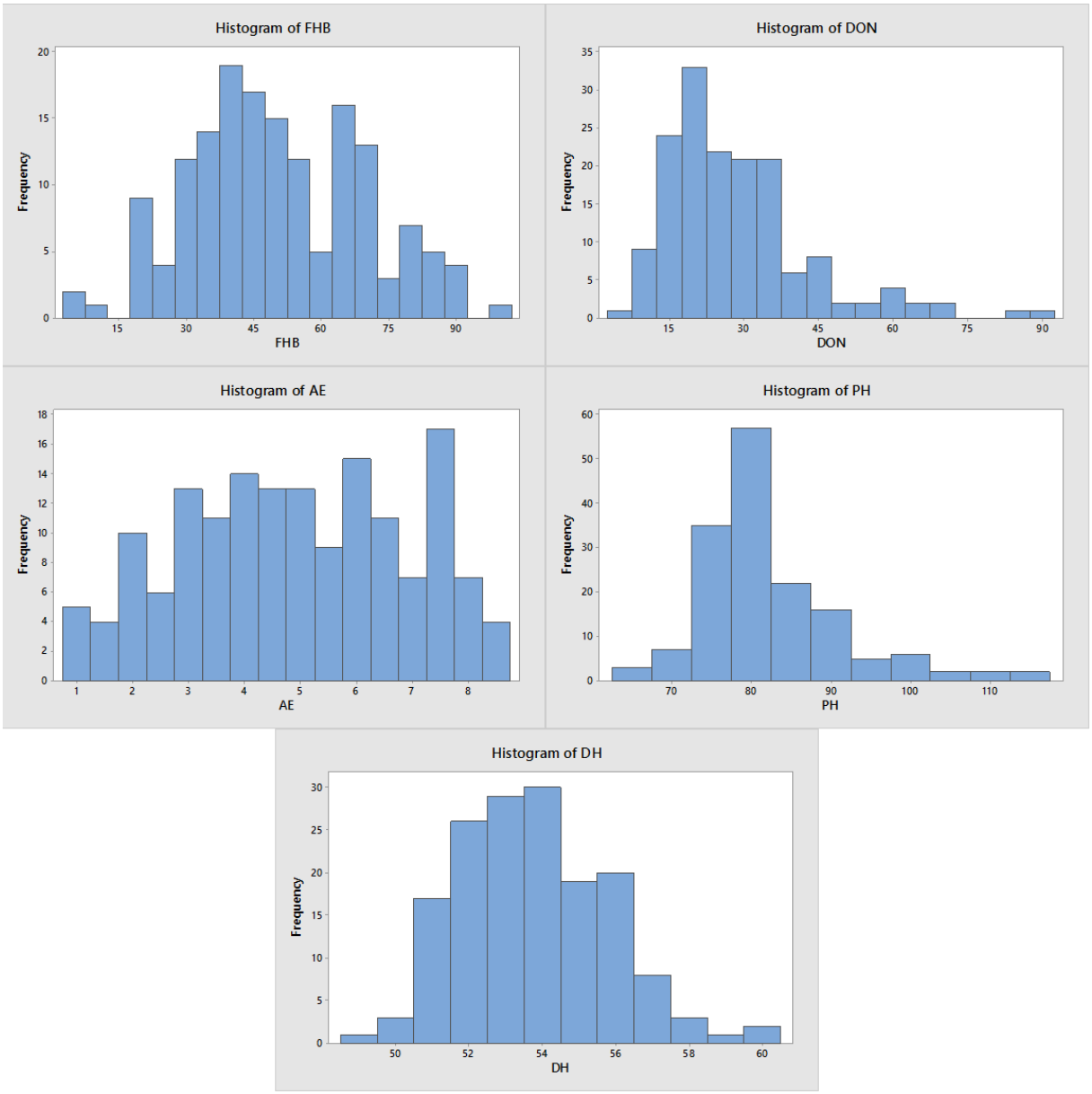

Figure 11: Histograms of phenotypic traits and frequencies of spring wheat in 2015

Table 3: ANOVA for FHB at Vollebekk in 2015

Source	DF	Adj SS	Adj MS	F-value	P-Value
Line	225	150695	669,8	4,12	0,000
Rep	1	899	898,9	1,91	0,179
Block(Rep)	46	15007	326,2	2,01	0,001
Error	207	33643	162,5		

Table 4: ANOVA for DH at Vollebekk in 2015

Source	DF	Adj SS	Adj MS	F-value	P-Value
Line	225	1494,29	6,64127	13,42	0,000
Rep	1	2,61	2,61305	1,22	0,278
Block(Rep)	46	63,03	1,37015	2,77	0,000
Error	207	102,41	0,49476		

Table 5: ANOVA for DON values at Vollebekk in 2015

Source	DF	Adj SS	Adj MS	F-value	P-Value
Line	225	77752	345,562	9,08	0,000
Rep	1	10	10,211	0,27	0,605
Block(Rep)	46	5979	129,988	3,41	0,000
Error	206	7842	38,067		

Table 3-5 show that Line is highly significant for DH, FHB and DON at Vollebekk in 2015, and has a large effect. Rep does not show significance, but Block nested in Rep show high significance, but not so high effect compared to line. This indicates that the alpha-lattice design helps correct for variation errors within reps, which then reduces the variation error in the field.

Table 6: ANOVA for PH at Staur in 2015

Source	DF	Adj SS	Adj MS	F-Value	P-Value
Line	174	21240,1	122,07	11,43	0,000
rep	1	114,3	113,29	10,70	0,001
block(rep)	68	1067,4	15,70	1,47	0,037
Error	106	1132,3	10,68		

Table 6 shows that line is very significant for PH at Staur in 2015 with a large effect. Rep also shows high significance and effect. Block nested in rep show far less effect, but still significant.

Table 7: ANOVA for FHB at Staur in 2015

Source	DF	Adj SS	Adj MS	F-Value	P-Value
Line	174	131864	757,8	3,93	0,000
rep	1	991	991,2	3,65	0,070
block(rep)	68	15785	232,1	1,20	0,195
Error	106	20454	193,0		

Table 7 shows that line is very significant for FHB at Staur in 2015 with a large effect. Rep also shows high significance and effect. Block nested in rep show far less effect, and is no significance

Table 8: ANOVA for DH at Staur in 2015

Source	DF	Adj SS	Adj MS	F-Value	P-Value
Line	174	3583,78	20,596	12,36	0,000
rep	1	31,50	31,500	5,62	0,023
block(rep)	68	247,38	3,638	2,18	0,000
Error	106	176,62	1,666		

Table 8 shows that line has a large effect and significance for DH at Staur in 2015. Rep and Block nested in rep also show significance, but has less effect.

Table 9: ANOVA for AE at Staur in 2015

Source	DF	Adj SS	Adj MS	F-Value	P-Value
Line	154	859,84	5,583	2,52	0,000
Rep	1	57,95	57,948	26,14	0,000
Error	174	385,77	2,217		

Table 9 shows that line and rep was very significant for both line and Rep for AE at Staur in 2015. But Rep had a larger effect that line. AE data were taken from a trial with a different field design that the others, so block is not included.

Table 10 shows how much of the phenotypic variation in spring wheat at Vollebekk and Staur in 2015 is due to genetic variation. DH and PH show a consistent high heritability (above 90%) for winter and spring wheat both in 2015, and over years(Table 10, 15, 19 and 23). FHB is over 10% lower in heritability than DON values. This difference is mainly due to errors in assessment, since DON is measured more accurately with LC-MS method in the lab while FHB is scored by visual assessments. Since different people score FHB between years, and within the same year, it is expected more errors. DON data are not as open to interpretation as FHB. AE shows the lowest heritability at 60%. This trait is largely affected by environmental factors and assessment errors.

Table 10: Broad sense heritability for spring wheat at Vollebekk and Staur in 2015

Trait and location	Broad sense heritability
DH Vollebekk	92%
FHB Vollebekk	75%
DON Vollebekk	88%
DH Staur	91%
PH Staur	91%
FHB Staur	74%
AE Staur	60%

2.1.2.Winter wheat 2015

Figure 12 shows that winter wheat data from 2015 have some non-normal tendencies. PH is closest to normal distributed. DH is a bit left skewed. AE and FHB have more than one peak along the x-axis.

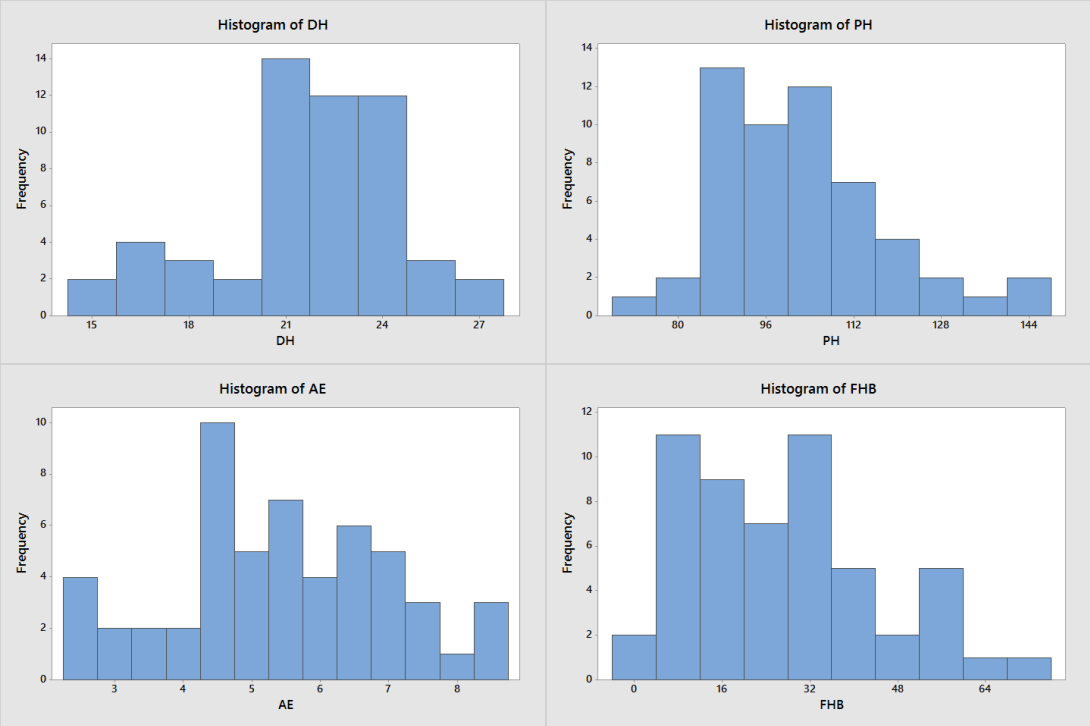

Figure 12: Histograms of phenotypic traits and frequencies of winter wheat in 2015

Table 11: ANOVA for DH at Vollebekk in 2015

Source	DF	Adj SS	Adj MS	F-Value	P-Value
Line	87	1288,34	14,8085	30,07	0,000
Rep	1	3,79	3,7931	8,98	0,049
Block(Rep)	14	6,36	0,4546	0,92	0,538
Error	89	43,83	0,4924		

Table 11 shows that Line is very significant for DH in winter wheat at Vollebekk in 2015. Line also shows a large effect. Rep shows less significance and effect that line, and Block nested in rep is not significant.

Table 12: ANOVA for PH at Vollebekk in 2015

Source	DF	Adj SS	Adj MS	F-Value	P-Value
Line	87	37518,9	431,25	31,63	0,000
Rep	1	19,2	19,18	1,06	0,349
Block(Rep)	14	224,6	16,04	1,18	0,307
Error	88	1199,7	13,63		

Table 13: ANOVA for AE at Vollebekk in 2015

Source	DF	Adj SS	Adj MS	F-Value	P-Value
Line	69	473,163	6,8574	7,13	0,000
Rep	2	0,906	0,4529	0,57	0,595
Block(Rep)	15	12,764	0,8509	0,88	0,583
Error	128	123,170	0,9623		

Table 12 and 13 shows that Line is highly significant for PH and AE at Vollebekk in 2015, and shows a large effect. Rep and Block nested in rep does not show significance.

Table 14: ANOVA for FHB at Vollebekk in 2015

Source	DF	Adj SS	Adj MS	F-Value	P-Value
Line	87	46217,5	531,236	5,60	0,000
Rep	1	4,0	4,042	0,01	0,930
Block(Rep)	14	4447,4	317,672	3,35	0,000
Error	86	8161,5	94.901		

Table 14 shows that line is highly significant for FHB at Vollebekk in 2015, and shows a large effect. Block nested in Rep is also significant, but has less effect. Rep does not show significance.

Table 15 shows how much of the phenotypic variation in winter wheat at Vollebekk in 2015 is due to genetic variation. All traits show very high heritability, with 86% for AE, 97% for PH, 96% for DH and 82% for FHB. AE showed a 26% higher heritability for winter wheat than spring wheat (Table 10). The scoring was done on two different locations, and by different people, which could mean that there is a larger environmental effect at Staur than Vollebekk, or that there is a difference in error during visual assessments. In addition, the lines used at the two sites were different, giving them different genetic backgrounds. FHB also showed higher heritability with 8% compared to spring wheat at Staur, and 7% to spring wheat at Vollebekk. One of the reasons for this could be, that there were two people who scored each rep in spring wheat at Vollebekk, while there were one who scored in winter wheat. The reason DH and PH had higher heritability in winter than spring (Table 10) wheat I believe is that winter wheat is less affected by environmental factors during the growth season. However, winter wheat is affected by winter conditions, which could increase the effects of environmental factors on winter wheat.

Table 15: Broad sense heritability for winter wheat at Vollebekk in 2015

Trait and location	Heritability
AE Vollebekk	86%
PH Vollebekk	97%
DH Vollebekk	96%
FHB Vollebekk	82%

2.1.3.Spring wheat 2013-2015

Figure 13 shows that the means spring wheat data from 2013-2015 are close to normally distributed. DON and PH have a slight right skewed tendency.

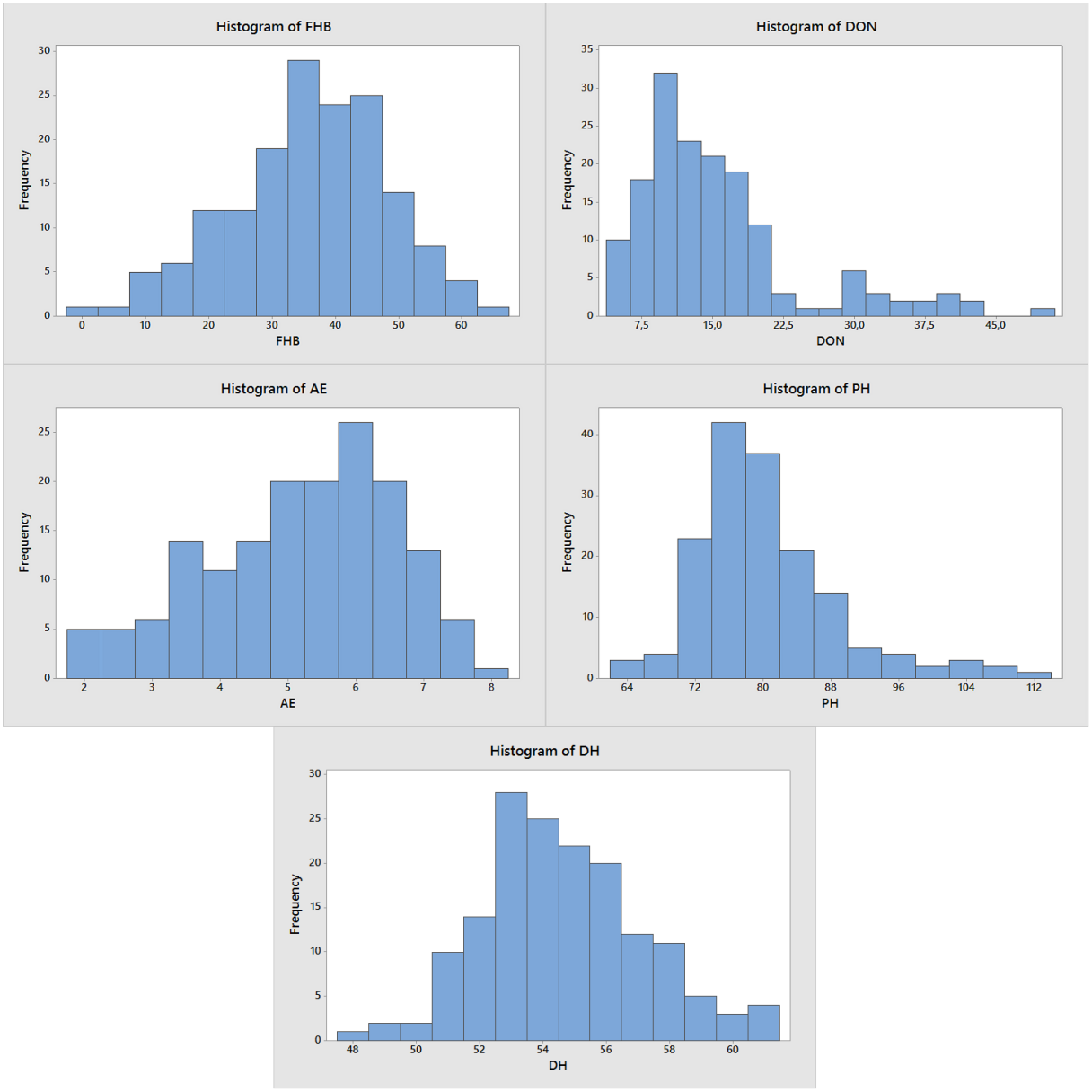

Figure 13: Histograms of phenotypic traits and frequencies of spring wheat in 2013-2015

Table 16: ANOVA for DH at Vollebekk in 2013-2015

Source	DF	Adj SS	Adj MS	F-Value	P-Value
Line	295	3772,5	12,788	8,86	0,000
Year	2	346,2	173,101	119,91	0,000
Error	370	534,1	1,444		

Table 17: ANOVA for FHB at Vollebekk in 2013-2015

Source	DF	Adj SS	Adj MS	F-Value	P-Value
Line	295	90974	308,4	1,88	0,000
Year	2	181293	90646,7	553,30	0,000
Error	370	60617	163,8		

Table 18: ANOVA for DON values at Vollebekk in 2013-2015

Source	DF	Adj SS	Adj MS	F-Value	P-Value
Line	295	47172	159,9	3,88	0,000
Year	2	52964	26482,1	642,41	0,000
Error	370	15253	41,2		

Table 16-18 shows that line and year is highly significant for DH, FHB and DON at Vollebekk in 2013-2015. However, year shows a much larger effect than line.

Table 19 shows how much of the variation in the field between 2013 and 2015 in spring wheat can be explained by genetic variation. The remaining percentage includes environmental conditions, error in assessment of the trait, and other errors. DH showed the highest heritability with 88%, while FHB and DON showed 46% and 74% respectively. This difference is mainly due to errors in assessment.

Table 19: Broad sense heritability for spring wheat at Vollebekk in 2013-2015

Trait and location	Heritability
DH Vollebekk	88%
FHB Vollebekk	46%
DON Vollebekk	74%

2.1.4.Winter wheat 2014-2015

Figure 14 shows that the means winter wheat data from 2014-2015 are mostly non-normal distributed except for AE. DH show a left skewed data. PH have two high peaks in the middle and to the left. FHB is also non-normal with a high flat area in the middle of the dataset.

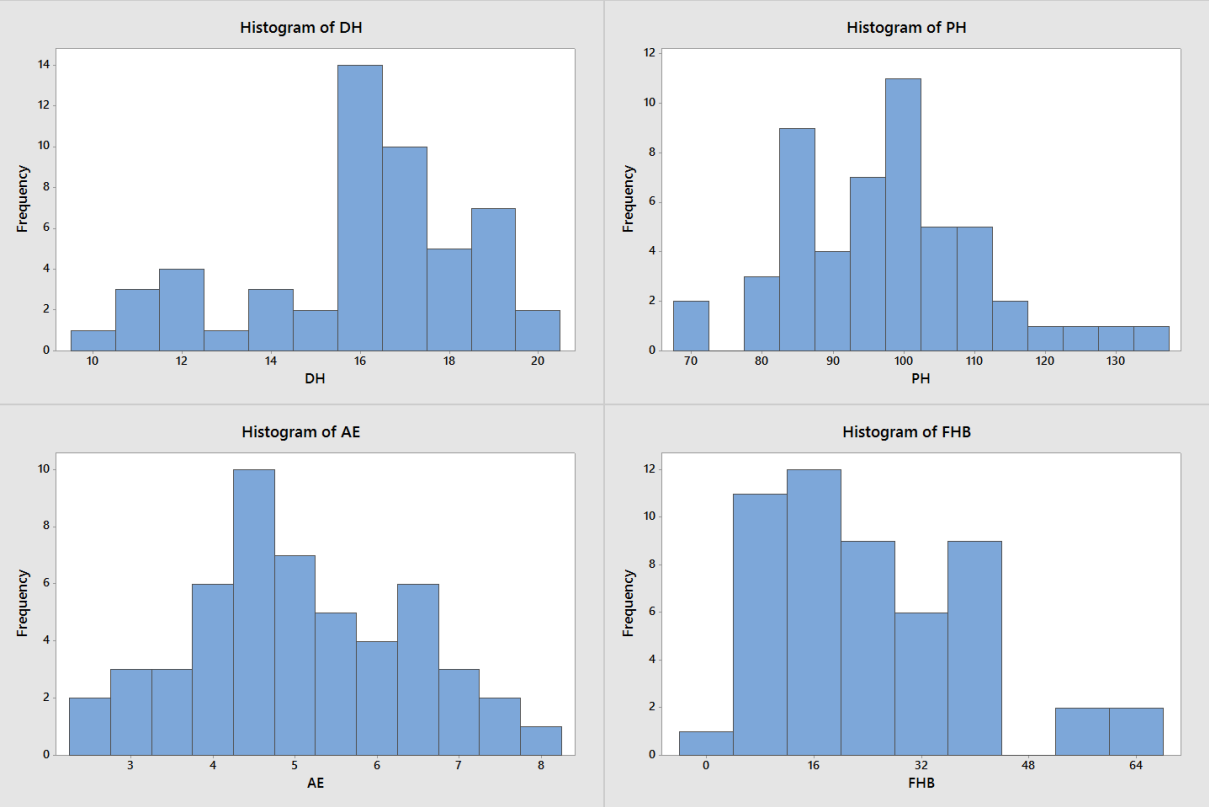

Figure 14: Histograms of phenotypic traits and frequencies of winter wheat in 2014-2015

Table 20: ANOVA for DH at Vollebekk in 2014-2015

Source	DF	Adj SS	Adj MS	F-Value	P-Value
Line	65	816,03	12,55	12,94	0,000
Year	1	3750,39	3750,39	3865,47	0,000
Error	55	53,36	0,97		

Table 21: ANOVA for PH at Vollebekk in 2014-2015

Source	DF	Adj SS	Adj MS	F-Value	P-Value
Line	65	29676	456,56	21,47	0,000
Year	1	3759	3759,22	176,74	0,000
Error	55	1170	21,27		

Table 22: ANOVA for FHB at Vollebekk in 2014-2015

Source	DF	Adj SS	Adj MS	F-Value	P-Value
Line	65	32259,2	496,29	5,27	0,000
Year	1	581,4	581,4	6,18	0,016
Error	54	5083,8	94,14		

Table 20-22 shows that line and year is highly significant for PH, DH and FHB in winter wheat at Vollebekk in 2014-2015. Year shows the largest effect in all cases, but has much larger effect for DH (F-value = 3865,47) compared to FHB (F-Value = 6,18)

Table 23 shows how much of the variation in the field between 2014 and 2015 in winter wheat can be explained by genetic variation. DH and PH show as expected a high heritability. This is mainly due to the small environmental effect on the trait, and that it is easy to assess. Plant height leaves no room for interpretation, as FHB does. FHB show a relatively high heritability compared to spring wheat in 2015(table 10) and spring wheat over years(table 19). It is however more or less the same as winter wheat in 2015(Table 15). This indicates that either does the environment have less effect on FHB in winter wheat, or there are less errors during assessment, or that there is a larger genetic variation in winter wheat than in spring wheat.

Table 23: Broad sense heritability for winter wheat at Vollebekk in 2014-2015

Trait and location	Heritability
DH	92%
PH	95%
FHB	81%

2.2. Correlation between trait and number of QTL

By studying the chromosome position of the significant markers from the association mapping, we can find how many QTL our mapping revealed. Then, the number of favorable allele for each QTL was found for each line in old MASBASIS. The lines were grouped together in number of QTLs, and compared with their mean phenotypic value from 2013-2015. The results are shown in figure 15-17. Since the QTLs that were found are based on the population they are compared with, it is not surprising that an increased number of favorable alleles increases anther extrusion and reduces DON and FHB values. Different QTLs also have different effects on the trait. But this test does show that the QTLs found in the AM have an effect, and largely show an additive effect. There is no apparent improvement in resistance from combining the favorable alleles of more than 13 QTL.

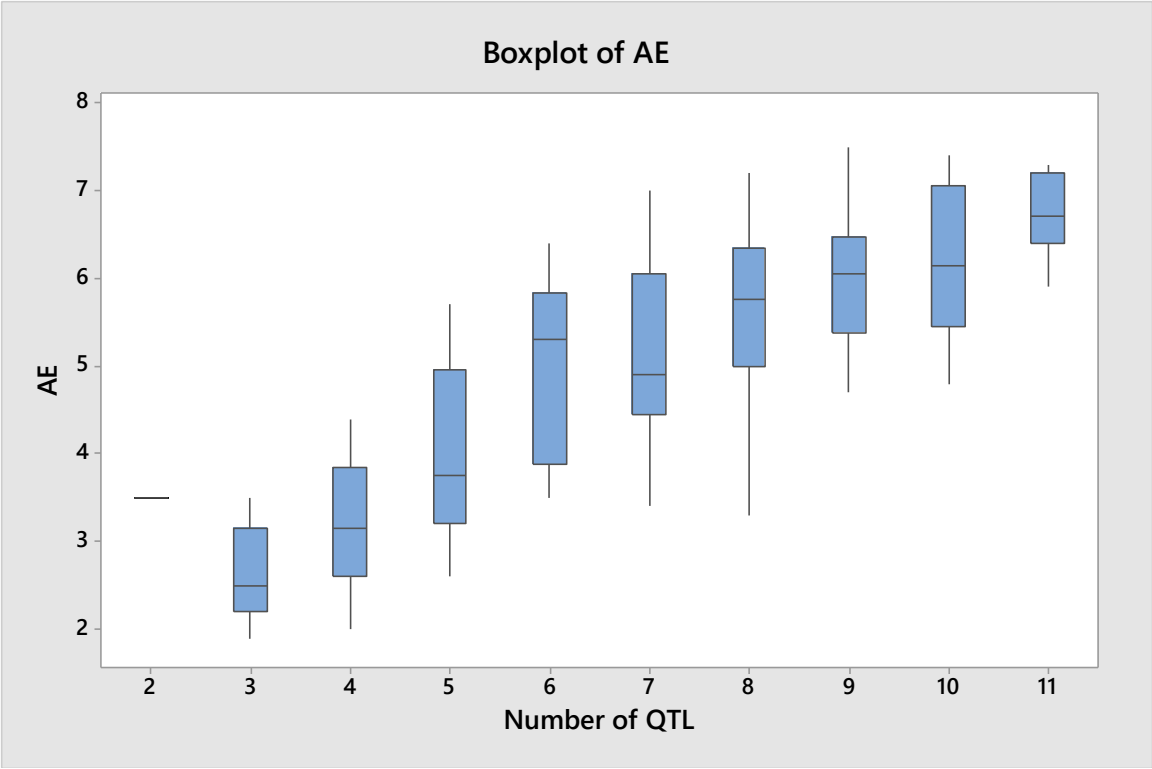

Figure 15: Shows AE scores on the Y-axis, and number of QTL on X-axis based on association mapping from 2013-2015.

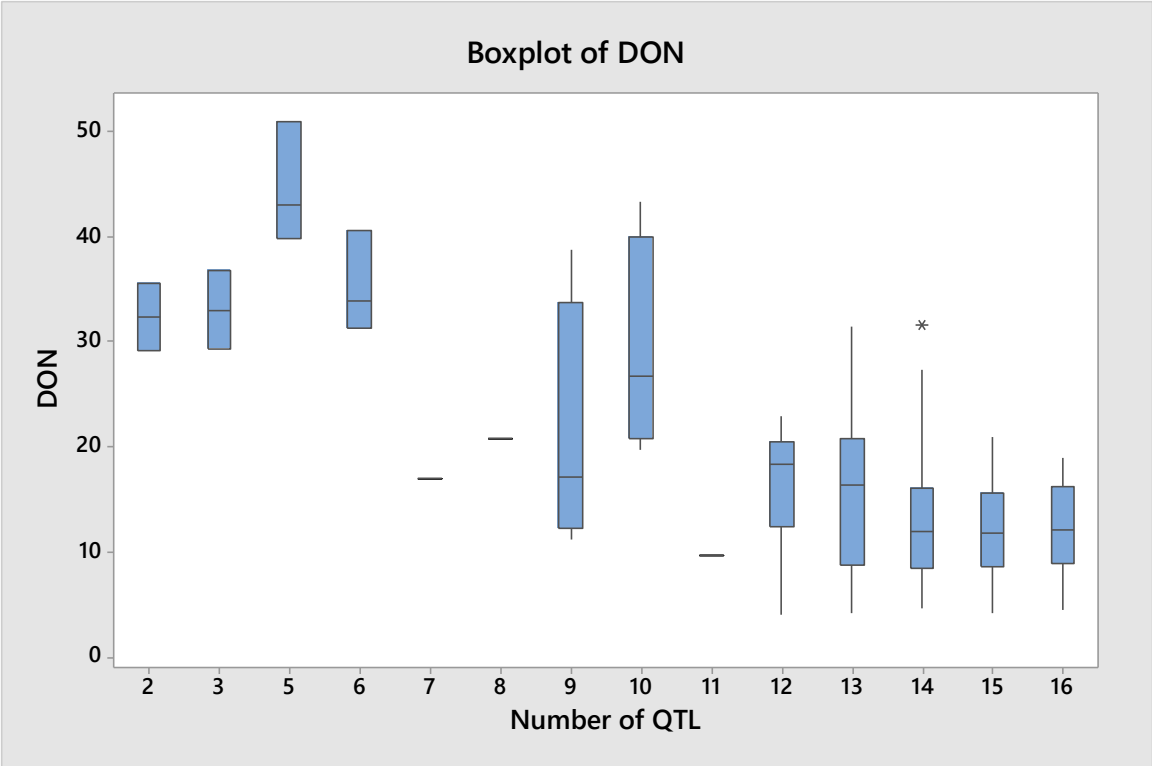

Figure 16: Shows DON values on the Y-axis, and number of QTL on X-axis, based on association mapping from 2013-2015.

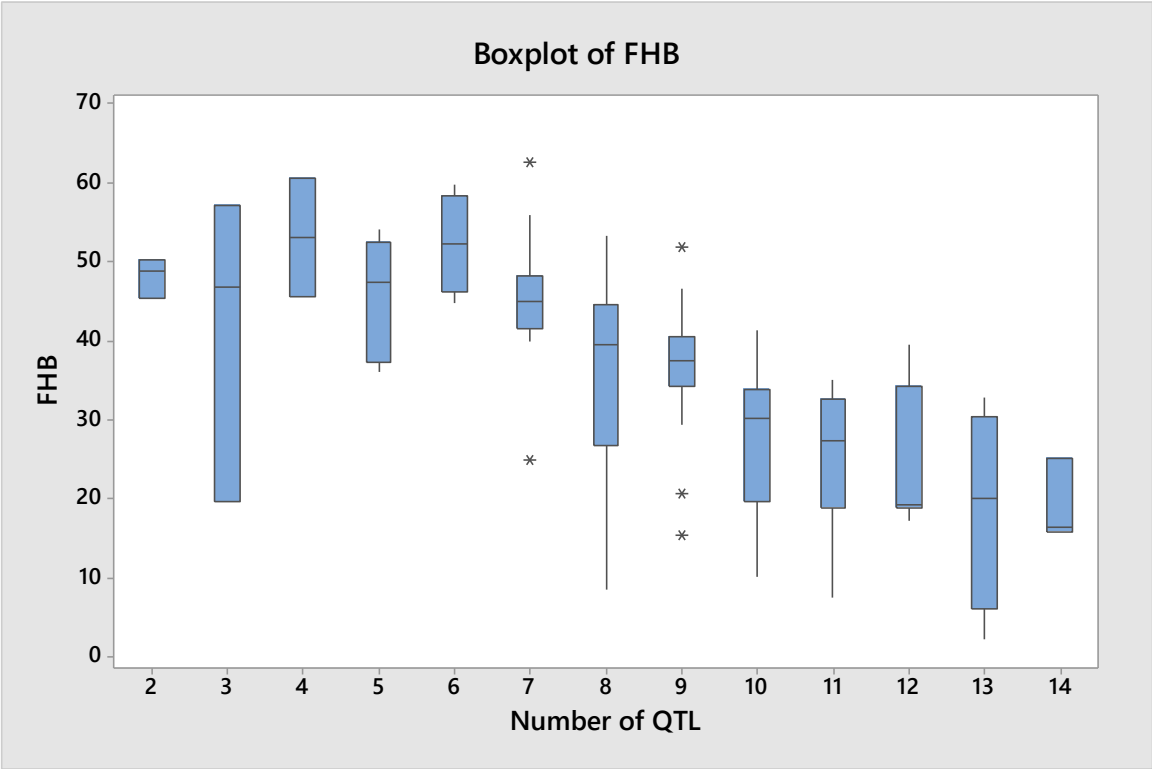

Figure 17: Shows FHB scores on the Y-axis, and number of QTL on X-axis based on association mapping from 2013-2015.

2.3. Correlations between traits

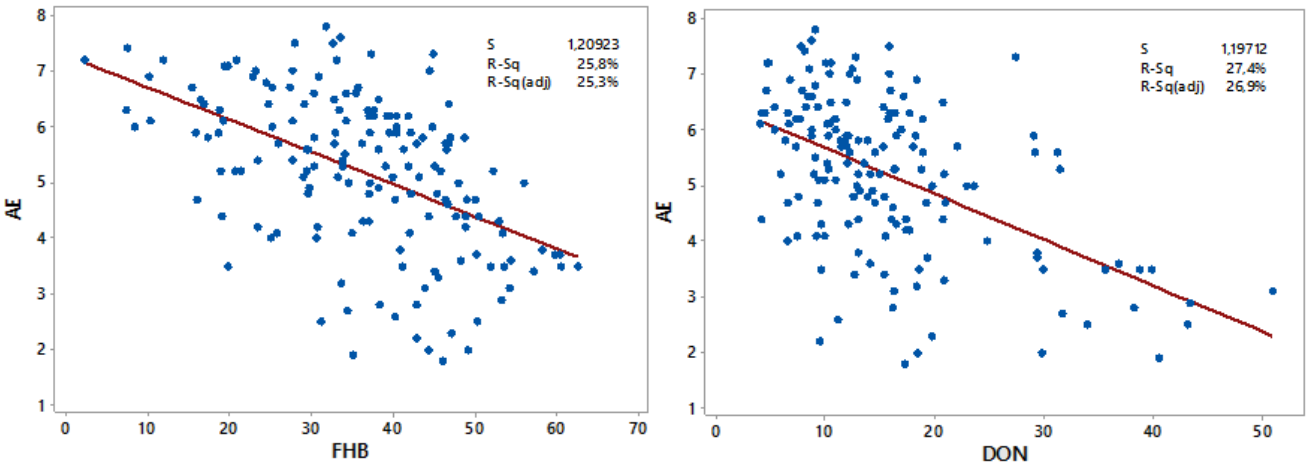

Figure 18: Correlation between AE and FHB and DON over years

Figure 18 shows how anther extrusion affects severity of fusarium head blight and DON accumulation. These data are mean values from 2013-2015. There is a clear trend that high anther extrusion is correlated with low fusarium infection, and low DON values. The data for

DON values are more clustered together, so if we focus on the area between 4 and 8 AE, we see no clear pattern. The FHB data are more evenly spread, giving stronger indication of this negative correlation between AE and FHB.

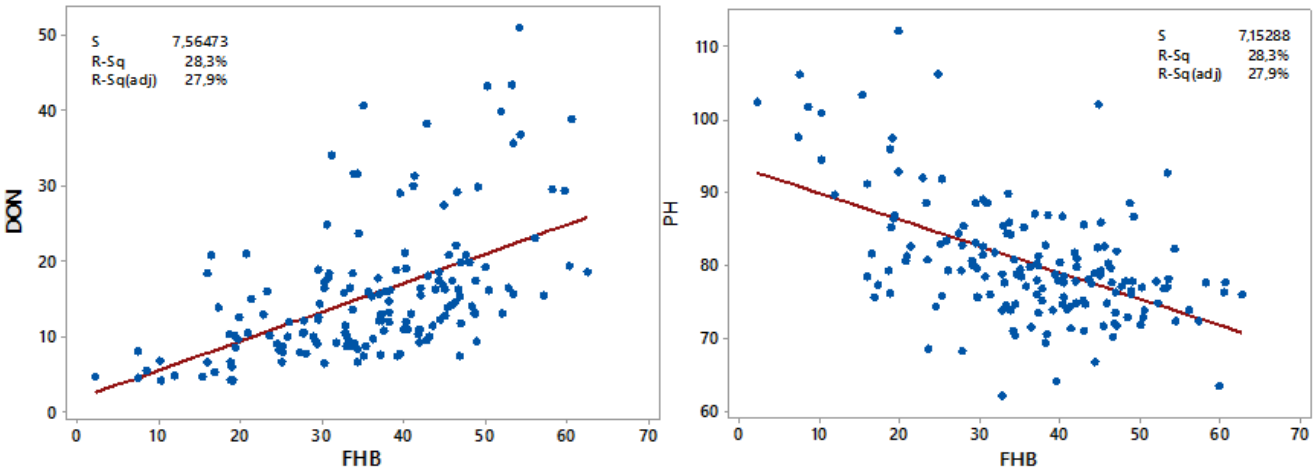

Figure 19: Correlation between FHB and DON and PH

Figure 19 shows that there is a general trend that higher FHB infection gives high DON values, and that taller plants have less FHB infection that shorter plants.

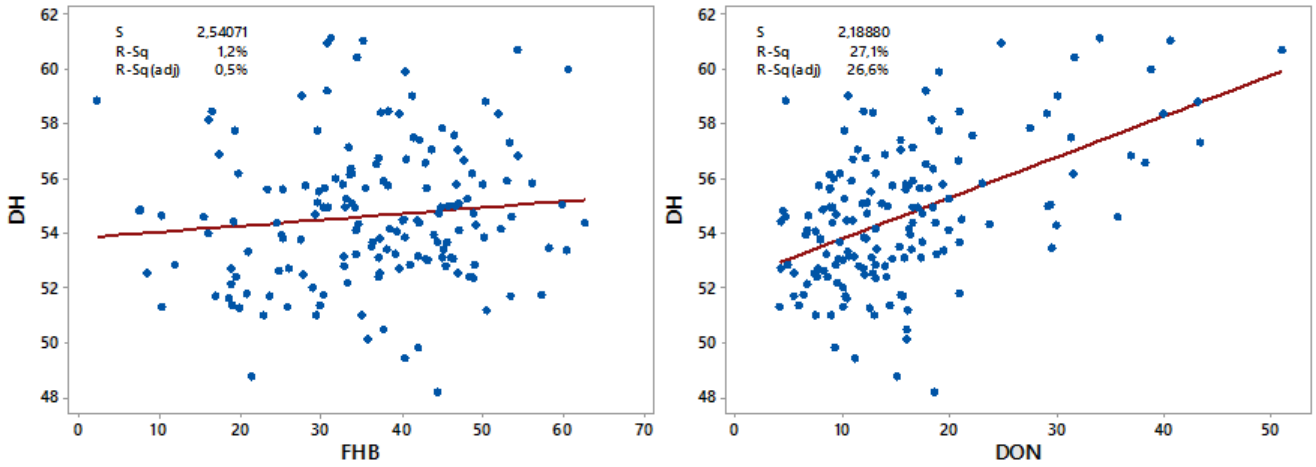

Figure 20: Correlation between DH and FHB and DON

Figure 20 shows no clear trend DH being correlated with FHB infection, but there is a small trend that plants that flower late has higher DON values then plants that flower early. But if we focus on the area of DON under 20, the trend is less clear.

Chapter 3: Association mapping

Phenotypic data from 2015 and 2013-2015 include DH, PH, AE, FHB, DON and residuals from a regression between FHB, and DH and PH, and between DON, and DH and PH. The regression was done to prevent the effect of DH and PH on marker significance of FHB. The genotypic data include 22 031 SNP markers from a 90K SNP chip. In the mixed linear model, phenotypic data, genotypic data, a kinship matrix based on the genotypic data, and population structure are included. The Manhatten plots in figure 27-52 shows each markers -10log p-value on the Y-axis, and the markers in correspondence to their chromosome and position on the X-axis. A threshold for significant markers is set somewhere between 2 and 3 based on when the p-value starts to deviate from the normal distribution. When the p-value deviates in the MLM over years and in 2015 is shown in figure 21-24. In addition to the QQ-plots, the threshold is set by looking at the Manhatten plots from the MLM and finding the most significant chromosomes. The threshold is then set so that these chromosomes have at least on marker included. Since DON data from 2015 were not initially included in the mean data set, a different MLM results were first presented for DON and DON_reg in figure 41 and 42 with a threshold of 3,0. After including data from 2015 in figure 39 and 40, the threshold were lowered to 2,5. Figure 25 and 26 show how the p-value deviates differently in the two MLM results. In figure 25 we see that the p-values start to deviate at 2,5 and have a generally low deviation from the normal distribution. In order to capture all the significant markers the threshold were set to 2,5. In figure 26 we see that the p-values start to deviate at 2,0 and have a generally high deviation from the normal distribution. In order to only capture the truly significant markers, and reduce the amount of markers with false significance, we set the threshold to 3,0 based on the Manhatten plot in figure 42.

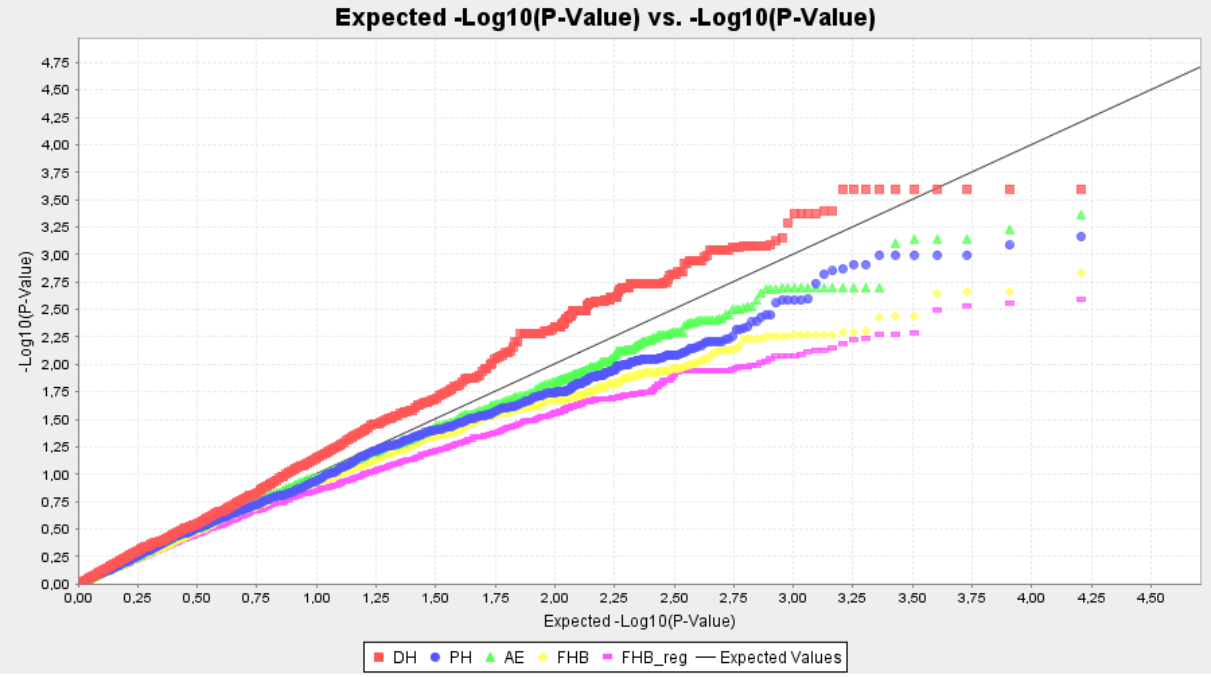

Figure 21: QQ-plot of p-values in the mixed linear model with phenotypic data from 2015 in winter wheat

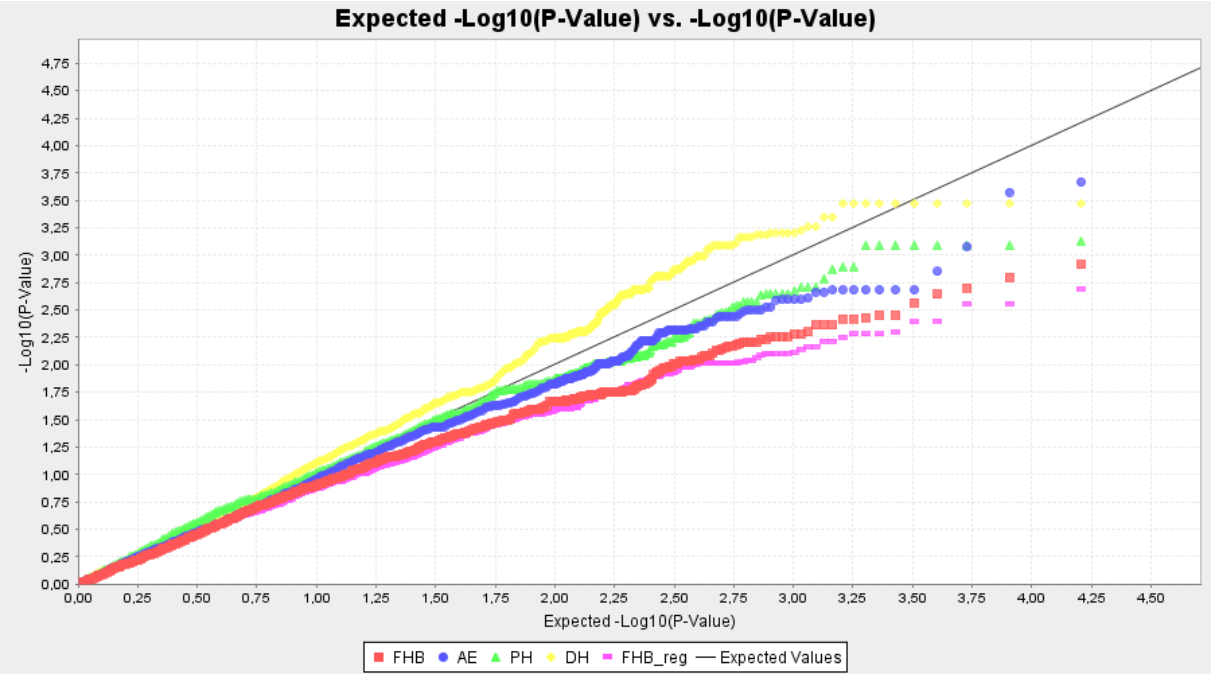

Figure 22: QQ-plot of p-values in the mixed linear model with phenotypic data over years in winter wheat

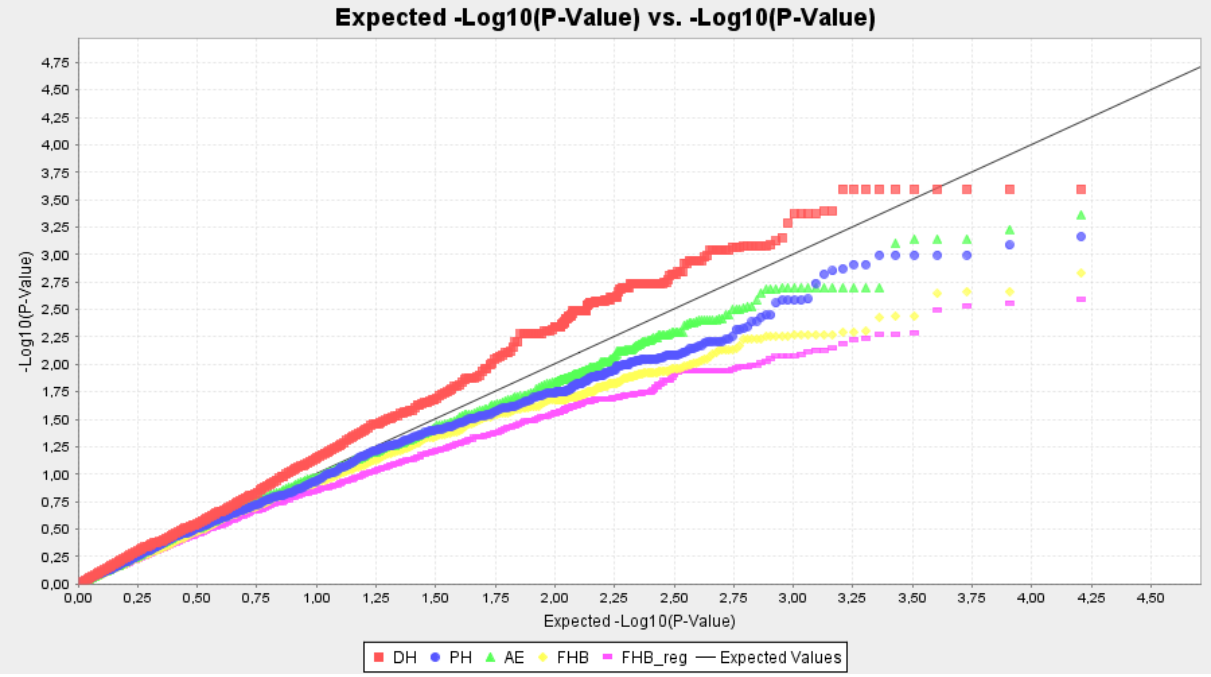

Figure 23: QQ-plot of p-values in the mixed linear model with phenotypic data from 2015 in spring wheat

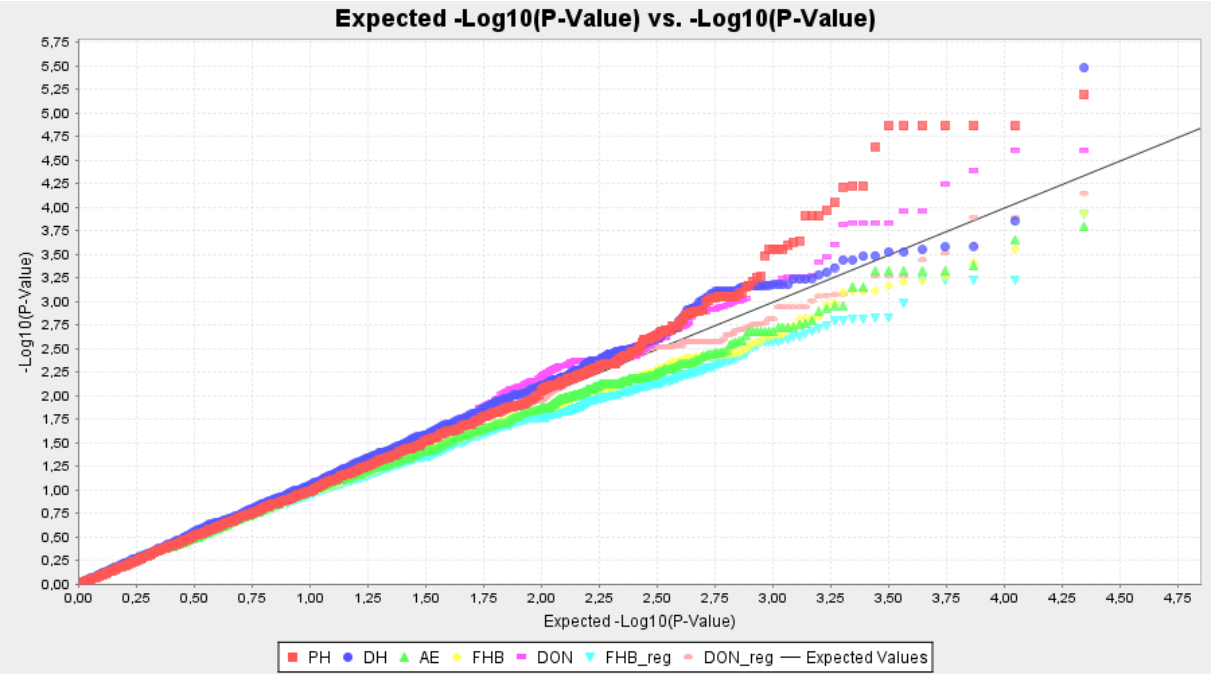

Figure 24: QQ-plot of p-values in the mixed linear model with phenotypic data over years in spring wheat

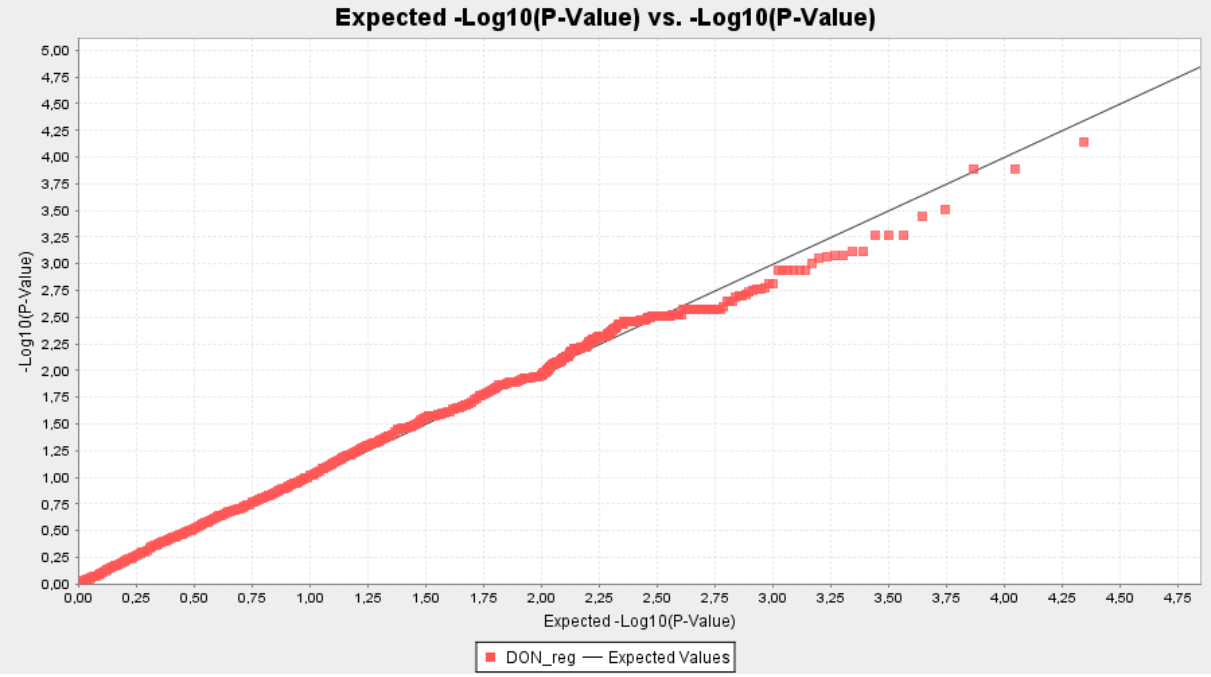

Figure 25: QQ-plot of p-values for DON_reg in the mixed linear model with phenotypic data from 2013-2015 in spring wheat.

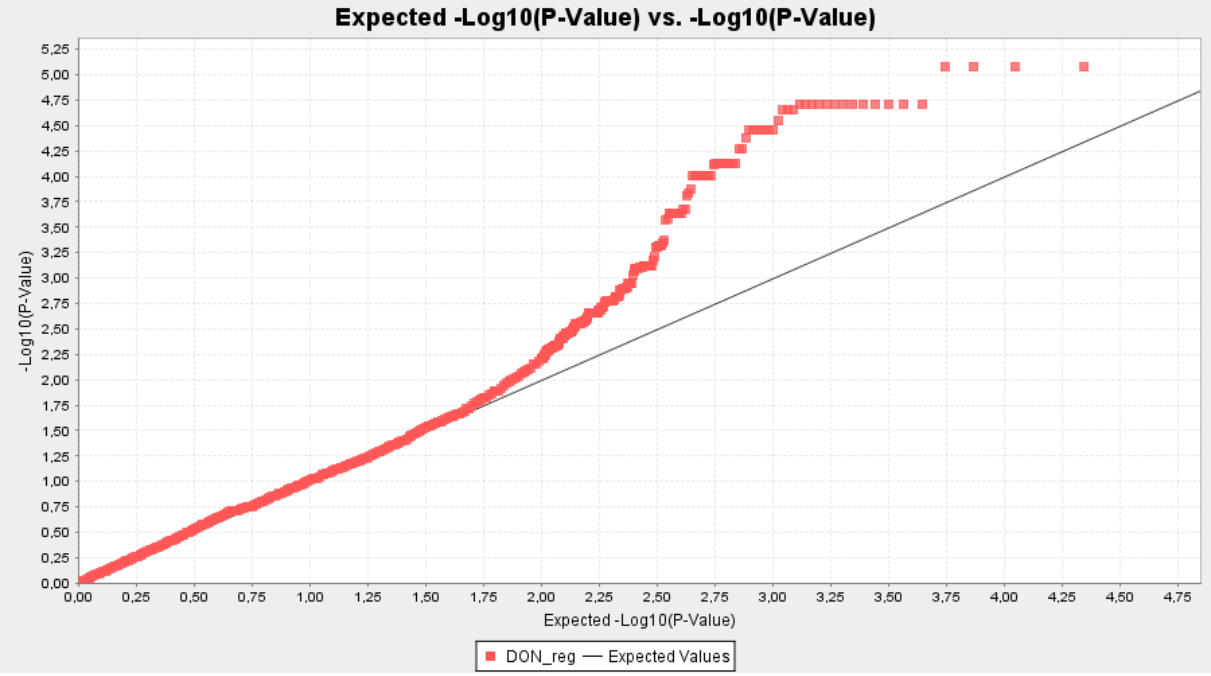

Figure 26: QQ-plot of p-values for DON_reg in the mixed linear model with phenotypic data from 2013-2014 in spring wheat.

The point of the threshold is to capture the significant markers, without including too many markers with false significance.

The least squared mean of all traits from 2013 to 2015 were used in a mixed linear model, and showed several significant markers for FHB, AE and DON. A complete list of significant markers are showed in Appendix 1 and 2.

3.1. Association mapping of spring wheat

3.1.1. 2015

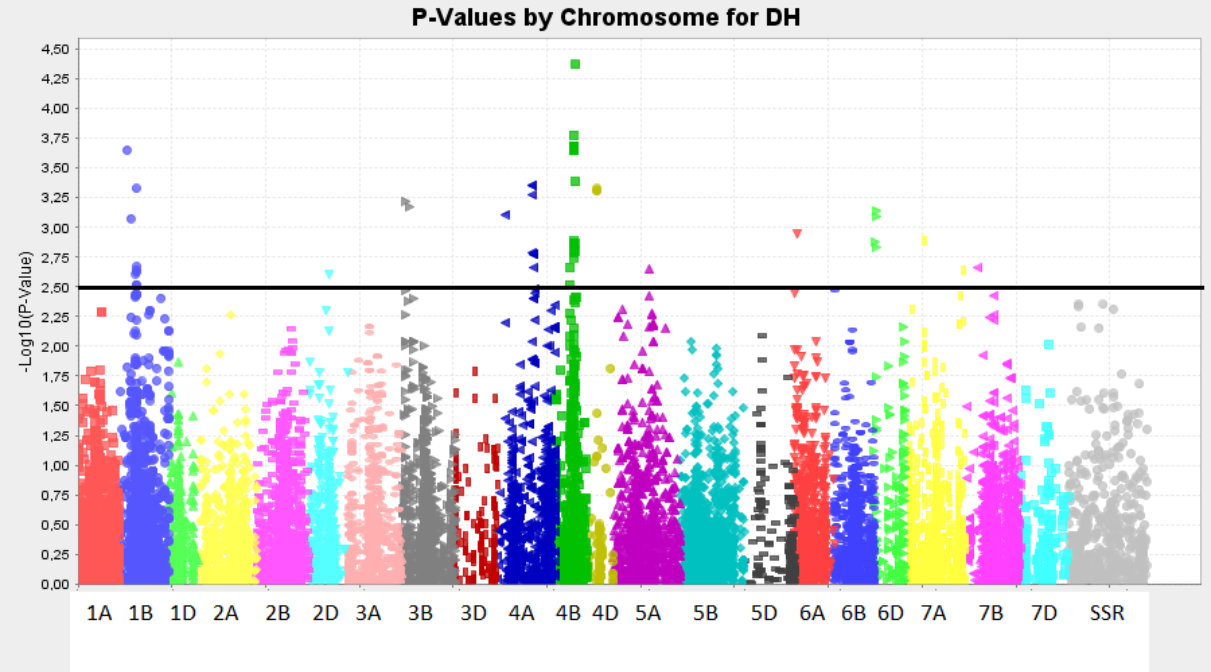

Figure 27: Manhatten plot displaying the markers for earliness (DH) in spring wheat in 2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log(P-value) of 2,5

Data from DH in 2015 shows a significant areas on 1BS, 2D, 3BS, on 4A, 4B, 4D, 5A, 6A, on the short arm of 6DS, 7A and 7B. Many of these are barely above the threshold. The ones that stand out as most important are 1BS, 3BS, 4A, 4B, 4D and 6D. The marker Rht-B1 which is the functional marker of the gibberellin insensitive dwarf gene *Rht-B1* on 4B was highly significant (Worland & Snape, 2001).

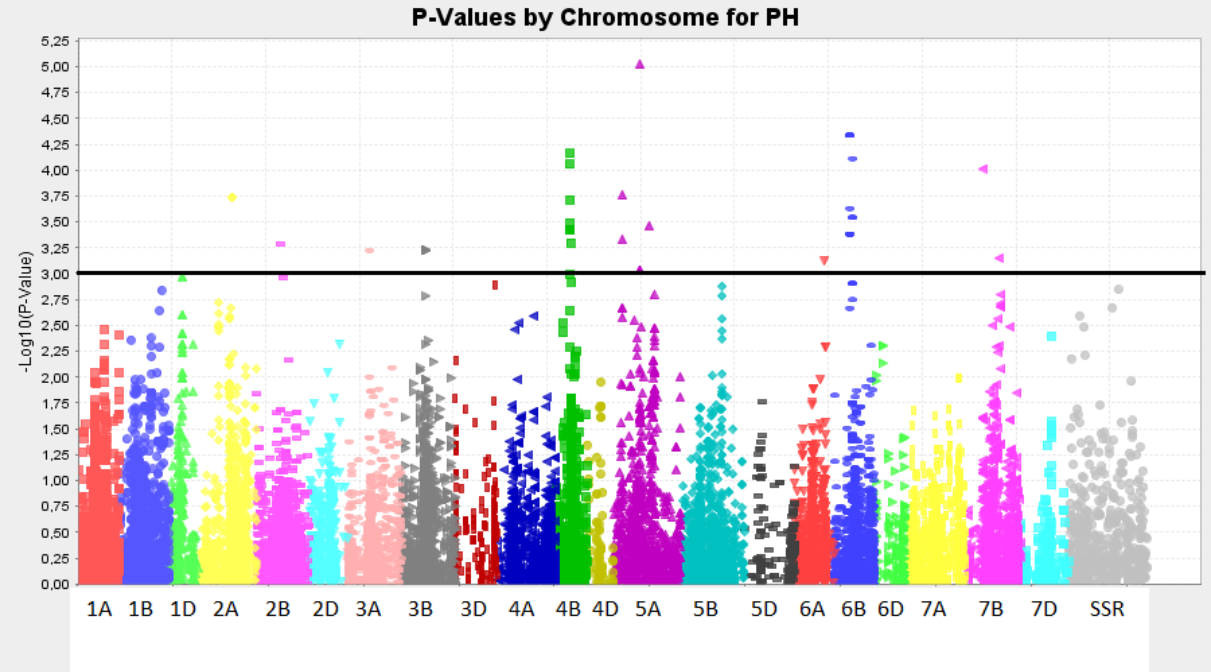

Figure 28: Manhatten plot displaying the markers for plant (PH) in spring wheat in 2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log(P-value) of 3,0

Data from PH in 2015 shows a significant areas on 2A, 2B, 3A, 3B, 4B, 4D, 6A, 6B and 7B. Of these 2A, 4B, 4D, 6B and 7B stand out as most significant. Rht-1B was once again highly significant, as expected when testing for plant height.

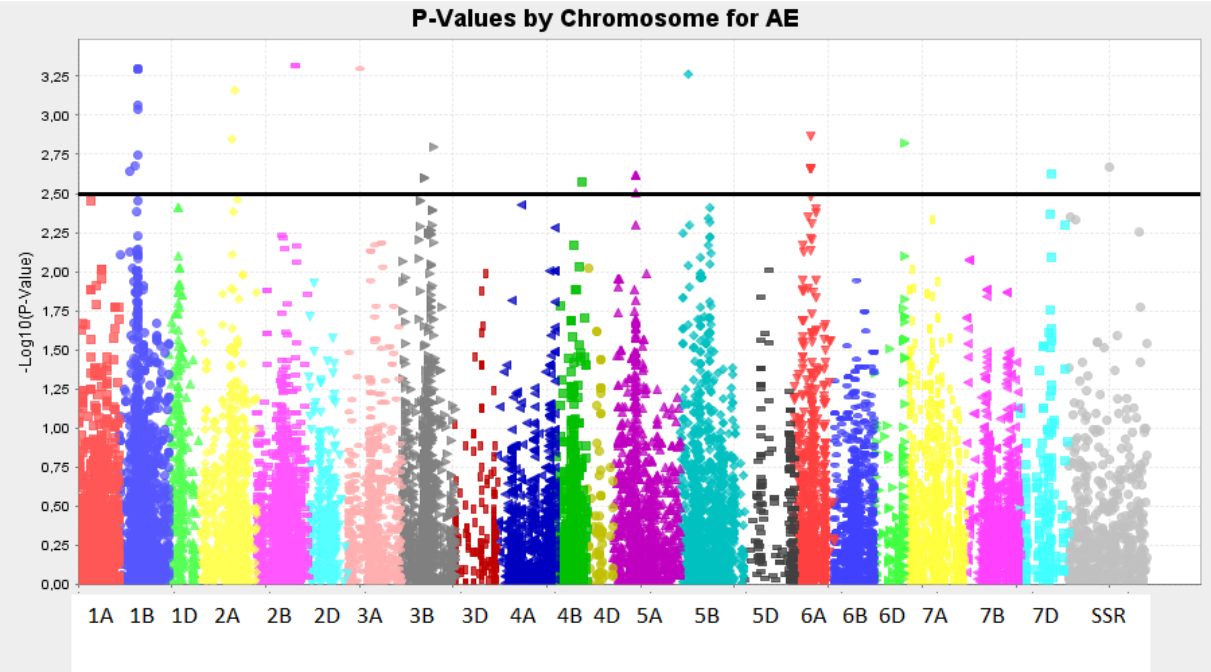

Figure 29: Manhatten plot displaying the markers for anther extrusion (AE) in spring wheat in 2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log(P-value) of 2,5

Data from AE in 2015 shows significant areas on 1BS, 2B, 3A, 3B, 4B, 5A, 5B, 6A, 7A and 7D. Of these the most significant areas are 1BS, 3A, 3B, and 5B. One SSR marker gwm320_275 was also significant.

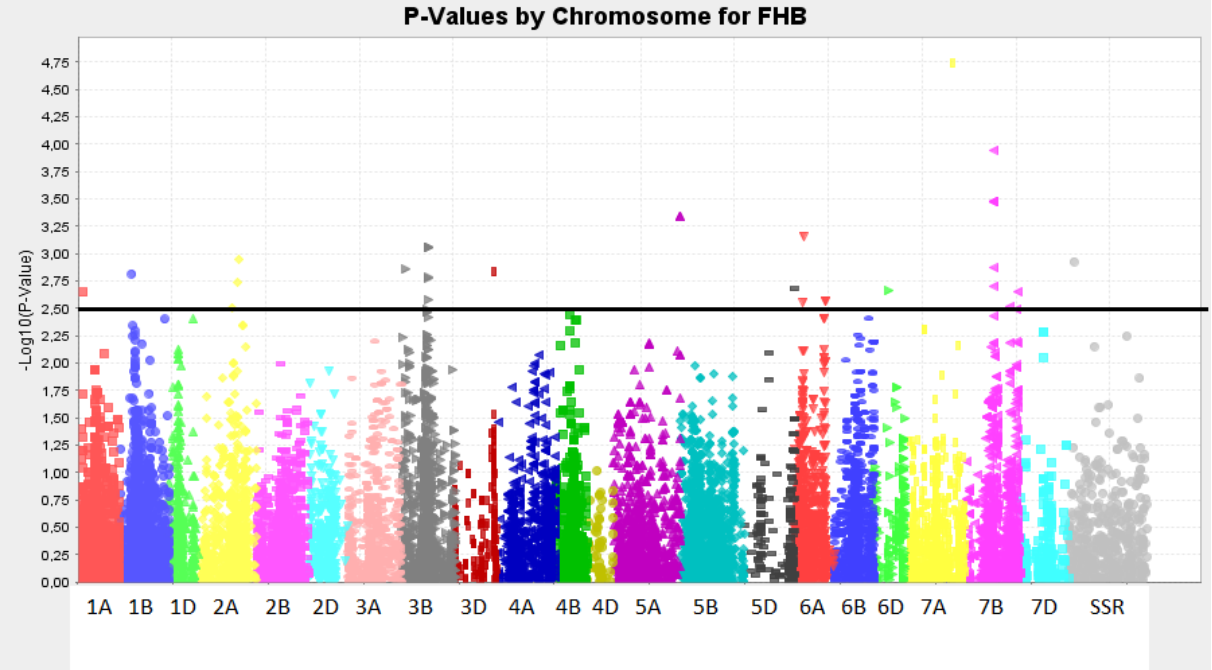

Figure 30: Manhatten plot displaying the markers for Fusarium head blight (FHB) in spring wheat in 2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log(P-value) of 2,5

Data from FHB in 2015 shows significant areas on 1A, 1BS, 2A, 3B, 3D, 5AL, 5DL, 6A, 6D and 7B. One SSR marker barc228_194 was also significant. The most interesting of these areas are 3B, 5A, 6A, and 7B.

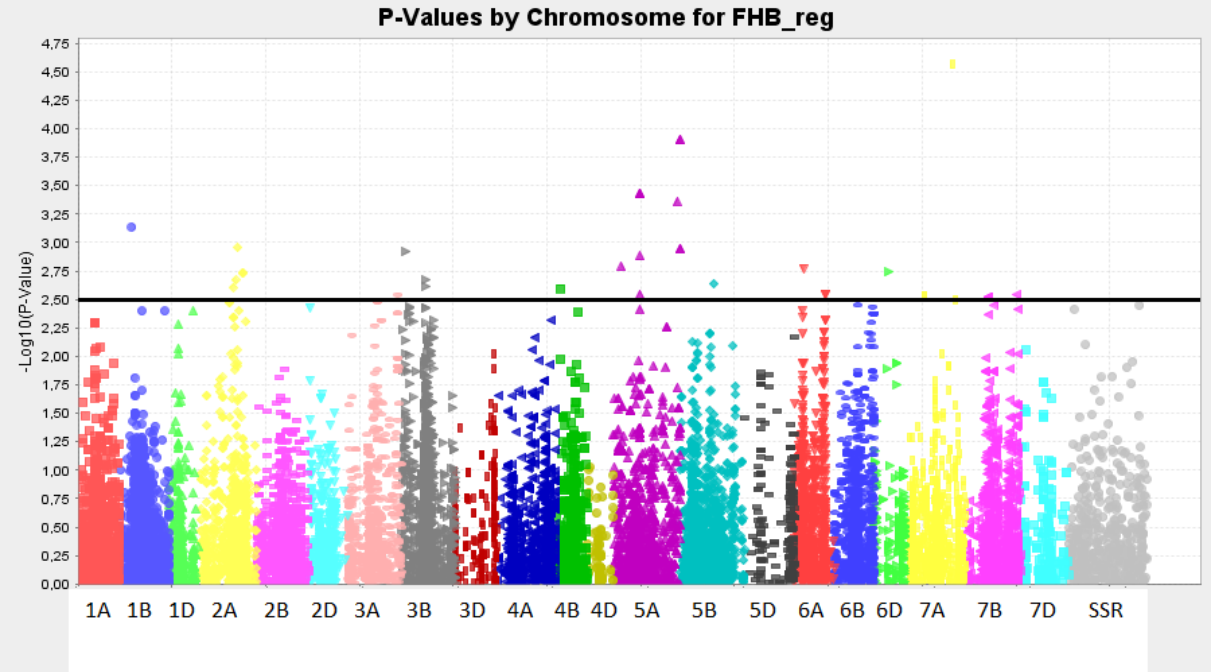

Figure 31: Manhatten plot displaying the markers for Fusarium head blight after regression (FHB_reg) in spring wheat in 2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log(P-value) of 2,5

Data from FHB in 2015 after regression shows significant areas on 1BS, 2A, 3B, 4B, 5A, 5B, 6A, 6D, 7A, and 7B. The most interesting of these areas are 1BS, 3B, 5A and 7A. Worth noticing is that the markers on 7B that were significant for FHB and PH around position 300, has dropped below the threshold line after regression. We would however, except the Rht-B1 marker on 4B to have an effect on FHB, and its effect to be reduced after regression.

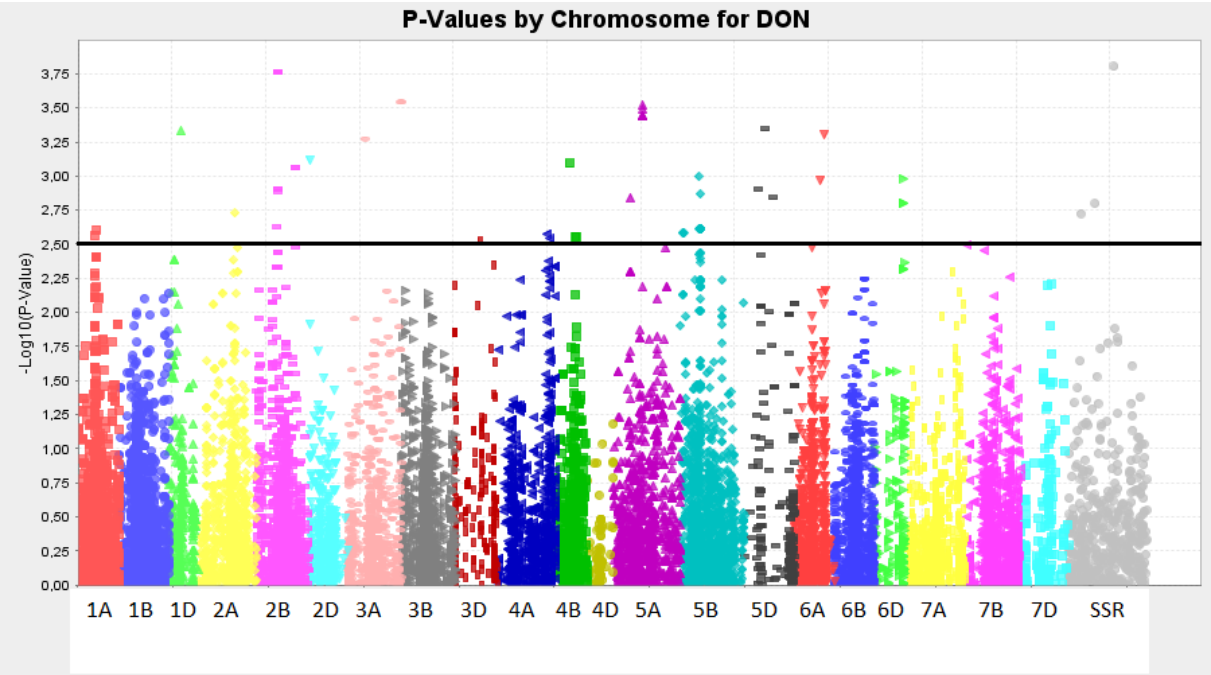

Figure 32: Manhatten plot displaying the markers for DON values (DON) in spring wheat in 2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log(P-value) of 2,75

Data from DON in 2015 shows significant areas on 1D, 2B, 2D, 3A, 4B, 5A, 5B, 5D, 6A and 6D. Two SSR markers, gwm410_372 and gwm148_184 were also significant. The significant marker on 4B is the dwarf gene Rht-B1. As expected, height is strongly correlated with Fusarium symptoms.

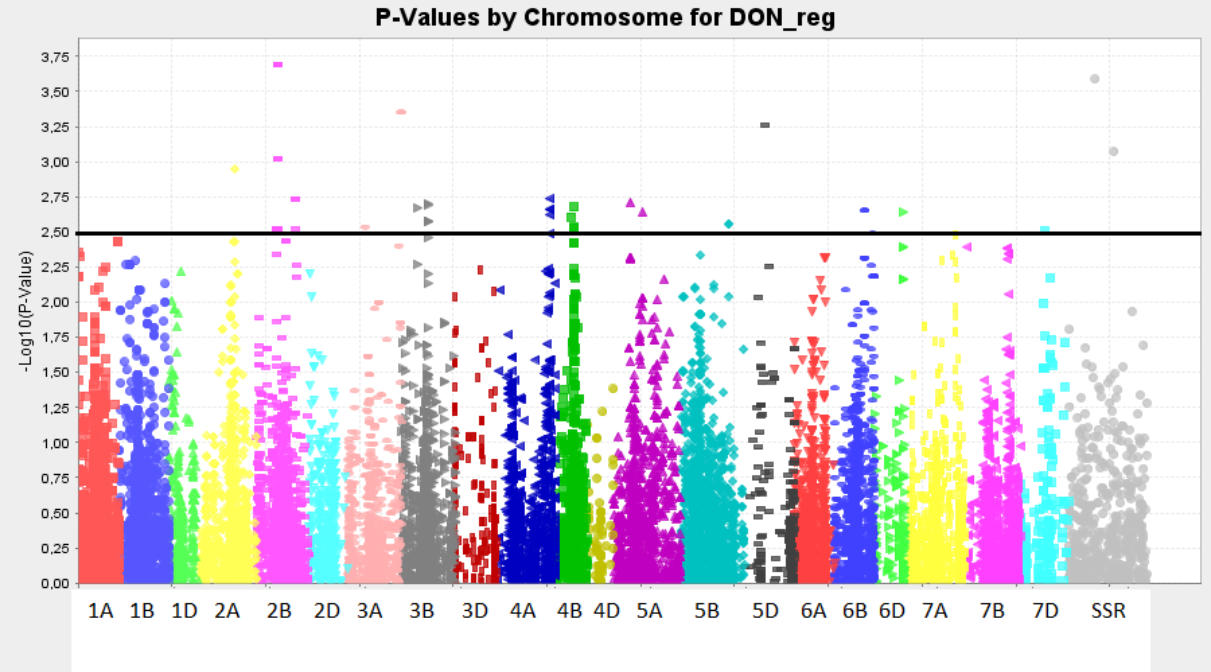

Figure 33: Manhatten plot displaying the markers for DON values after regression (DON_reg) in spring wheat in 2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log(P-value) of 2,75

Data from DON in 2015 after regression shows significant areas on 2A, 2B, 3A and 5D. Two SSR markers, gwm410_372 and gwm148_184 were significant 2BS. The SSR markers were also significant before regression. All areas except for 2A were significant before regression. Areas that are no longer significant include 1D, 2D, 4B 5A, 5B, 6A and 6D. Since Rht-1B is included in these areas we can presume that the others also has some effect on DH and PH.

3.1.2. 2013-2015

Another mixed linear model was run based on mean data from 2013, 2014 and 2015. Significant markers were selected from AE, FHB_reg and DON_reg for further genotyping on new MASBASIS, and development of new KASP-markers. Markers were selected based on chromosome and position, in order to capture as many significant QTLs as possible. For each QTL a maximum of 3 markers were chosen, in case some markers did not work during genotyping. Lastly, some significant QTL for each trait were not included due to limited time for genotyping. Markers for DON_reg were selected based on mean data from 2013 and 2014, since data from 2015 was not ready until May 2016. A complete list of significant markers and their values is provided in table 31-48 in Appendix 1 and 2. The markers selected for genotyping are presented in table 24-26.

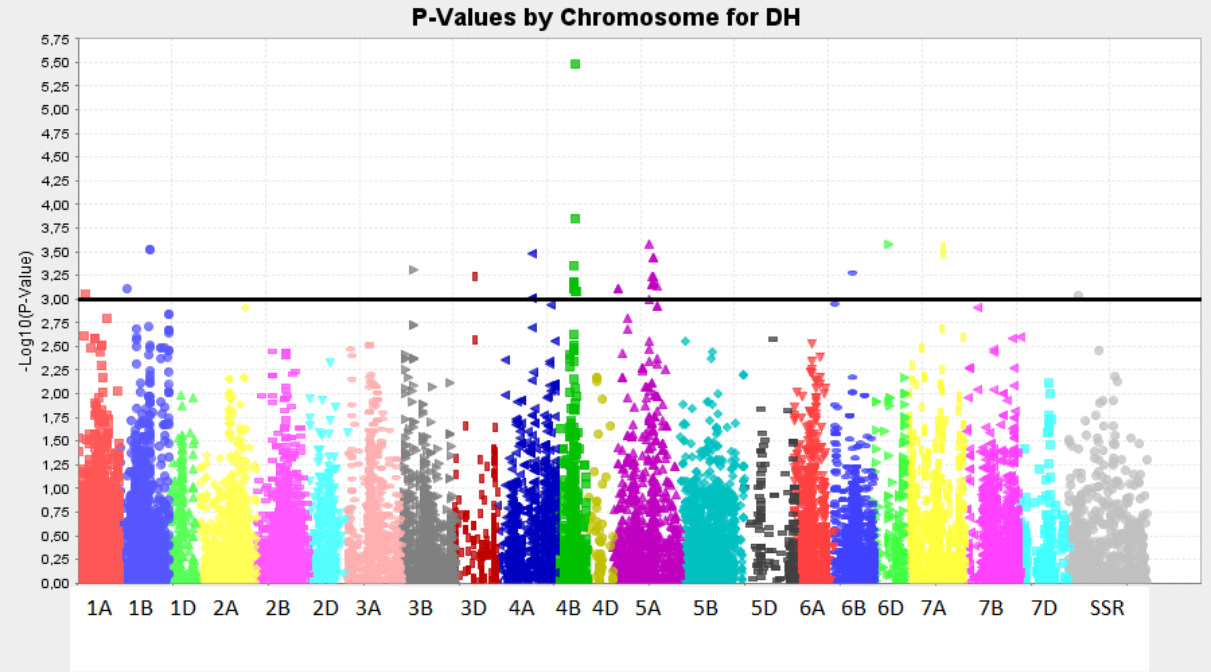

Figure 34: Manhatten plot displaying the markers for earliness (DH) in spring wheat from 2013-2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log (P-value) of 3,0

Data for DH over years show significant areas on 1B, 3B, 3D, 4A, 4B, 5A, 6B and 6D. One SSR marker, cfd018b_198 were significant on 5DS. Of these, 4B and 5A are the most interesting because of their high significance and high number of significant markers. It is worth noting that the dwarf gene Rht-B1 on chromosome 4B is not significant, indicating that there are other mechanisms for earliness located on 4B.

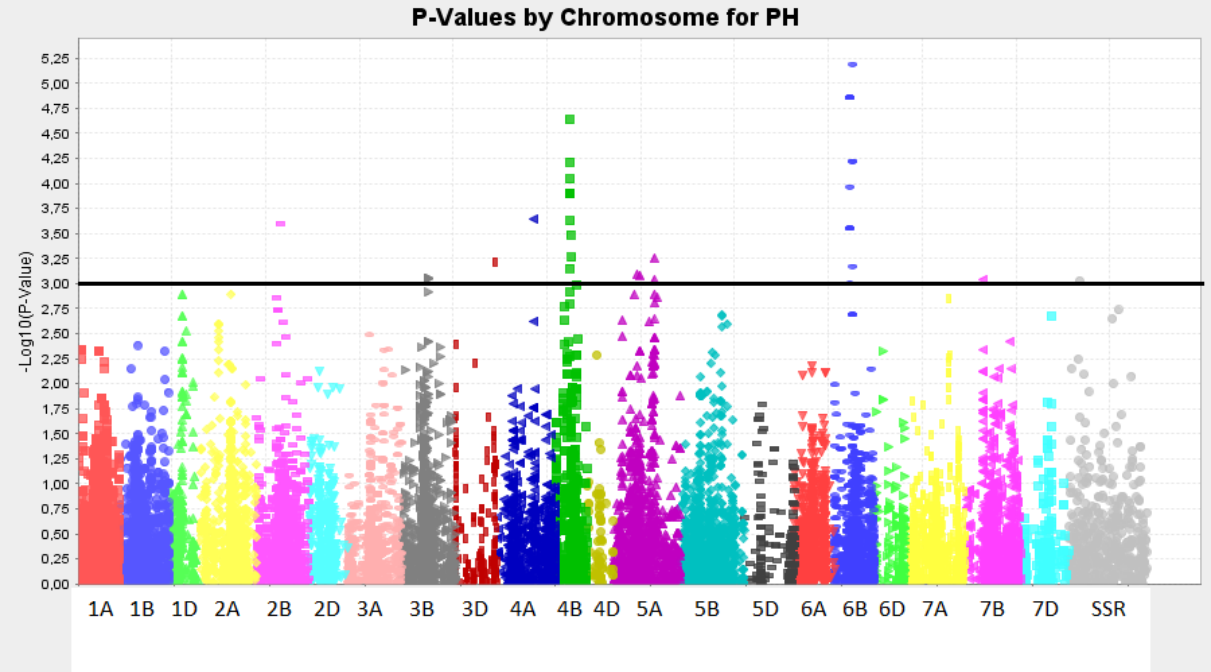

Figure 35: Manhatten plot displaying the markers for plant height (PH) in spring wheat from 2013-2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log(P-value) of 3,0

Data for PH over years shows significant areas on 2B, 3B, 3D, 4A, 4B, 5A, 6B and 7B. One SSR marker, cfd26_286 were significant on 5DL. Of these areas, 4B and 6B are most interesting due to high significant level and high number of significant markers. As expected, Rht-B1 is the significant QTL on 4B.

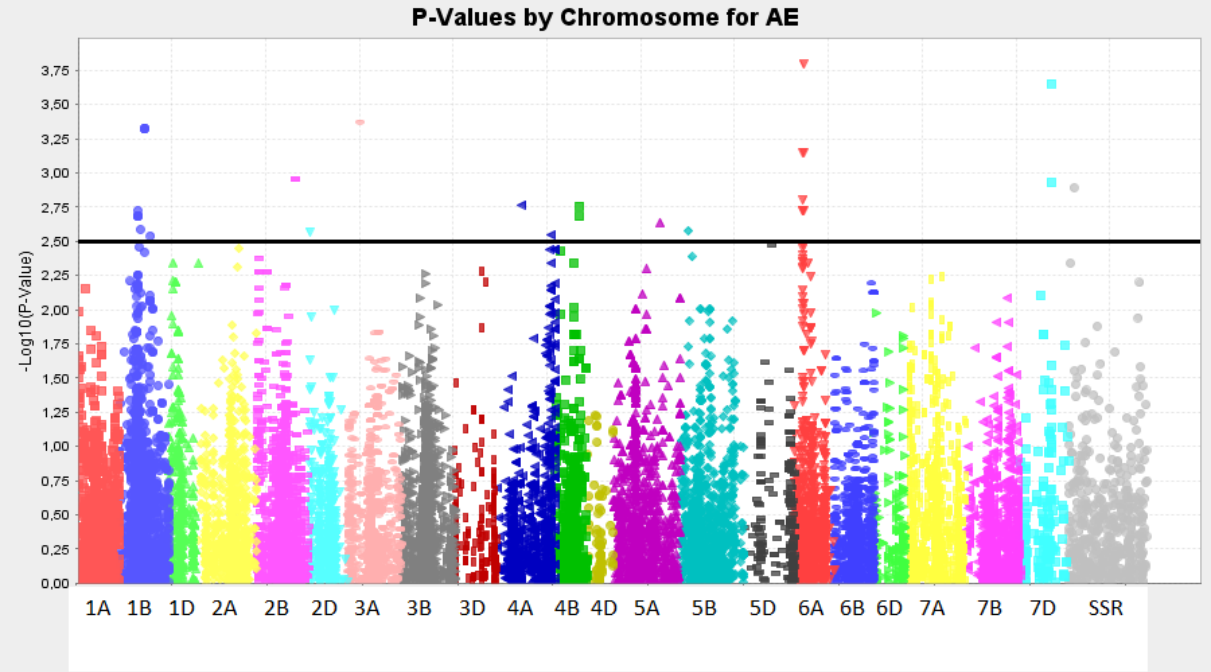

Figure 36: Manhatten plot displaying the markers for anther extrusion (AE) in spring wheat from 2013-2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log (P-value) of 2,5

Data for AE over years show significant areas on 1B, 2B, 2D, 3A, 4A, 4B, 5A, 5B, 6A and 7D. One SSR marker, barc228_194 were also significant. Areas that have dropped in significance after regression are 1A, 1B, 4A, 4B, 5A, 6A, 7B, 7D and the SSR marker hbe248a_227. Areas that has increased or remained the same in significance after regression are 3A, 3B, 5B and 6B. No markers for 5A and 5B were selected for genotyping.

Table 24: Markers selected for genoyping onto new MASBASIS based on marker significance, chromosome and positon from the MLM based on AE data from 2013-2015

Marker	Chromosome	position	-10log p-value
BS00066338_51	1B	287	3.32
BS00069125_51	1B	287	3.32
IACX2852	1B	287	3.32
Excalibur_c7964_1290	2B	458	2.95
Tdurum_contig57254_254	2B	458	2.95
barc228_194	2D	58	2.89
wsnp_Ex_c18883_27772081	3A	169	3.37
Ku_c10913_2542	4A	293	2.77
RAC875_c107130_384	4B	265	2.76
GENE-1584_692	4B	264	2.68
wsnp_Ex_c1011_1931797	6A	104	3.79
Kukri_c35255_1312	6A	104	3.15
BS00023150_51	7D	332	3.65
RAC875_rep_c106588_205	7D	332	2.93

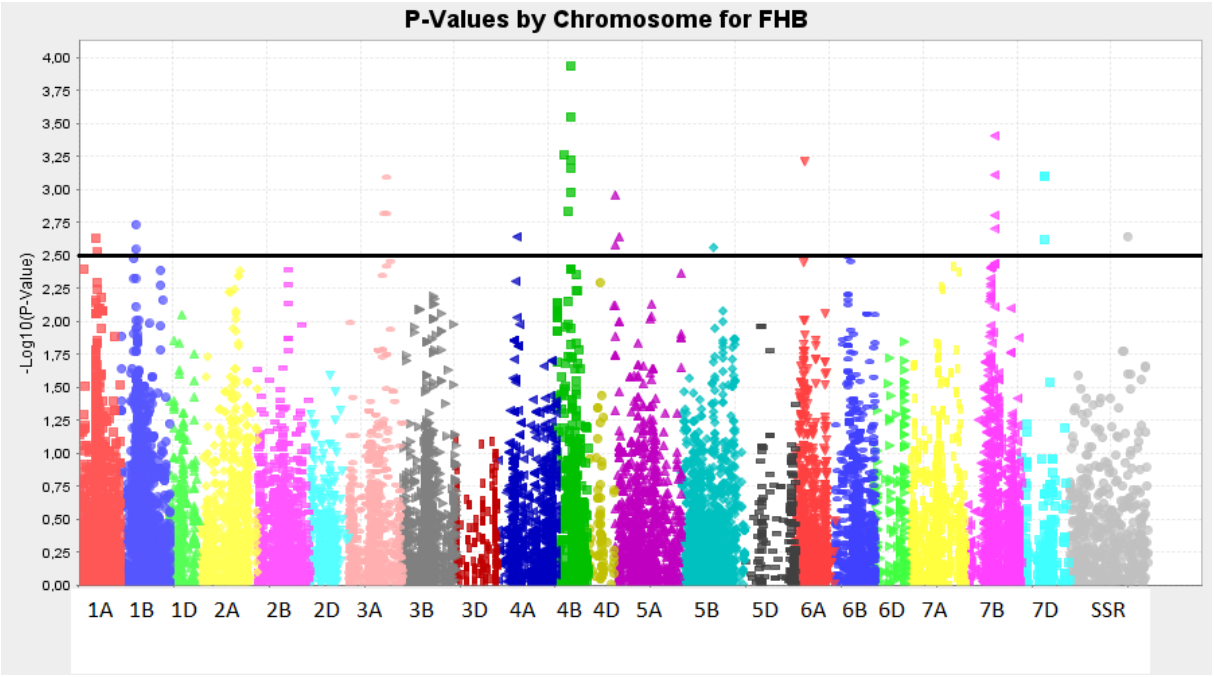

Figure 37: Manhatten plot displaying the markers for Fusarium head blight (FHB) in spring wheat from 2013-2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log (P-value) of 2,5

Data for FHB over years show significant areas on 1A, 1B, 3A, 4A, 4B, 5A, 5B, 6A, 7B and 7D. One SSR marker, hbe248a_227 were significant on 1BL. Marker Rht-B1 were highly significant as expected. What areas that are most interesting will become clearer after correcting for earliness and plant height.

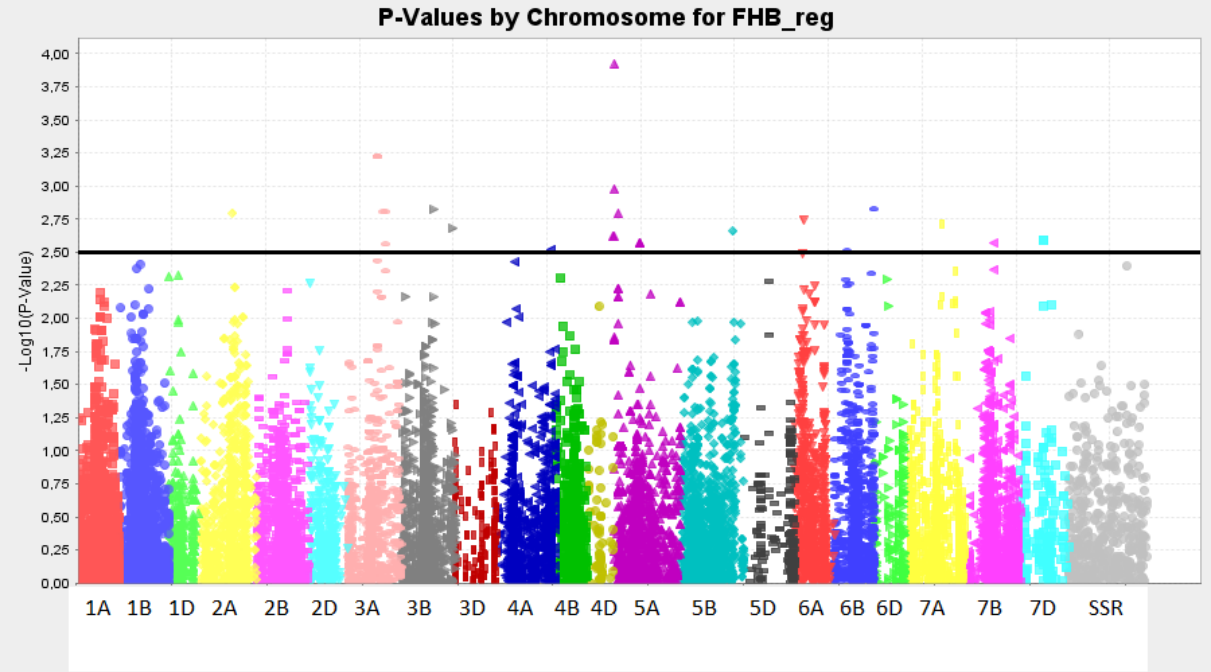

Figure 38: Manhatten plot displaying the markers for Fusarium head blight after regression (FHB_reg) in spring wheat from 2013-2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log (P-value) of 2,5

Data for FHB over years after regression shows significant areas on 3A, 3B, 4A, 5A, 5B, 6A, 6B, 7A, 7B and 7D. Areas that have dropped in significance after regression are 1A, 1B, 4A, 4B, 5A, 6A, 7B, 7D and the SSR marker hbe248a_227. Areas that has increased or remained the same in significance after regression are 3A, 3B, 5B and 6B. Markers selected for further genotyping into new MASBASIS are shown in table 25.

Table 25: Markers selected for genoyping onto new MASBASIS based on marker significance, chromosome and positon from the MLM based on FHB_reg data from 2013-2015

Marker	Chromosome	position	-10log p-value
BobWhite_c4743_63	2A	362	2.80
Excalibur_c39002_242	3A	347	3.22
wsnp_BF292596A_Ta_1_3	3A	347	3.22
wsnp_Ku_c458_954940	3A	346	3.22

BS00022459_51	3A	439	2.81
BS00110550_51	3A	414	2.81
IAAV5302	3B	347	2.82
Excalibur_c766_705	3B	558	2.68
Excalibur_c26997_272	5A	44	3.92
wsnp_Ex_c6209_10838456	5A	43	2.98
wsnp_Ex_c6209_10838852	5A	81	2.79
RFL_Contig3285_1009	5B	565	2.66
wsnp_Ex_c1011_1931797	6A	104	2.74
RAC875_c17011_373	6B	419	2.83
Tdurum_contig46334_832	7A	447	2.71

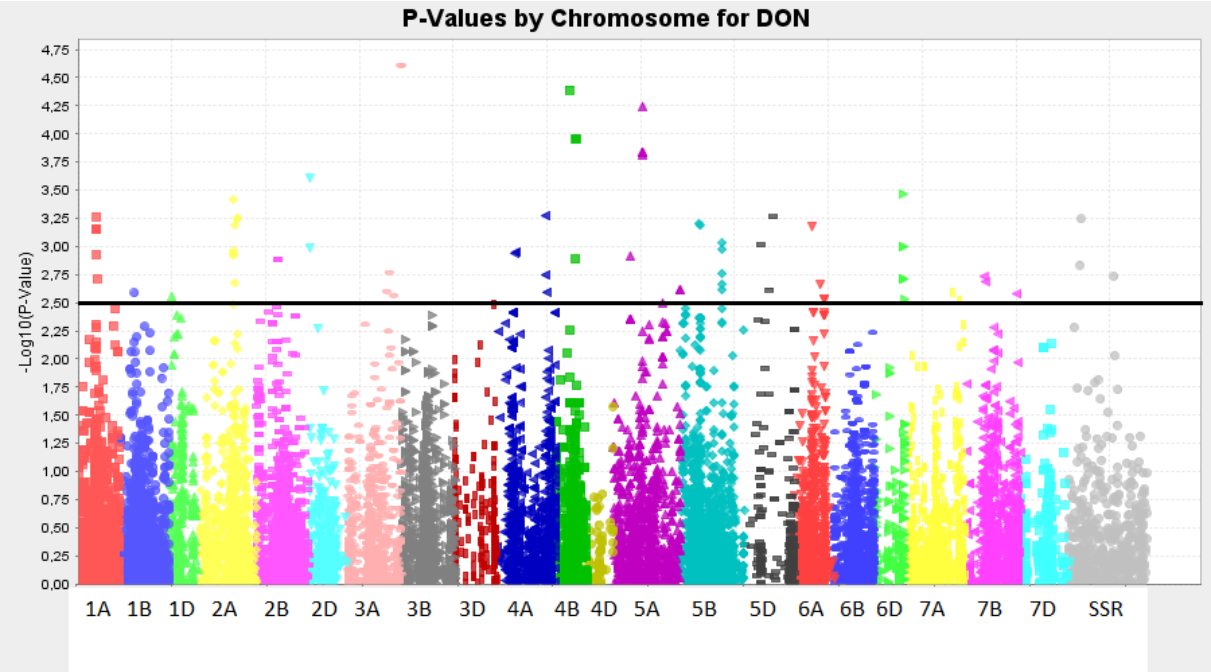

Figure 39: Manhatten plot displaying the markers for Don values (DON) in spring wheat from 2013-2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log (P-value) of 2,5

Data for DON over years show significant areas on 1A, 1B, 1D, 2A, 2B, 2D, 3A, 4A, 4B, 5A, 5B, 5D, 6A, 6D, 7A and 7B. Three SSR markers gwm410_372, cfd47_213 and cfd56_271 were also significant. As expected, Rht-1B is highly significant on chromosome 4B. What areas that are most interesting will become clearer after correcting for earliness and plant height.

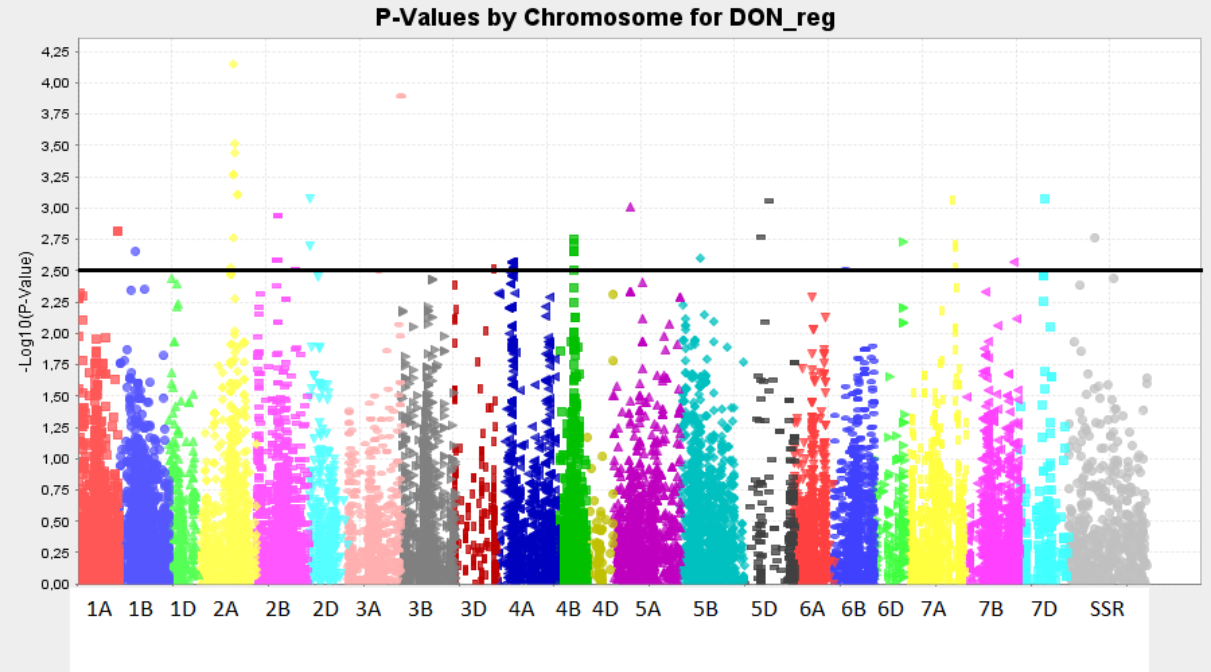

Figure 40: Manhatten plot displaying the markers for DON values after regression (DON_reg) in spring wheat from 2013-2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log (P-value) of 2,5

Data for DON over years after regression show significant areas on 1A, 1B, 2A, 2B, 2D, 3A, 4A, 4B, 5A, 5B, 5D, 6D, 7A, 7B and 7D. One SSR marker, gwm148_184 are also significant. Areas that have decreased in significance after regression are 1A, 1D, 4A, 4B, 5A, 5B, 6A, 6D, 7B and all 3 SSR markers. Areas that has increased or remained relatively the same after regression are 1B, 2A, 2B, 2D, 3A, 5D, 7A, 7D and the SSR marker gwm148_184. As previously mentioned, no markers were chosen for genotyping based on this data, since these were not ready at the time. Markers based on DON data after regression were chosen from 2013 and 2014. These markers are shown in figure 41 and 42.

3.1.3. DON 2013-2014

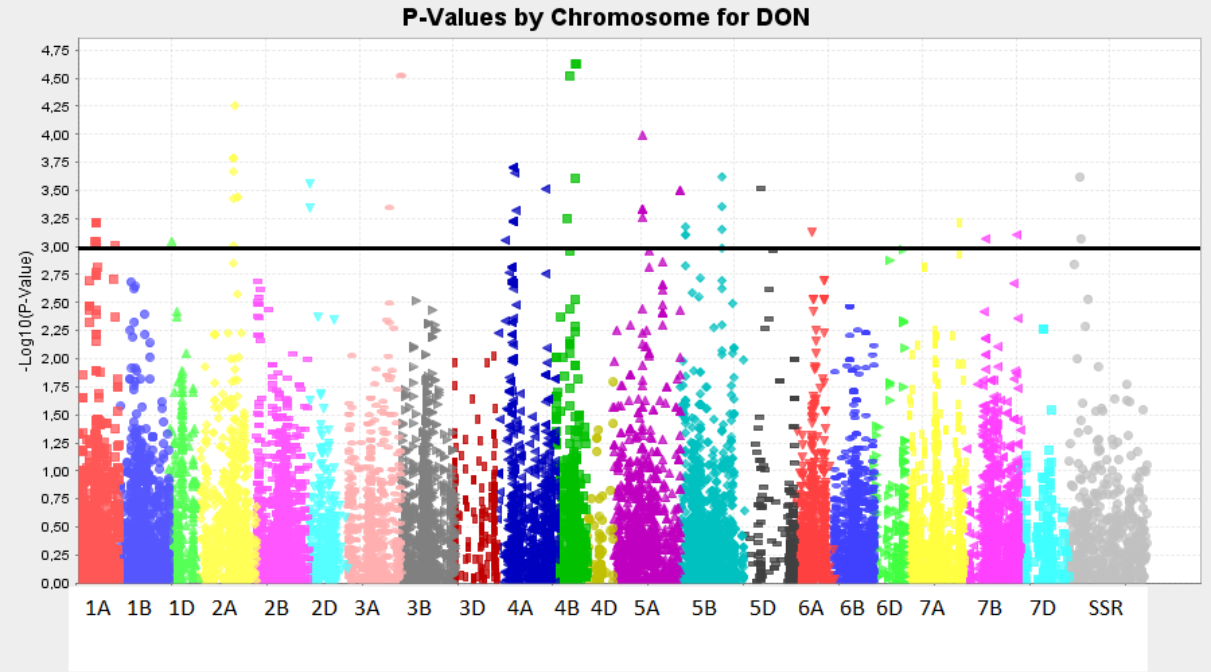

Figure 41: Manhatten plot displaying the markers for DON values (DON) in spring wheat from 2013-2014 derived from Tassel with marker positions on chromosome and significance threshold at -10log (P-value) of 3,0

Data for DON values from 2013-2014 shows significant areas on 1A, 1D, 2A, 2D, 3A, 4A, 4B, 5A, 5B, 5D, 6A, 7A and 7B. Two SSR markers cfd47_213 and cfd56_271 were also significant. What areas that are most interesting will become clearer after correcting for earliness and plant height.

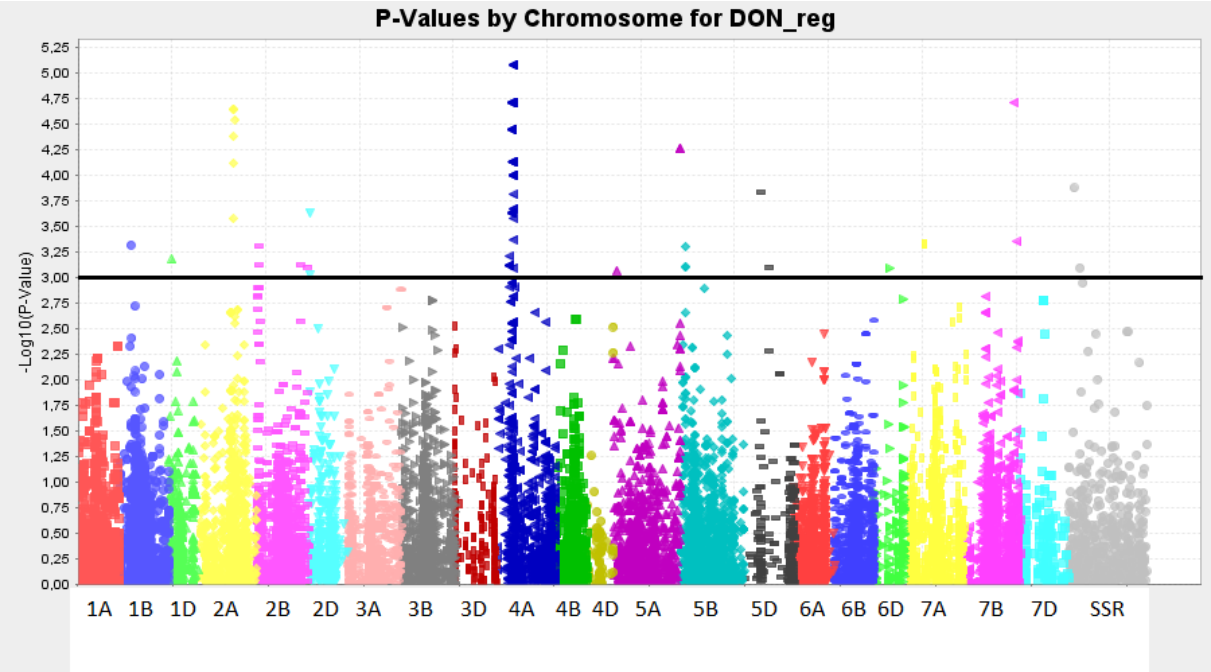

Figure 42: Manhatten plot displaying the markers for DON values after regression (DON_reg) in spring wheat from 2013-2014 derived from Tassel with marker positions on chromosome and significance threshold at -10log (P-value) of 3,0

Data for DON values after regression from 2013-2014 shows significant areas on 1B, 1D, 2A, 2B, 2D, 4A, 5A, 5B, 5D, 6D, 7A and 7B. Three SSR markers, barc228_194, cfd47_213 and csLV46G22_0 were also significant. Areas that decreased after regression were 1A, 3A, 4B, 5A, 5B and 6A. Areas that increased or remain relatively the same after regression were 1B, 1D, 2A, 2D, 4A, 5D, 7A and 7B. Markers selected for further genotyping into new MASBASIS are shown in table 26.

Table 206: Markers selected for genoyping onto new MASBASIS based on marker significance, chromosome and positon from the MLM based on DON_reg data from 2013-2014

Marker	Chromosome	position	-10log p-value
RAC875_c140_872	1B	142	3.32
csLV46G22_0	1BL	155	2.95
wsnp_Ra_c2633_5017265	1D	39	3.18
BS00012320_51	2A	368	4.65
RAC875_c38018_278	2A	368	4.65
RFL_Contig4517_1300	2A	368	4.65
wsnp_JD_rep_c49438_33652645	2B	61	3.31
IAAV5743	2B	504	3.12
Excalibur_c17250_751	2B	61	3.12
RFL_Contig2324_729	2B	583	3.11
Excalibur_rep_c109101_94	2D	6	3.63
D_contig17313_245	2D	6	3.03
barc228_194	2D	58	3.88
cfd47_213	2DL	124	3.10
BobWhite_c13322_215	4A	200	5.08
wsnp_Ex_c1563_2986030	4A	200	5.08
wsnp_Ex_rep_c101638_86971861	4A	200	5.08
Kukri_c80869_122	4A	160	3.21
BobWhite_c47401_491	5A	737	4.27
wsnp_Ex_c20899_30011827	5A	737	4.27
Excalibur_c47920_249	5A	64	3.07
Tdurum_contig53796_360	5B	56	3.30
IAAV731	5B	56	3.10
Tdurum_contig8695_379	5B	56	3.10
BobWhite_c6328_410	5D	178	3.83
Excalibur_c49805_63	5D	270	3.10
BS00063175_51	6D	185	3.09
Kukri_rep_c70864_638	7A	256	3.32
wsnp_Ex_c13248_20898211	7A	256	3.32
wsnp_Ku_c44600_51841068	7B	502	4.71

Kukri_c77849_131	7B	540	3.35

3.2. Association mapping of winter wheat

3.2.1 2015

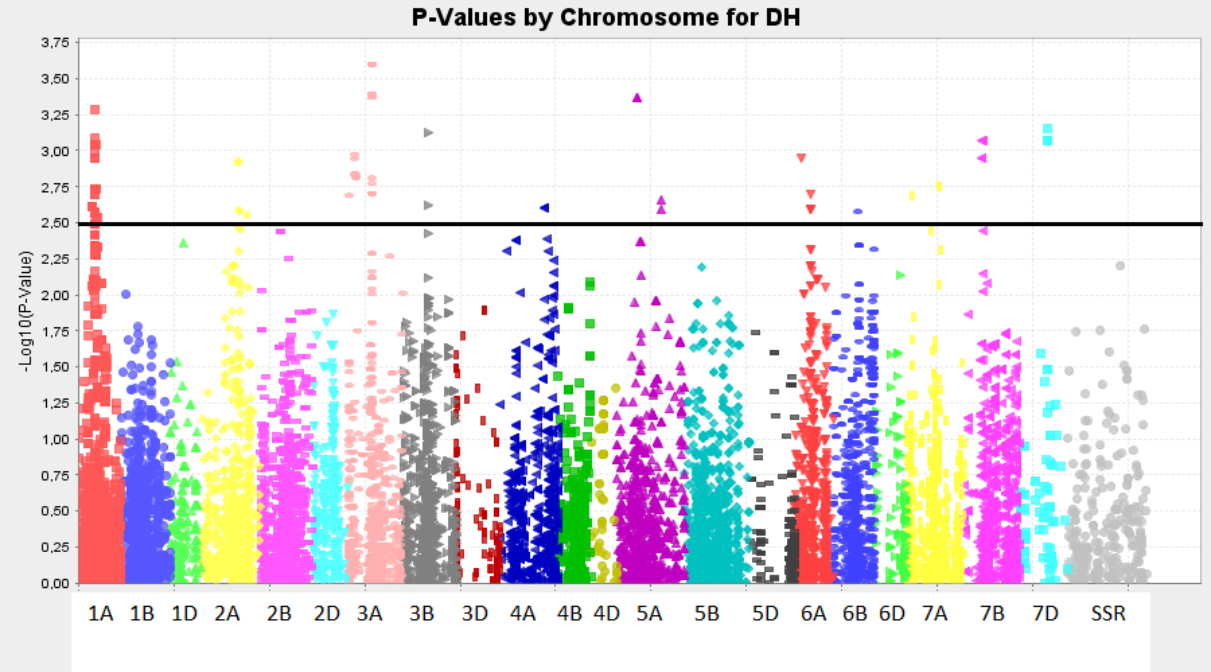

Figure 43: Manhatten plot displaying the markers for days to heading (DH) in winter wheat from 2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log (P-value) of 2,5

Data for DH from 2015 show significant areas on 1A, 2A, 3A, 3B, 4A, 5A, 6A, 6B, 7A, 7B and 7D. The most interesting areas are 1A and 4A, because of their high number of significant markers.

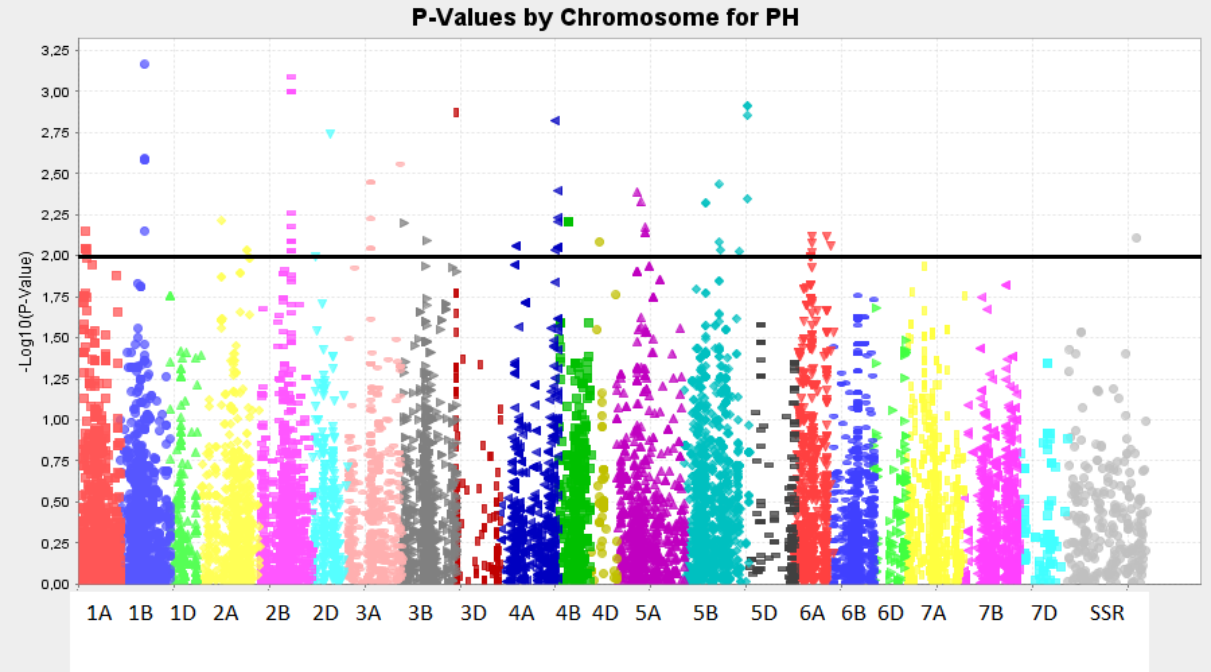

Figure 44: Manhatten plot displaying the markers for plant height (PH) in winter wheat from 2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log (P-value) of 2,0

Data for PH in 2015 shows significant areas on 1A, 1B, 2A, 2B, 2D, 3A, 3B, 3D, 4A, 4B, 4D, 5A, 5B and 6A. One SSR marker wmc044_282 were also significant. The significant marker on 4D is the functional marker Rht-D1 for the gibberellin insensitive dwarf gene *Rht-D1 (Worland & Snape, 2001).*

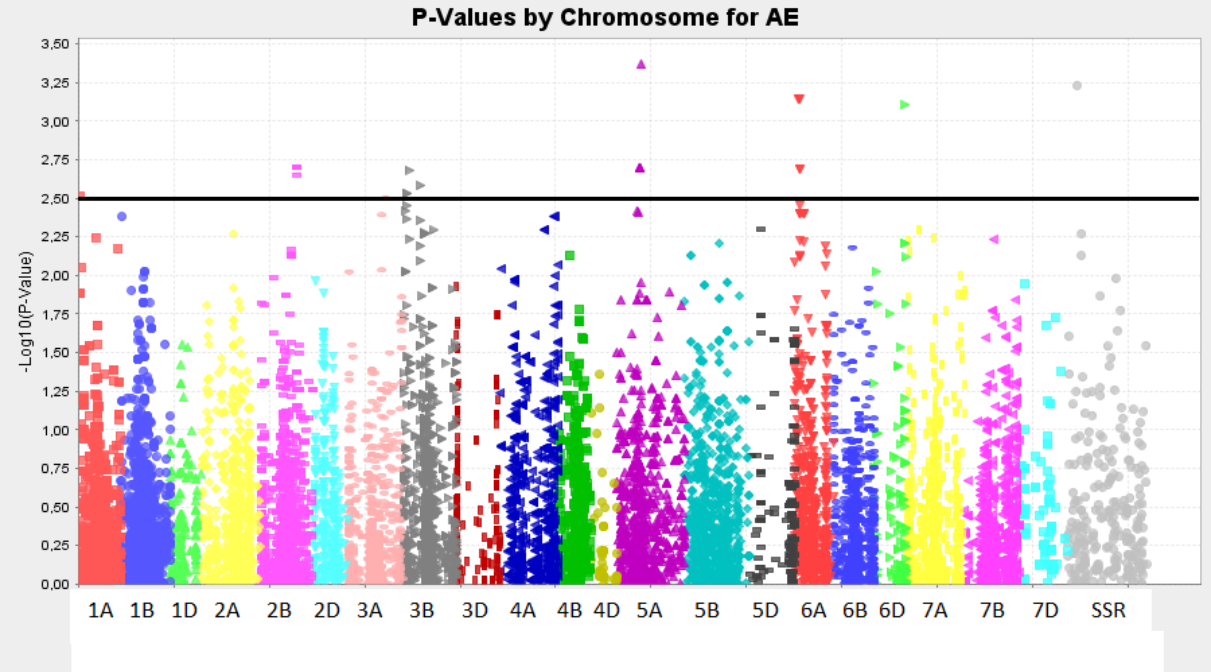

Figure 45: Manhatten plot displaying the markers for anther extrusion (AE) in winter wheat from 2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log (P-value) of 2,5

Data for AE in 2015 shows significant areas on 1A, 2B, 3B, 5A, 6A and 6D. One SSR marker cfd018b_207 were also significant.

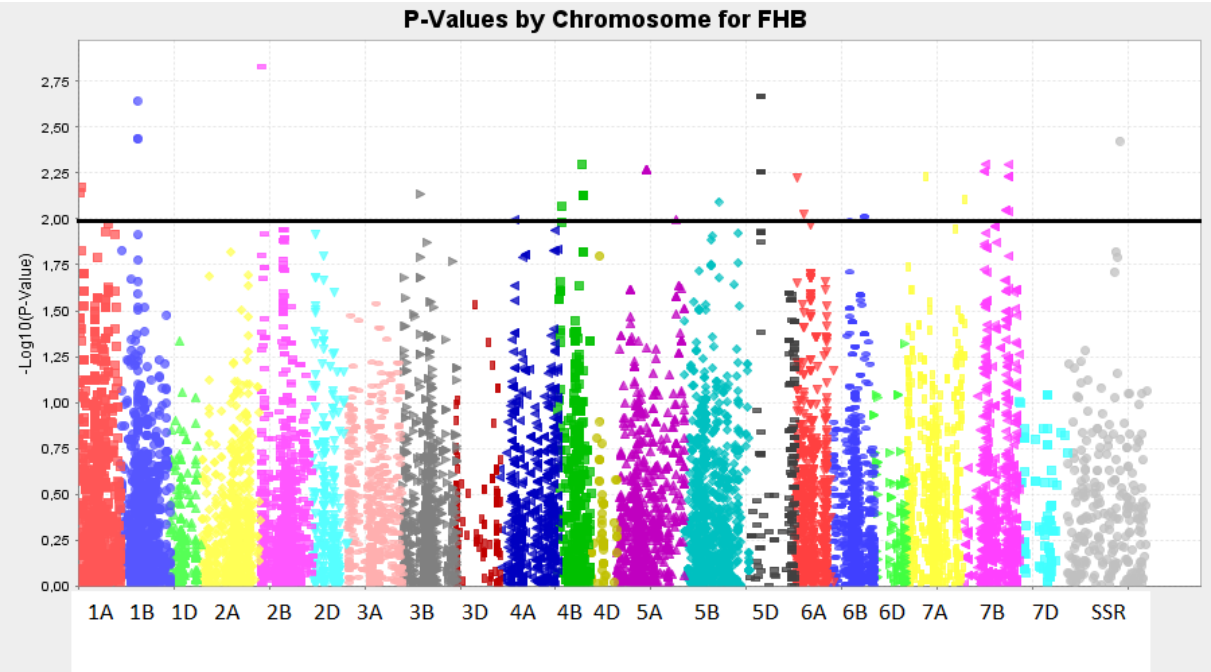

Figure 46: Manhatten plot displaying the markers for fusarium head blight (FHB) in winter wheat from 2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log (P-value) of 2,0

Data for FHB in 2015 show significant areas on 1A, 1B, 2B, 3B, 4B, 5A, 5B, 5D, 6A, 6B, 7A and 7B. One SRR marker gwm644_164 were also significant.

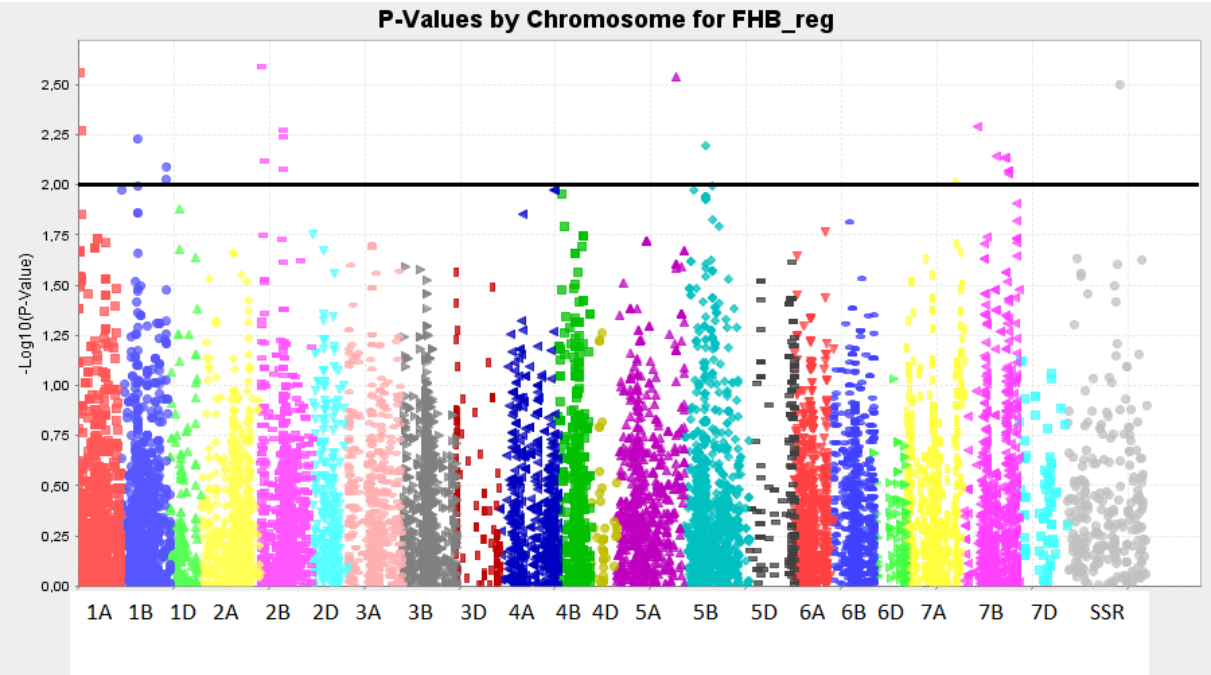

Figure 47: Manhatten plot displaying the markers for fusarium head blight after regression (FHB_reg) in winter wheat from 2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log (P-value) of 2,0

Data for FHB in 2015 after regression show significant areas on 1A, 1B, 2B, 5A, 5B and 7B. One SSR marker gwm644_164 were also significant. The SSR marker were also significant before regression. Areas that are no longer considered significant after regression are 3B, 4B, 5D, 6A, 6B and 7A.

3.2.2. 2014-2015

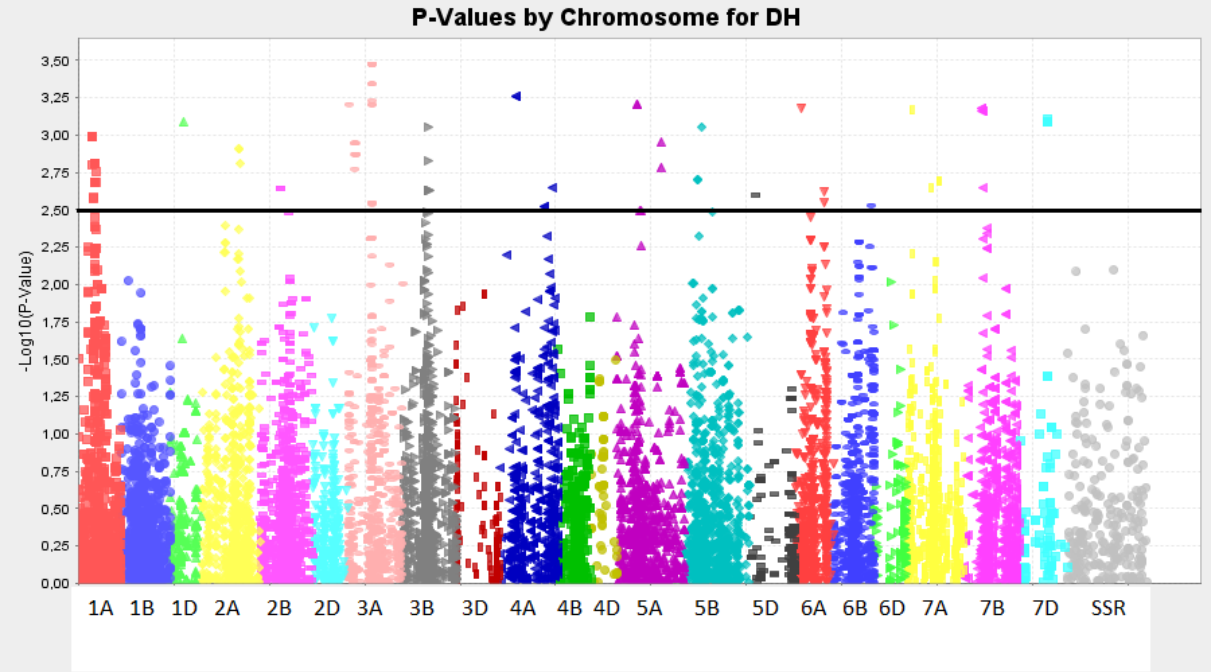

Figure 48: Manhatten plot displaying the markers for days to heading (DH) in winter wheat from 2013-2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log (P-value) of 2,5

Data for DH in 2013-2015 shows significant areas on 1A, 1D, 2A, 2B, 3A, 3B, 4A, 5A, 5B, 5D, 6A, 6B, 7A, 7B and 7D.

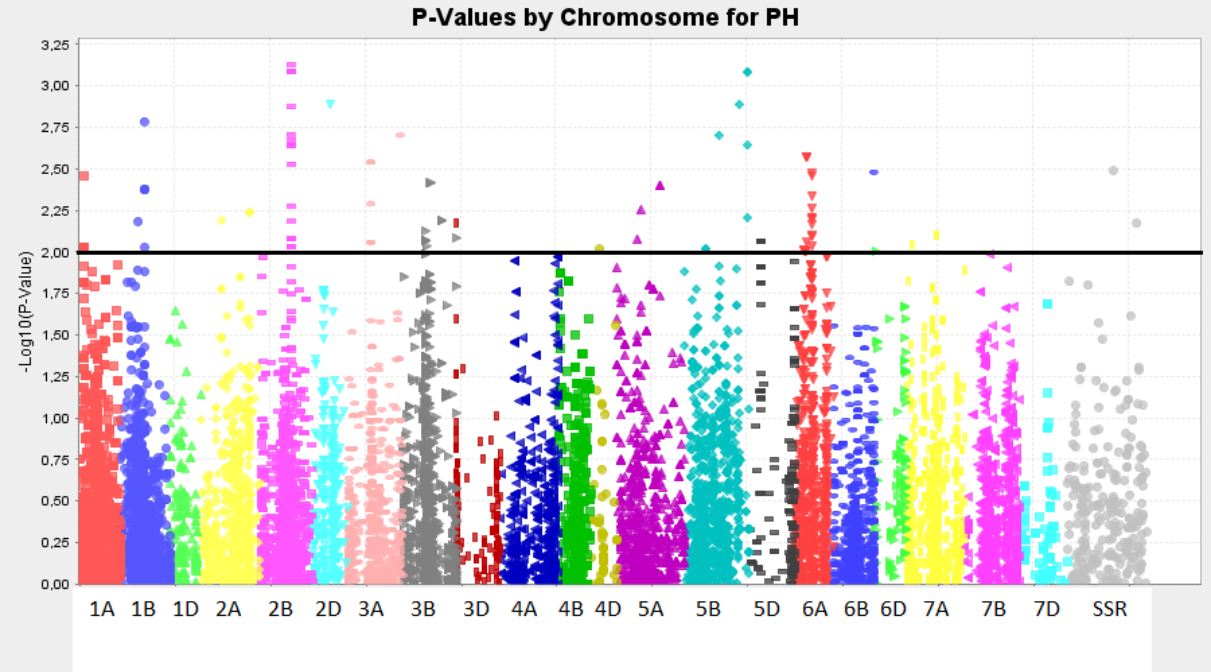

Figure 49: Manhatten plot displaying the markers for plant height (PH) in winter wheat from 2013-2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log (P-value) of 2,0

Data for PH in 2013-2015 shows significant areas on 1A, 1B, 2A, 2B, 2D, 3A, 3B, 3D, 4D, 5A, 5B, 5D, 6A, 6B and 7A. Two SSR markers, gwm410_355 and wmc044_282 were also significant. The significant marker on 4D is the functional marker Rht-D1.

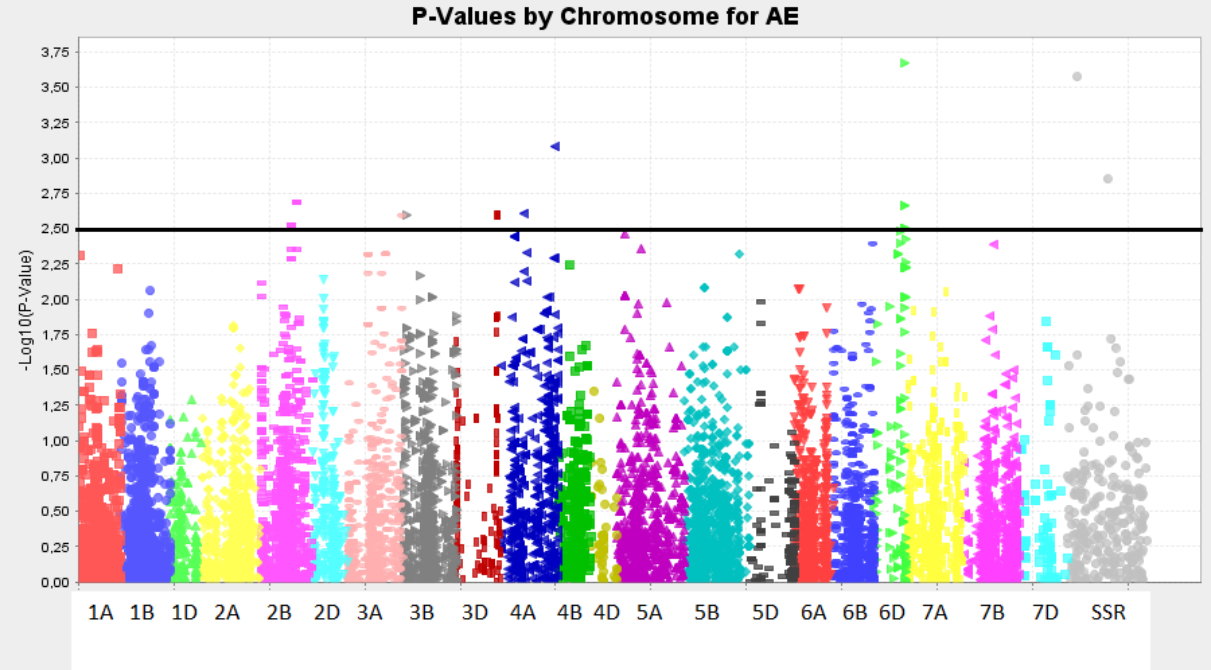

Figure 50: Manhatten plot displaying the markers for anther extrusion (AE) in winter wheat from 2013-2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log (P-value) of 2,5

Data for AE in 2013-2015 show significant areas 2B, 3A, 3B, 3D, 4A and 6D. Two SSR markers cfd018b_207 and gwm301_239 were also significant.

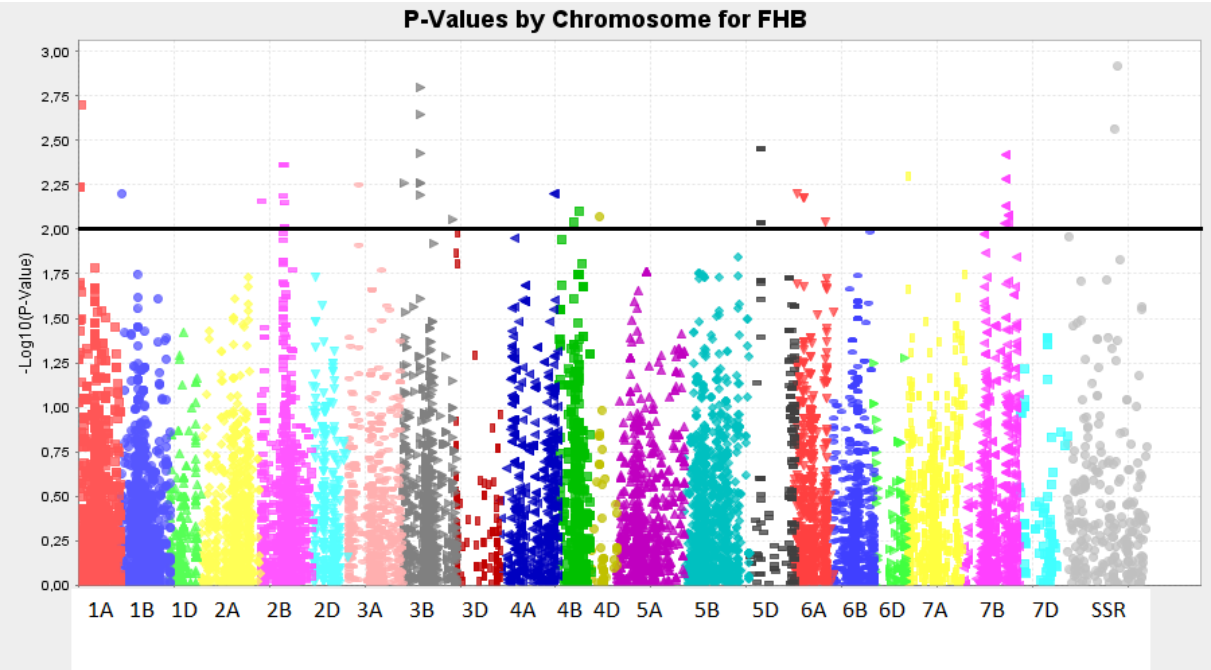

Figure 51: Manhatten plot displaying the markers for fusarium head blight (FHB) in winter wheat from 2013-2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log (P-value) of 2,0

Data for FHB in 2013-2015 show significant areas on 1A, 1B, 2B, 3A, 3B, 4A, 4B, 4D, 5D, 6A, 7A and 7B. Two SSR markers, gwm427_232 and gwm617a_146 were also significant. The significant marker on 4D is the functional marker Rht-D1.

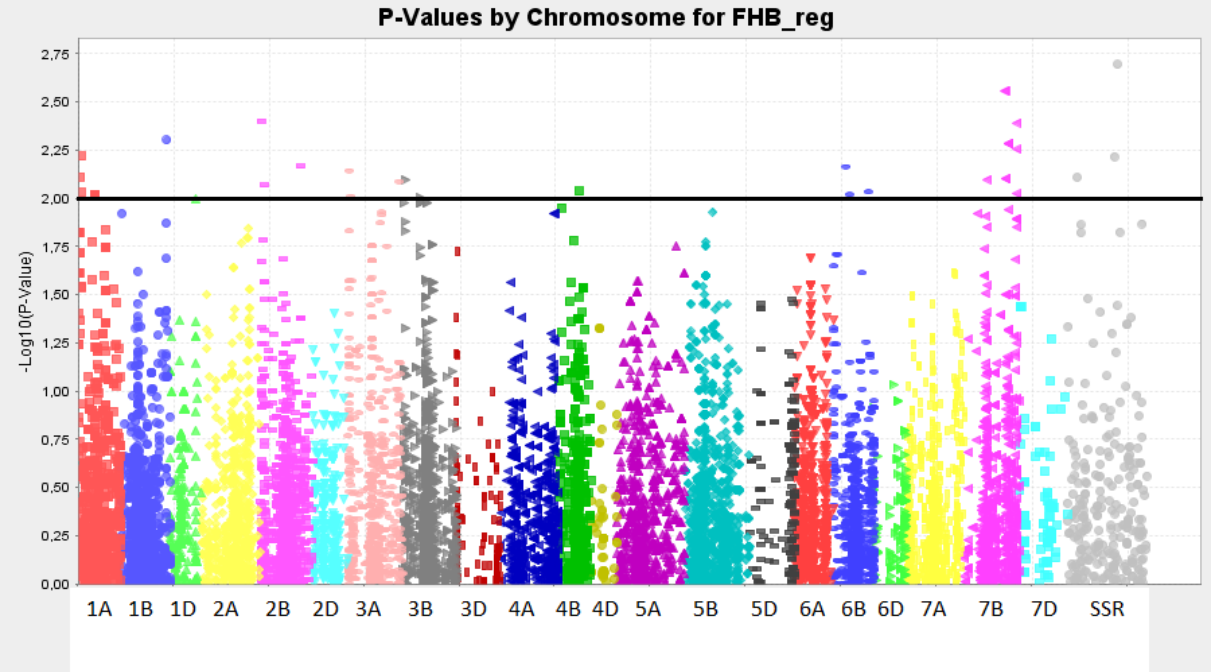

Figure 52: Manhatten plot displaying the markers for fusarium head blight after regression (FHB_reg) in winter wheat from 2013-2015 derived from Tassel with marker positions on chromosome and significance threshold at -10log (P-value) of 2,0

Data for FHB in 2013-2015 after regression show significant areas on 1A, 1B, 2, 3A, 3B, 4B, 6B and 7B. Three SSR markers, gwm617a_146, gwm427_232 and cfd018b_207 were also significant. gwm617a_146 and gwm427_232 were also significant before regression. Areas that are no longer considered significant after are 4A, 4D, 5D, 6A and 7A. Areas are considered significant after regression but not before are 6B.

Chapter 4: Validation test

After the most significant markers from the association mapping had been genotyped on the entire MASBASIS, phenotypic data from the new MASBASIS lines from 2013-2015 were used to validate the markers significance. Validation was performed using ANOVA in minitab, using each fenotypic trait for each year as the response, and each marker as factor. If the markers showed significance for FHB, DON or AE over two or more years, they pass the test. The reason for this validation test is to estimate the marker effects on an entirely new

genetic background. For a marker to be valid, it should show a large effect no matter which line it is tested on, and not just on the population used in the association mapping.

The results from the genotyping gave variable results. Not all markers gave the same results as the 90k chip, not all were amplified, and some showed no clear clustering pattern. This resulted in 36 of 58 markers that were successfully genotyped. Of these 36 markers, most only showed significance for FHB or DON in one year. Others showed significance to earliness and plant height. Some of the markers that showed significance for FHB and/or DON for more years had low segregation. 4 lines that show high marker effect, is not representative for marker effect to be valid. 5 lines showed high significance over years, and a minor allele frequency of 5 or more. Three of these are located on chromosome 4A, position 200. One is located on 5D, positon 270. And one is located on 7B, position 502. A complete list of the results from the validation test is showed in table 27.

Table 27: results from genotyping and validation test. Markers with significant effect of FHB and/or DON over years, and have minor allele frequency of 5 or more are shown with green areas. Allele frequency include all lines in MASBASIS.

Trait	Marker	Chr	Pos	n=a	n=b	allele frequence (A/T)	results from validation test
AE	BS00066338_51	1B	287	6	117	*	No clear clustering path
AE	BS00069125_51	1B	287	6	117	19/364	Significant for PH in 2014, and FHB in 2015
AE	IACX2852	1B	287	6	117	*	No clear clustering pattern
AE	Excalibur_c7964_1290	2B	458	19	104	*	gives results very different from the 90K chip
AE	Tdurum_contig57254_254	2B	458	19	104	*	gives results very different from the 90K chip
AE	barc228_194	2D	58	117	6	*	Not significant for any trait
AE	wsnp_Ex_c18883_27772081	3A	169	97	26	*	No clear clustering pattern
AE	Ku_c10913_2542	4A	293	97	26	323/74	significant for FHB 2013
AE	GENE-1584_692	4B	264	60	63	123/269	not significant for any trait
AE	RAC875_c107130_384	4B	265	61	62	133/261	not significant for any trait
AE	wsnp_Ex_c1011_1931797	6A	104	88	35	295/74	not significant for any trait

AE	Kukri_c35255_1312	6A	104	78	45	*	No clear clustering pattern
AE	BS00023150_51	7D	332	103	20	208/84	Significant for DH and DON in 2013
AE	RAC875_rep_c106588_205	7D	332	101	22	*	No clear clustering path
DON_reg	RAC875_c140_872	1B	142	10	113	28/343	Not significant for any trait
DON_reg	wsnp_Ra_c2633_5017265	1D	39	27	96	39/349	Not significant for any trait
DON_reg	BS00012320_51	2A	368	19	104	*	Not amplified
DON_reg	RAC875_c38018_278	2A	368	19	104	57/339	Not significant for any trait
DON_reg	RFL_Contig4517_1300	2A	368	104	19	345/57	significant for FHB 2013
DON_reg	wsnp_JD_rep_c49438_33652645	2B	61	86	37	208/119	Significant for AE at Vollebekke in 2014, and DH in 2015.
DON_reg	Excalibur_c17250_751	2B	61	85	38	223/139	Significant for DH in 2015.
DON_reg	IAAV5743	2B	504	22	101	*	No clear clustering pattern
DON_reg	RFL_Contig2324_729	2B	583	96	27	*	gives results very different from the 90K chip
DON_reg	Excalibur_rep_c109101_94	2D	6	112	11	338/56	not significant for any trait
DON_reg	D_contig17313_245	2D	6	26	97	*	not amplified.
DON_reg	barc228_194	2D	58	117	6	*	Not significant for any trait
DON_reg	Kukri_c80869_122	4A	160	78	45	299/86	not significant for any trait
DON_reg	BobWhite_c13322_215	4A	200	11	112	19/308	significant for DON in 2013, 2014 and 2015, PH in 2014, and FHB in 2015
DON_reg	wsnp_Ex_c1563_2986030	4A	200	11	112	20/332	significant for DON in 2013, 2014 and 2015, PH in 2014, and FHB in 2013 and 2015
DON_reg	wsnp_Ex_rep_c101638_86971861	4A	200	11	112	20/377	significant for DON in 2013 and 2014, PH in 2014, FHB and DON in 2015
DON_reg	Excalibur_c47920_249	5A	64	117	6	*	No clear clustering path

DON_reg	BobWhite_c47401_491	5A	737	15	108	20/375	Significant for DON in 2013 and 2014, and FHB in 2015. Low segregation
DON_reg	wsnp_Ex_c20899_30011827	5A	737	108	15	370/19	not significant for any trait
DON_reg	Tdurum_contig53796_360	5B	56	95	28	*	No clear clustering pattern
DON_reg	IAAV731	5B	56	96	27	*	No clear clustering pattern
DON_reg	Tdurum_contig8695_379	5B	56	96	27	*	gives results very different from the 90K chip
DON_reg	BobWhite_c6328_410	5D	178	12	111	16/385	significant for DON in 2013 and 2014, and FHB in 2013 and 2015. Low segregation.
DON_reg	Excalibur_c49805_63	5D	270	101	22	363/31	significant for DH in 2013 and 2015, PH in 2014, DON in 2013, 2014 and 2015, and FHB in 2013 and 2015
DON_reg	cfd47_213	6D	124	111	12	*	Not significant for any trait
DON_reg	BS00063175_51	6D	185	110	13	379/22	Significant for DON in 2013 and 2014. Low seggeregation.
DON_reg	Kukri_rep_c70864_638	7A	256	14	109	17/383	significant for PH in 2014, DON in 2014 and FHB in 2015. Low seggeregation.
DON_reg	wsnp_Ex_c13248_20898211	7A	256	14	109	*	Dominant Y allele
DON_reg	wsnp_Ku_c44600_51841068	7B	502	111	12	340/21	significant for DON in 2013, 2014 and 2015, PH in 2014, and FHB in 2013 and 2015
DON_reg	Kukri_c77849_131	7B	540	16	107	*	gives results very different from the 90K chip
FHB_reg	BobWhite_c4743_63	2A	362	22	101	*	markes does not match the 90k chip

FHB_reg	wsnp_Ku_c458_954940	3A	346	12	111	*	gives results very different from the 90K chip
FHB_reg	Excalibur_c39002_242	3A	347	12	111	16/363	significant for in DH 2013 and 2015, and PH 2014. Low seggeregation
FHB_reg	wsnp_BF292596A_Ta_1_3	3A	347	12	111	18/382	significant for in DH 2013. Low seggeregation
FHB_reg	BS00110550_51	3A	414	83	40	293/100	Significant for AE at Staur in 2015
FHB_reg	BS00022459_51	3A	439	83	40	295/102	Significant for AE at Staur in 2015
FHB_reg	IAAV5302	3B	347	92	31	262/130	only significant for FHB in 2015
FHB_reg	Excalibur_c766_705	3B	558	46	77	206/198	significant for PH in 2013, and AE at Staur in 2015
FHB_reg	wsnp_Ex_c6209_10838456	5A	43	62	61	*	gives results very different from the 90K chip
FHB_reg	Excalibur_c26997_272	5A	44	49	74	*	gives results very different from the 90K chip
FHB_reg	wsnp_Ex_c6209_10838852	5A	81	22	101	48/331	significant for DH in 2013 and 2015
FHB_reg	RFL_Contig3285_1009	5B	565	67	56	182/205	not significant for any trait
FHB_reg	wsnp_Ex_c1011_1931797	6A	104	88	35	295/74	not significant for any trait
FHB_reg	RAC875_c17011_373	6B	419	40	83	*	not amplified
FHB_reg	Tdurum_contig46334_832	7A	447	33	90	106/266	significant for DH in 2013 and 2015, and AE at Staur in 2015

Table 28: Significant markers after validation test using one-way ANOVA, with significant years and traits, their p-value and the allele effects.

Marker	year and trait	p-value	mean effect X	mean effect Y
BobWhite_c13322_215	DON 2013	0,000	21,93	8,861
	PH 2014	0,002	73,35	79,334
	DON 2014	0,000	7,09	2,317
	FHB 2015	0,001	58,98	40,94
	DON 2015	0,000	34,28	20,79
Excalibur_c49805_63	DH 2013	0,012	55,87	53,822
	FHB 2013	0,028	37,13	24,62
	DON 2013	0,000	23,40	8,731
	PH 2014	0,015	73,91	79,175
	DON 2014	0,000	8,67	2,267
	DH 2015	0,004	54,718	53,247
	FHB 2015	0,001	58,93	41,09
	DON 2015	0,000	40,54	20,29
wsnp_Ex_c1563_2986030	FHB 2013	0,038	35,63	23,92
	DON 2013	0,000	21,93	8,991
	PH 2014	0,002	73,35	79,392
	DON 2014	0,000	7,09	2,330
	FHB 2015	0,002	58,98	41,49
	DON 2015	0,000	34,28	20,96
wsnp_Ku_c44600_51841068	FHB 2013	0,028	24,76	38,55
	DON 2013	0,000	9,131	23,20
	PH 2014	0,002	79,586	73,15
	DON 2014	0,000	2,364	7,58
	FHB 2015	0,000	40,84	61,36
	DON2015	0,001	21,32	33,14
wsnp_Ex_rep_c101638_86971861	DON 2013	0,000	21,93	8,861
	PH 2014	0,002	73,35	79,334
	DON 2014	0,000	7,09	2,317
	FHB 2015	0,001	58,98	41,17
	DON 2015	0,000	34,28	20,88

After the significant markers were genotyped on MASBASIS, they were tested on another MASBASIS population in using a one-way ANOVA in order to validate the markers as significant. The criteria for a significance marker is that it shows significance for either FHB or DON over 2 or more years, and that the alleles segregates into more than 5 lines. Of all 33 selected markers, only 5 passed these criteria in the validation test. These markers are BobWhite_c13322_215, Excalibur_c49805_63, wsnp_Ex_c1563_2986030, wsnp_Ku_c44600_51841068 and wsnp_Ex_rep_c101638_86971861. The markers, their significant trait and effect on that trait is shown in table 28. BobWhite_c13322_215, wsnp_Ex_c1563_2986030, wsnp_Ex_rep_c101638_86971861 are all located on position 200

on chromosome 4A. Excalibur_c49805_63 is located on position 270 on chromosome 5D. wsnp_Ku_c44600_51841068 is located on position 502 on chromosome 7B.

Table 29 shows the lines in MASBASIS that have the susceptible allele. This means that every other line in MASBASIS has a resistant allele, except for those that did not get amplified during genotyping of the new MASBASIS lines. These lines are shown in table 30.

Table 29: Lines in MASBASIS with susceptible allele of the significant markers.

Marker	Line	Name
BobWhite_c13322_215	1048	Saar-1
wsnp_Ex_c1563_2986030	1050	Filin-1
wsnp_Ex_rep_c101638_86971861	1054	Pfau-Milan-1
	1073	Avocet-YrA-1
	1127	ONSCDH-03(1)
	1131	ONSCDH-04(2)
	1158	CD87-3
	1161	Chara-3
	1164	Kukri-3
	1306	GN07581
	1320	GN08647
	1332	C80.1/3*QT4522//2*ATTILA
	1407	GN08530
	1421	BJY/COC//CLMS/GEN
	1422	HAHN/PRL//AUS1408
	1423	TUI/RL4137
	1562	GN12701
	1577	GN12645
	1631	NG8675/CBRD//SHA5/WEAVER
	1632	TRAP#1/BOW//TAIGU DERIVATIVE
	1634	GAMENYA
wsnp_Ku_c44600_51841068	1048	Saar-1
	1050	Filin-1
	1054	Pfau-Milan-1
	1073	Avocet-YrA-1
	1127	ONSCDH-03(1)
	1131	ONSCDH-04(2)
	1141	ONSCDH-07(3)
	1158	CD87-3
	1161	Chara-3
	1164	Kukri-3
	1168	ONPMSYDER-05
	1306	GN07581
	1332	C80.1/3*QT4522//2*ATTILA

	1407	GN08530
	1421	BJY/COC//CLMS/GEN
	1422	HAHN/PRL//AUS1408
	1423	TUI/RL4137
	1562	GN12701
	1577	GN12645
	1632	TRAP#1/BOW//TAIGU DERIVATIVE
	1634	GAMENYA
Excalibur_c49805_63	1041	Naxosx3
	1048	Saar-1
	1052	Milan-1
	1054	Pfau-Milan-1
	1057	Bagula-Milan-2
	1058	Dulus-1
	1063	Catbird-2
	1121	ONSCDH-01(1)
	1124	ONSCDH-02(1)
	1127	ONSCDH-03(1)
	1131	ONSCDH-04(2)
	1134	ONSCDH-05(2)
	1141	ONSCDH-07(3)
	1158	CD87-3
	1164	Kukri-3
	1168	ONPMSYDER-05
	1309	GN08533
	1312	GN08554
	1315	GN08568
	1322	Sabin
	1331	RB07
	1332	C80.1/3*QT4522//2*ATTILA
	1333	C80.1/3*QT4522//2*PASTOR
	1422	HAHN/PRL//AUS1408
	1423	TUI/RL4137
	1531	GN12628
	1571	GN12630
	1626	EMB16/CBRD//CBRD
	1633	IVAN/6/SABUF/5/BCN/4/RABI//GS/CRA/3/AE.SQUARROSA (190)
	1634	GAMENYA
	1635	WHEAR/2*KRONSTAD F2004
	1636	T.DICOCCON PI94625/AE.SQUARROSA (372)//TUI/CLMS/3/2*PASTOR/4/EXCALIBUR

Table 30: unamplified lines of the new MASBASIS lines

Marker	unamplfied lines	Marker	unamplfied lines
wsnp_Ku_c44600_51841068	1039	wsnp_Ex_c1563_2986030	1510
	1172		1511
	1272		1512
	1408		1513
	1430		1514
	1505		1515
	1509		1521
	1511		1522
	1514		1523
	1516		1524
	1517		1525
	1518		1526
	1527		1527
	1539		1553
	1542		1606
	1546		1607
	1547		1608
	1548		1609
	1553		1610
	1557		1611
	1570		1618
	1572		1619
	1593		1620
	1595		1621
	1613		1622
	1615		1623
	1701		1714
	1719		1715
	1734		1716
	1747		1717
BobWhite_c13322_215	1339		1718
	1553		1719
Excalibur_c49805_63	1553		1725
	1589		1726
	1608		1727
	1612		1728
	1741		1729
	1744		1730
wsnp_Ex_rep_c101638_86971861	1553		1731
	1600		1741
	1742		
	1743		

Chapter 5: Marker analysis

5.1. AE

The association mapping for AE revealed significant markers for 11 QTLs on chromosome 1B, 2BL, 2DS, 3AS, 4ALc, 4AL 4BL, 5AL, 5BS, 6AS and 7DL, where markers for eight QTLs were selected for genotyping. The markers and their positions are listed in table 43. Figure 15 shows that there is a clear additive pattern of these 11 specific QTLs in MASBASIS. Maria and Hermann Buerstmayr performed a mapping of QTLs for anther extrusion among other traits in 2015 and found three QTLs on chromosome 4AL, 6BL, and 5AS(Buerstmayr & Buerstmayr, 2015). 4AL and 6BL overlapped with QTLs for FHB. Figure 18 shows a high correlation between AE and FHB, and less correlation between AE and DON. So we would expect some of the significant markers for AE to overlap with markers for FHB. Our AM shows significant markers for AE on 4A and 5A, but not 6B. The marker on 4ALc is located on position 293, and does not overlap with any markers in the same position in DON or FHB. However, another significant marker that were not selected for genotyping on 4AL position 603 is located on the same position as another marker that were significant for FHB. This QTL is likely the same Buerstmayr found on 4AL. The significant marker on 5A is located on position 530, and was not selected for genotyping. This is not the same QTL as Buerstmayr found on 5AS.

Lu et al. evaluated FHB resistance in a cross between SHA3/CBRD and the German line Naxos in 2013, confirming that high AE is associated with low FHB infection(Lu et al, 2013). This association is mainly for type 1 resistance, except for one QTL on 2DLc which was associated with resistance in all inoculation methods. The QTLs their study revealed for AE were 1BL, 2DLc, 3DL, 4AL, 4BS, 5AL, 5BL, 6AS, 6ASc and 7AL. The QTLs our studies have in common are 4AL, 5AL, and 6AS, all of which is associated with FHB. Our AM showed two QTL common to both AE and FHB, which is 6AS on position 104, and 4AL on position 603. The marker wsnp_Ex_c1011_1931797 on 6AS was significant for both traits.

The validation test of the selected markers in table 27 showed no clear significant markers for AE in more than one trial. The QTLs that showed significance in one trial were 2BS, 3AL, 3BL and 7AL. The QTL on 7AL was also found in the study by Lu et al. in 2013, and was associated with both FHB and AE. Four of the five markers that were significant for AE in the validation test were initially selected for FHB, which shows the strong association between these two traits. None of the markers selected for AE showed significance during the validation test. One of the reasons for this is that seven of the fourteen selected markers gave

no clear results during genotyping, and seven of the thirty-three markers used in the validation were monomorphic within the testing population (Table 53 and 54). This means that the significant markers on 2BL and 3AS could not be tested.

5.2 FHB

The association mapping for FHB revealed significant markers for 15 QTLs on chromosome 2AL, 3AL, 3ALc, 3BL, 3BLc, 4AL, 5AS, 5ALc, 5BL, 6AS, 6BS, 6BL, 7AL, 7Bc and 7Dc, where nine of them were selected for genotyping. The markers and their positions are listed in table 44. Figure 17 shows that there is some effect of these QTLs, and that they are additive. Two major resistance QTLs can be speculated to be significant in this AM. These are *fhb2* on 6BS, and *fhb5* on 5A. There are no significant markers on 3BS, or 4B, meaning that *fhb1* and *fhb4* are not significant in this AM. Of the meta QTLs found by Liu et al in 2009 3A, 5A, 5B, 6BS, 6B and 7A seem to be overlapping among the confirmed QTL (Liu et al, 2009). Among the unique QTLs from the same study, 2A, 3A, 5AL, 5B, 7A and 7B seem to overlap.

The mapping done by Buerstmayr in 2015 revealed some small and medium effect QTL on 1BS, 3BS, 4AL and 6BL (Buerstmayr & Buerstmayr, 2015). 4AL and 6BL were also present in our AM. In the study by Lu et al in 2013, 19 QTLs were associated with FHB resistance. Of these 15, 4AL, 5AS, 5AL, 5BL, 6AS and 7AL were similar to the results in our study (Lu et al, 2013).

From the validation test on the selected markers in table 27, we see that none of the markers selected for FHB were significant for FHB in any of the years. The reason for this could be that the testing population does not show large enough variation the markers to be significant. Table 52 shows that there were no significant markers at all for FHB in 2014. 2014 had a generally low FHB infection compared to 2013 and 2015. It is worth mentioning that the two markers BS00110550_51 and BS00022459_51 on 3A on position 414 and 439, respectively, show very low p-values for FHB, and is also significant for AE. The markers that show significance for FHB in 2013 and 2015 were initially selected for their association with DON and AE. In figure 19 we see that there is a clear correlation between DON values and FHB infection. So we would expect some of the markers selected for DON to be significant for FHB, since the pathogen used the mycotoxin to attack the host, making them more susceptible to fungal spread.

5.3. DON

The association mapping for DON revealed significant markers for 21 QTLs on chromosome 1AL, 1BSc, 2AL, 2ALc, 2BSc, 2BL, 2DS, 3AL, 3ALc, 3DL, 4A, 4B, 5A, 5B, 5DS, 5DL, 6BS, 6DL, 7AL, 7BL and 7D. These QTLs are based on DON data from 2013-2015. The significant markers selected for genotyping were based on data from 2013-2014 and is listed in table 26. The most noticeable differences in figure 40 and 42, is that by adding data from 2015 to the MLM is that we get significant markers on 1AL, 3AL and 7D. Other QTSs get less significant, such as 1D, 4A and 7B. There is also a generally lower significance level in the data from 2013-2015 than in the data from 2013-2014.

The meta-analysis in table 2 by Liu et al. in 2009 revealed 3 QTLs for DON accumulation resistance on 2A, 3BS and 5A(Liu et al., 2009). The QTLs on 3BS and 5A showed association to type 1 and 2 resistance as well, while the QTL on 2A only showed effect for DON accumulation. Our AM revealed no QTL on 3BS, which is likely the major QTL *fhb1* from Sumai 3. Our AM did reveal two QTL on 2A and one on 5A, which could be the same as were found in the meta-analysis. The marker on 5A did show a -10log (p-value) of 1,7 for FHB. Even though this is not considered significant by the threshold we set, it could still be a minor QTL for FHB. The markers for the two QTLs on 2A showed similar significance for FHB. The marker BS00022896_51 on 2AL position 266 actually lies fairly close to the most significant marker for FHB on 2A BobWhite_c4743_63 on position 268.

A QTL analysis by Jiang et al in 2007 revealed 2 new QTL for DON accumulation resistance on 1AS and 2DL (Jiang et al., 2007B). These do not show significance in our AM, as our significant markers on 1A are located on position 462, and position 6 for chromosome 2D. Another QTL study on winter wheat by Draeger et al in 2007, revealed three QTLs for DON resistance on 4DS, 6BL and 7DL (Draeger et al., 2007). The QTL on 4DS is the functional marker for the dwarf gene Rht-D1. Our AM revealed significant markers on 6B position 115, which is likely the short arm of the chromosome, and 7D position 263, which is probably on the long arm. QTL found on 7D could be the same as our study revealed.

The validation test in table 27 showed that many of the significant markers selected for DON showed significant effects on the testing population. A total of five markers shown in table 27 and 28 had significant effect for DON values in all three years, and had a high enough minor allele frequency that we can say that their significance was not by chance. 3 of the markers were located on chromosome 4A position 200. And even though these markers were less significant when we added DON data from 2015, they are still among the most significant

markers on 4A in the AM from 2013-2015. The markers were also significant for PH in 2014 and FHB in 2015. Another marker on 5D position 270 showed significance for DON in all the years, as well as DH in 2013 and 2015, PH in 2014 and FHB in 2013 and 2015. This marker is still highly significant in the AM for 2013-2015. The last marker to pass the validation test is located on 7B position 502, and this marker is also considered significant in the AM for 2013-2015. Table 27 also shows that there were three markers on 5A position 737, 5D position 178 and 6D position 185 that were not considered significant because of a minor allele frequency lower than 6 in the testing population. When the number of lines carrying an allele gets too low, we cannot say if the phenotypic variation is by chance or if it is the effect of the allele.

5.4. Spring and winter wheat

Spring wheat and winter wheat are two distinct genetic populations, and show different significant areas for AE and FHB. One of the most noticeable QTLs is the dwarf gene Rht-D1 on 4D that is significant for PH and FHB in winter wheat but not in spring wheat. The opposite is true for the dwarf gene Rht-B1 on 4B that is significant for PH and FHB in spring wheat but not in winter wheat. The degree of fixation of these genes in the winter and spring wheat populations can explain why they show difference in significance, since Rht-D1 is present in larger degree in winter wheat than spring wheat, and Rht-B1 is present in a larger degree in spring wheat.

The QTLs that spring and winter wheat have in common for AE are on 2BL, 4ALc and 4AL. The markers on 2BL were selected for genotyping in spring wheat but were not in the validation test due problems during genotyping. Both the study Buerstmayr in 2015 and Lu et al. in 2013 confirmed significant markers for AE on 4AL (Buerstmayr & Buerstmayr, 2015)(Lu et al., 2013). The significant marker for 4AL in winter wheat is located on position 603, which is the same position as significant markers for both AE and FHB in spring wheat. There are no significant marker for FHB on 4A in winter wheat. The QTLs that spring and winter wheat have in common for FHB are on 6BS, 6BL and 7BLc. The meta analysis by Liu et al. in 2009 revealed a QTL for FHB on 6BS. 6BL was confirmed in the mapping done by Buerstmayr in 2015 (Buerstmayr & Buerstmayr, 2015). The QTL analysis of winter wheat variety Arina by Draeger et al. in 2007 confirms a QTL for FHB resistance on 7BL(Draeger et al., 2007). Most of the QTLs for AE and FHB in spring and winter wheat are different, except for the six mentioned above that are all confirmed in previous QTL studies, except for 2BL for AE.

Chapter 6: Discussion

6.1. Association mapping

Association mapping (AM) is a way to identify marker alleles that has statistical association with a trait. For a marker to become significant, it needs to be closely linked to a gene responsible for the variation observed in the phenotype. But factors like selection and genetic relationship between lines can cause markers to show significance when they are not actually linked to the favorable QTL. A large selection factor is breeding, which fixates large portions of chromosome within breeding lines. And with breeding programs in different parts of the world, we get populations that have different parts of the genome in common. Within MASBASIS, there are five populations in spring wheat from Norway, Sweden, Europe, China and CIMMYT. By adding the population structure, and a kinship matrix based on the genotypic data of the SNP chip, we can reduce the number of false significant markers that is due to relationship between lines.

Genetic resolution depends on the amount of recombination within the experimental population. In populations with distantly related individuals, many generations has passed since the last common ancestor. Therefore, resolution will generally be higher in an association mapping population than in a simple biparental population. A biparental population can increase its resolution by intercrossing and increasing the number of progeny. However, this increases both the time and labor of the experiment, making association mapping more cost efficient than biparental crossing.

Some of the main factors affecting the accuracy of AM is the number of markers, the coverage of the markers, the allele frequency within the population, the phenotypic variation within the population, the accuracy of trait assessment and environmental conditions. AM has in the last 10 years become useful, especially for studies of complex traits that has several genes that contribute with moderate to low effect on the phenotype. One of the reasons for the increasing use of AM is availability of SNP chips, which contains several thousand markers that covers the large portions of the genome.

In our AM we use a 90K SNP chip, which contain 27 000 SNPs that have a high minor allele frequency in our population. The population used is called MASBASIS and contains around 400 lines of winter and spring wheat from Norway, Sweden, Europe and China. This population shows a high degree of phenotypic variation. There are mainly three traits that we study in this AM, anther extrusion, fusarium head blight resistance, and DON accumulation

resistance. Anther extrusion and Fusarium head blight severity is scored visually, and can have high assessment errors depending on the experience on the person scoring. DON is measured more accurately with LC-MS method in a lab, giving this trait a generally lower assessment error. The difference in assessment errors for the traits could be one of the reasons we have very few significant markers that show significance in the validation test for AE and FHB compared to DON (Table 27).

Both FHB and AE are strongly affected by the environment. In figure 5 we see how much the DON values varies between years. More importantly, how the phenotypic variation between lines varies between years. In 2009 at Vollebekk the phenotypic variation between the five cultivars in figure 5 is almost none existing, while just one year later in the same location, Zebra and Demonstrant showed almost twice as much DON content as the others. Because the phenotypic variation in even the most accurate measuring factor like DON can vary so much between years, it is important to use mean values from several years. Mean values should increase the accuracy of the data used in the AM. In our AM we used the least square mean values from three years in the same location. And as we see in table 50, 52 and 55 the FHB and DON data from 2014 are very low compared to 2013 and 2015. The reason for this is mainly a lower amount of infected oat grains in the trial in 2014, in combination with dry conditions after inoculation that did not favor fungal growth. Before we had DON data from 2015, we used data from 2013 and 2014. By comparing the results from 2013-2014 in figure 42 and the results from 2013-2015 in figure 40, we see that significance level has in general gone down with the addition of the data from 2015. The reason for this difference is likely due to some very high levels of DON in some of the susceptible cultivars in 2014, a year with generally low infection. The large variation in DON then increases the significance of markers in these few lines. In 2015, the variation is not as high, making the general significance level lower. In addition, some of peaks that were highly significant in 2013-2014, like 5AL and 7AL are no longer considered significant with the addition of data from 2015. Other areas that were not significant in 2013-2014, like 1AL and 3AL are now considered highly significant with the addition of data from 2015. These significant markers from 2013-2014 is likely connected to special factors like environment for those years. So data from 2013-2015 are considered more accurate, and tell us more about the general differences in resistance between lines, instead of showing significant markers that is connected to special conditions.

6.2. Challenges of association mapping

The quality of the phenotypic data is very important, and one of the biggest challenges with AM (Rafalski, 2010). FHB and AE are strongly affected by environmental conditions. In our experiments, we consider environment by using mean data for several years, using mist irrigation to make a good condition for fungal growth and use an alpha-lattice design to correct for differences in field conditions.

Another big challenge of AM, is the number of false significant markers. The goal of the AM is to find markers that are closely linked to a QTL for the trait we are looking at. But some association can be explained by other traits than the one we are interested in. For example, plant height, time of flowering and anther extrusion have shown to be highly correlated with FHB. So when looking at only the FHB data, we also get significant markers for the other traits that are linked to FHB. The model correct for DH and PH by running a regression against these traits. AE is not being corrected for, since higher AE does not have any known undesirable effects, like tall plants.

Relationship between lines can also increase the number of false significant markers, since there have been fewer recombinations between them, and will therefore have larger part of its genomes in common. The population structure and kinship is used to correct for this factor. A problem with this approach is that you can overcorrect markers that are truly significant, making them not significant. An example of this is the major FHB resistance QTL *fhb1* on chromosome 3BS, that have not been detected in our AM. Both Sumai 3 and CJ9306 are present in the population, but its effect is being corrected for by population structure since it is not present in any other breeding material than the ones from China. Other reason for a resistance QTL to lack significance is that its effect is generally too small to be detected. Sometimes, QTLs can be in linkage disequilibrium with each other, even when they are not on the same chromosome. This linkage is more difficult to correct for, because it is not necessarily connected to relationship between lines.

For a marker to be truly associated with a trait, its effect can be validated in a different population. If a marker show significance in a different genetic background for the same trait, it has true association with the trait. One of the challenges of this approach, is to have a large enough testing population, with large enough variation for the marker to be significant. Also the population needs to have high minor allele frequency for the significant marker. If the minor allele frequency is too small, we cannot say if the effect of the allele is due to genetics

or other factors like environment or linked traits. For rare alleles it is recommended to map them using biparental segregation.

6.3. Genomic selection

Genomic selection is a new method for improving quantitative traits in a breeding population, by using a set of high-density markers that include both SNP markers and genotype-by-sequencing markers(CIMMYT, 2016). The marker set should be dense enough so that each trait locus is in linkage disequilibrium with at least one marker. The genomic prediction is being made based on marker data, phenotypic data and pedigree (if available). The way it works in practice is that a reference population or training population is being phenotyped in different environmental conditions. These data are being used to calculate the effect of each marker in this reference population. Kinship between breeding lines is also calculated into the model. A validation population derived from the reference population is then being genotyped and selected purely on the genetic information and not the phenotypic information. And selection from that point on should only be done by genotyping. Considering the reduced cost of genotyping over the last 10 years, which is predicted to continue to drop, genomic selection could save the breeders a lot of money from field trials and phenotyping. Additionally, it could be able to capture the effect of minor QTLs that association mapping cannot (Korte & Farlow 2013). Some of the challenges of this method in bread wheat is that the genome is very large. Bread wheat is hexaploid, with three different genomes, and a total genome size of 17 GB. It would prove difficult to get a dense enough marker set to capture all the genetic diversity in such a large genome. In addition, many traits in wheat are associated with each other, making selection on one trait effect others. For instance, if we make genomic selection for fusarium head blight alone we will end up with a very tall population, since height has such a large effect on FHB. The model would need to be trained again to keep the selection from going in the wrong direction. It is however a method that has proved more cost effective in other areas like cattle, and could potentially work in wheat with a dense enough marker set. However, as the environment affects the phenotypic traits in such a high degree, a large reference population will be needed in different growing condition in order to properly train the model. And if the model needs to be trained again in a few years, then the cost would increase. One of the main point of genomic selection, is that you don’t need phenotyping. In addition, for the model to be able to make selection based on genotype alone, it should be able to score the markers differently, so that undesired traits associated with the desired trait are not selected for. Genomic selection is a very promising tool for plant breeders, and has yet to

be implemented here I Norway. With reduced cost of genotyping, and a well calculated model, could genomic selection reduce time and labor for breeding companies. However, association mapping is still a cost effective way to map populations for QTSs. Information gathered from association mapping could increase accuracy of genomic selection by modifying the score of known QTLs.

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Appendix 1

Spring wheat 2015

Table 31: Significant markers for anther extrusion (AE) at a-LOG(p-value) threshold of 2,5 with position on chromosome (cM) and allele effects for spring wheat lines in 2015 where n number of 'a' lines are indicated by a positive effect and 'b' by a negative effect.

Marker	Chr	Pos	p-value	R^2	n=a	n=b	Effect
RAC875_c44365_203	3B	270	0.0005	0.105	69	54	0.67
BS00073407_51	3B	271	0.0009	0.094	40	83	-0.96
RAC875_c24113_591	3B	271	0.0010	0.093	86	37	0.88
Kukri_c4599_482	3B	270	0.0012	0.090	70	53	0.56
Ku_c24974_674	3B	363	0.0013	0.089	74	49	0.29
IAAV1291	3B	271	0.0013	0.089	92	31	0.49
IAAV1270	3D	329	0.0015	0.087	29	94	1.29
BobWhite_c20558_413	4A	591	0.0015	0.087	103	20	-0.96
Kukri_c3948_209	4A	447	0.0016	0.086	25	98	-0.33
RAC875_c5834_235	4A	591	0.0019	0.083	102	21	-0.83
BobWhite_c10610_149	4A	392	0.0021	0.081	76	47	-0.50
Excalibur_c6749_694	4A	392	0.0021	0.081	76	47	-0.50
IAAV8683	4A	392	0.0022	0.080	24	99	0.23
Ku_c1125_814	4A	392	0.0022	0.080	24	99	0.23
IACX20775	5B	557	0.0022	0.080	70	53	0.91
BS00060460_51	5B	561	0.0022	0.080	69	54	0.74
BobWhite_c10956_71	5B	565	0.0023	0.080	68	55	0.79
wsnp_Ex_c7781_13255634	5B	565	0.0023	0.080	68	55	0.79
BobWhite_c5782_825	6A	158	0.0026	0.078	118	5	3.10
wsnp_Ex_c1011_1931797	6A	104	0.0026	0.078	88	35	1.30
barc125_170			0.0030	0.075	118	5	3.10

Table 32: Significant markers for days to heading (DH) at a-LOG(p-value) threshold of 2,5 with position on chromosome (cM) and allele effects for spring wheat lines in 2015 where n number of 'a' lines are indicated by a positive effect and 'b' by a negative effect.

Marker	Chr	Pos	p-value	R^2	n=a	n=b	Effect
BobWhite_c17044_155	1B	102	0.0002	0.119	47	76	1.59
Ra_c48966_260	1B	201	0.0005	0.106	110	13	-2.81
IAAV3430	1B	142	0.0008	0.096	18	105	2.61
BS00022180_51	1B	206	0.0021	0.081	19	104	2.64
IAAV2452	1B	201	0.0023	0.080	19	104	2.27
Excalibur_c111213_145	1B	208	0.0024	0.079	105	18	-2.65
BS00067201_51	1B	195	0.0025	0.078	23	100	1.88
BS00013901_51	1B	201	0.0030	0.075	20	103	2.24
BS00093736_51	1B	201	0.0030	0.075	20	103	2.24
Excalibur_c2426_931	2D	215	0.0025	0.078	84	39	1.54
BS00105741_51	3B	56	0.0006	0.102	21	102	1.74
wsnp_Ex_rep_c66766_65123941	3B	90	0.0007	0.100	22	101	1.69
Excalibur_c4325_1150	4A	402	0.0004	0.107	89	34	1.72
Excalibur_c4325_466	4A	402	0.0004	0.107	89	34	1.72
BobWhite_c7217_317	4A	402	0.0005	0.104	86	37	1.78
wsnp_BE405275A_Ta_1_1	4A	116	0.0008	0.098	12	111	2.15
CAP11_c18_238	4A	402	0.0016	0.085	87	36	1.55
wsnp_CAP11_c8366_3622210	4A	414	0.0017	0.085	114	9	2.66
RAC875_c35453_201	4A	420	0.0017	0.085	114	9	2.66
RAC875_c35979_263	4A	420	0.0017	0.085	114	9	2.66
TA003110-1046	4A	420	0.0017	0.085	114	9	2.66
tplb0046a02_804	4A	420	0.0022	0.080	115	8	2.88
CAP12_c2983_140	4B	223	0.0000	0.148	17	106	2.20
Kukri_c15910_159	4B	203	0.0002	0.124	46	77	1.63
IAAV163	4B	203	0.0002	0.120	46	77	1.60
RAC875_c104414_76	4B	203	0.0002	0.120	46	77	1.60
RAC875_c15807_669	4B	203	0.0002	0.120	46	77	1.60
wsnp_Ra_rep_c69724_67278233	4B	208	0.0002	0.120	46	77	1.60
Excalibur_c38012_393	4B	203	0.0002	0.119	47	76	1.59
Kukri_c32064_629	4B	203	0.0002	0.119	47	76	1.59
RAC875_c54178_90	4B	203	0.0002	0.119	47	76	1.59
wsnp_Ex_c296_573976	4B	203	0.0002	0.119	47	76	1.59
BS00068851_51	4B	208	0.0002	0.119	47	76	1.59
wsnp_Ex_c32127_40841791	4B	221	0.0004	0.108	11	112	2.10
Tdurum_contig86933_317	4B	206	0.0013	0.089	40	83	1.45
BS00087144_51	4B	206	0.0014	0.088	41	82	1.45
wsnp_Ku_rep_c104382_90867406	4B	206	0.0014	0.088	41	82	1.45
RAC875_rep_c72961_977	4B	220	0.0014	0.088	27	96	1.57
wsnp_Ku_c7453_12833586	4B	206	0.0016	0.086	40	83	1.44
wsnp_Ex_c26807_36031771	4B	220	0.0016	0.086	28	95	1.54
wsnp_Ex_c296_574790	4B	203	0.0017	0.085	80	43	-1.41
Tdurum_contig47552_957	4B	206	0.0018	0.084	42	81	1.39
IAAV971	4B	167	0.0022	0.080	41	82	1.33
Rht-B1	4B	159	0.0030	0.075	78	45	-1.22
RAC875_rep_c105718_304	4D	119	0.0005	0.106	56	67	1.50
RAC875_rep_c105718_585	4D	119	0.0005	0.105	68	55	-1.48
RAC875_rep_c105718_672	4D	119	0.0005	0.105	68	55	-1.48
RFL_Contig1284_640	5A	414	0.0023	0.080	48	75	-1.14
BS00009514_51	6A	40	0.0011	0.091	31	92	1.28

BS00022523_51	6D	52	0.0007	0.099	53	70	1.25
BS00021983_51	6D	52	0.0008	0.097	69	54	-1.23
IACX9471	6D	39	0.0013	0.089	53	70	1.16
wsnp_Ku_c2637_5009091	6D	41	0.0015	0.087	48	75	1.22
IACX17522	7A	260	0.0013	0.089	92	31	1.44
wsnp_JD_c1635_2290177	7A	676	0.0023	0.080	106	17	1.75
GENE-4833_102	7B	122	0.0022	0.080	30	93	1.34

Table 33: Significant markers for Fusarium head blight (FHB) at a-LOG(p-value) threshold of 2,5 with position on chromosome (cM) and allele effects for spring wheat lines in 2015 where n number of 'a' lines are indicated by a positive effect and 'b' by a negative effect.

Marker	Chr	Pos	p-value	R^2	n=a	n=b	Effect
RAC875_c57939_175	1A	95	0.0023	0.080	109	14	-16.48
wsnp_Ex_c14273_22230844	1B	153	0.0015	0.086	80	43	-12.86
BS00079611_51	2A	431	0.0011	0.091	14	109	19.62
wsnp_Ex_c59095_60108097	2A	417	0.0018	0.083	111	12	-20.62
Kukri_rep_c90581_382	2A	355	0.0031	0.075	110	13	15.51
Excalibur_c55414_254	3B	297	0.0009	0.095	87	36	-16.62
Ku_c47648_1403	3B	297	0.0009	0.095	36	87	16.62
Ra_c106076_67	3B	297	0.0009	0.095	36	87	16.62
wsnp_Ex_c8825_14757625	3B	297	0.0009	0.095	36	87	16.62
RAC875_c46966_193	3B	298	0.0009	0.095	36	87	16.62
Tdurum_contig10608_1081	3B	56	0.0014	0.088	40	83	11.52
wsnp_Ex_c6129_10723211	3B	297	0.0017	0.085	89	34	-15.57
Kukri_c7087_896	3B	289	0.0017	0.085	113	10	-23.02
wsnp_Ku_c50833_56310020	3B	300	0.0026	0.077	112	11	-20.82
wsnp_Ku_rep_c102135_89174746	3D	416	0.0015	0.087	37	86	15.11
BobWhite_c47401_491	5A	737	0.0004	0.107	15	108	19.57
wsnp_Ex_c20899_30011827	5A	737	0.0004	0.107	108	15	-19.57
Excalibur_rep_c106082_272	5D	532	0.0021	0.081	20	103	-12.02
wsnp_Ex_c1011_1931797	6A	104	0.0007	0.100	88	35	-14.60
GENE-3689_680	6A	338	0.0027	0.077	118	5	-25.95
Kukri_c79905_1112	6A	338	0.0027	0.077	118	5	-25.95
RFL_Contig5693_646	6A	103	0.0028	0.077	49	74	12.84
RFL_Contig4626_873	6D	180	0.0022	0.080	22	101	13.77
Excalibur_c1142_724	7A	555	0.0000	0.163	6	117	34.27
BS00079076_51	7B	296	0.0001	0.131	16	107	-22.92
BS00066484_51	7B	296	0.0003	0.112	15	108	-21.83
BobWhite_rep_c49050_1890	7B	296	0.0003	0.112	15	108	-21.83
Excalibur_c29124_598	7B	296	0.0003	0.112	15	108	-21.83
GENE-4958_195	7B	296	0.0003	0.112	15	108	-21.83
GENE-4958_208	7B	296	0.0003	0.112	15	108	-21.83
TA004145-0795	7B	296	0.0003	0.112	15	108	-21.83
GENE-4796_696	7B	296	0.0014	0.088	15	108	-18.87
BS00029789_51	7B	296	0.0020	0.082	16	107	-17.77
Tdurum_contig62213_423	7B	547	0.0022	0.080	22	101	-15.53
tplb0035h03_1251	7B	463	0.0031	0.075	59	64	-10.51
barc228_194		58	0.0012	0.090	117	6	-26.44

Table 34: Significant markers for Fusarium head blight after regression (FHB_reg) at a-LOG(p-value) threshold of 2,5 with position on chromosome (cM) and allele effects for spring wheat lines in 2015 where n number of 'a' lines are indicated by a positive effect and 'b' by a negative effect.

Marker	Chr	Pos	p-value	R^2	n=a	n=b	Effect
wsnp_Ex_c14273_22230844	1B	153	0.0007	0.098	80	43	-12.57
wsnp_Ex_c59095_60108097	2A	417	0.0011	0.092	111	12	-19.25
Tdurum_contig60298_219	2A	464	0.0019	0.083	112	11	-19.43
Tdurum_contig60205_806	2A	466	0.0019	0.083	112	11	-19.43
wsnp_Ex_c45_97816	2A	466	0.0019	0.083	112	11	-19.43
BS00029332_51	2A	392	0.0022	0.081	48	75	-13.49
BS00022896_51	2A	366	0.0025	0.078	106	17	-15.61
Tdurum_contig50577_620	3A	574	0.0029	0.076	71	52	-9.26
Tdurum_contig10608_1081	3B	56	0.0012	0.090	40	83	10.79
BobWhite_c11540_60	3B	268	0.0021	0.081	60	63	-10.98
wsnp_Ex_c2580_4800027	3B	269	0.0024	0.079	70	53	10.38
BobWhite_c1656_845	4B	63	0.0025	0.078	117	6	-21.89
BobWhite_c47401_491	5A	737	0.0001	0.129	15	108	19.37
wsnp_Ex_c20899_30011827	5A	737	0.0001	0.129	108	15	-19.37
JD_c20036_865	5A	314	0.0004	0.110	7	116	27.63
Ra_c700_1024	5A	314	0.0004	0.110	116	7	-27.63
Ra_c700_2210	5A	314	0.0004	0.110	7	116	27.63
RAC875_c8642_231	5A	709	0.0004	0.107	26	97	18.14
Excalibur_c2171_2728	5A	742	0.0011	0.091	22	101	15.75
wsnp_Ex_c2171_4074003	5A	742	0.0011	0.091	22	101	15.75
wsnp_Ku_c15816_24541162	5A	314	0.0013	0.089	109	14	-16.75
TA006089-0703	5A	117	0.0016	0.085	108	15	-14.67
BS00043532_51	5A	314	0.0028	0.076	112	11	-17.51
GENE-2689_215	5B	359	0.0023	0.080	12	111	-15.60
wsnp_Ex_c1011_1931797	6A	104	0.0017	0.085	88	35	-12.00
GENE-3689_680	6A	338	0.0029	0.076	118	5	-21.93
Kukri_c79905_1112	6A	338	0.0029	0.076	118	5	-21.93
RFL_Contig4626_873	6D	180	0.0018	0.083	22	101	13.08
Excalibur_c1142_724	7A	555	0.0000	0.156	6	117	30.01
Kukri_rep_c70864_638	7A	256	0.0030	0.075	14	109	16.94
wsnp_Ex_c13248_20898211	7A	256	0.0030	0.075	14	109	16.94
Tdurum_contig54832_139	7A	592	0.0032	0.074	108	15	16.42
tplb0060b03_432	7B	534	0.0029	0.076	60	63	-10.40
BobWhite_c29953_89	7B	229	0.0030	0.075	118	5	-21.92
BobWhite_c44558_325	7B	229	0.0030	0.075	5	118	21.92
Kukri_rep_c113231_244	7B	229	0.0030	0.075	5	118	21.92
RAC875_c18513_376	7B	229	0.0030	0.075	5	118	21.92
RAC875_rep_c71932_86	7B	229	0.0030	0.075	5	118	21.92
wsnp_Ku_c18780_28136150	7B	229	0.0030	0.075	118	5	-21.92

Table 35: Significant markers for plant height (PH) at a-LOG(p-value) threshold of 3,0 with position on chromosome (cM) and allele effects for spring wheat lines in 2015 where n number of 'a' lines are indicated by a positive effect and 'b' by a negative effect.

Marker	Chr	Pos	p-value	R^2	n=a	n=b	Effect
BS00021739_51	2A	355	0.00018	0.125	11	110	9.55
BS00079443_51	2A	355	0.00018	0.125	11	110	9.55
RAC875_rep_c73925_276	2A	355	0.00018	0.125	11	110	9.55
BS00070120_51	2B	291	0.00052	0.106	27	94	9.08
wsnp_JD_c9434_10274598	3A	271	0.00060	0.104	99	22	7.27
Excalibur_rep_c113157_316	3B	269	0.00060	0.104	10	111	10.61
RAC875_c30414_343	3B	269	0.00060	0.104	10	111	10.61
RAC875_rep_c105184_88	3B	269	0.00060	0.104	10	111	10.61
wsnp_BQ168706B_Ta_2_1	3B	269	0.00060	0.104	10	111	10.61
wsnp_BQ168706B_Ta_2_2	3B	269	0.00060	0.104	10	111	10.61
wsnp_Ex_c21499_30644485	3B	269	0.00060	0.104	10	111	10.61
wsnp_Ku_c10291_17065480	3B	269	0.00060	0.104	10	111	10.61
BS00021984_51	4B	163	0.00007	0.142	69	52	7.59
Rht-B1	4B	159	0.00009	0.137	78	43	7.87
IAAV971	4B	167	0.00019	0.123	39	82	-7.75
BobWhite_rep_c49034_167	4B	163	0.00032	0.114	79	42	7.21
Tdurum_contig42229_113	4B	162	0.00037	0.112	78	43	7.19
RAC875_rep_c105718_430	4B	163	0.00037	0.112	78	43	7.19
Tdurum_contig33737_157	4B	163	0.00037	0.112	78	43	7.19
Excalibur_c56787_95	4B	169	0.00051	0.107	35	86	-7.14
Kukri_rep_c103857_458	5A	314	0.00001	0.178	4	117	24.35
BS00023008_51	5A	126	0.00017	0.125	10	111	11.29
RAC875_c23340_2243	5A	410	0.00034	0.113	14	107	11.20
BS00066403_51	5A	126	0.00047	0.108	112	9	-10.96
JD_c20036_865	5A	314	0.00094	0.096	5	116	16.36
Ra_c700_1024	5A	314	0.00094	0.096	116	5	-16.36
Ra_c700_2210	5A	314	0.00094	0.096	5	116	16.36
Ra_c3356_506	6A	332	0.00075	0.100	19	102	7.48
BS00067590_51	6B	168	0.00005	0.149	11	110	14.32
GENE-0221_350	6B	168	0.00005	0.149	11	110	14.32
GENE-0221_721	6B	168	0.00005	0.149	11	110	14.32
Kukri_c31032_897	6B	168	0.00005	0.149	11	110	14.32
Kukri_c32307_481	6B	168	0.00005	0.149	11	110	14.32
TA005332-1378	6B	168	0.00005	0.149	11	110	14.32
RAC875_c17559_3102	6B	198	0.00008	0.140	13	108	12.06
BS00047044_51	6B	168	0.00023	0.120	13	108	11.21
BS00084314_51	6B	198	0.00029	0.116	13	108	11.18
TA002465-0455-w	6B	198	0.00029	0.116	13	108	11.18
Excalibur_s111479_146	6B	168	0.00042	0.110	112	9	-13.66
RAC875_c10650_90	6B	168	0.00042	0.110	112	9	-13.66
RAC875_rep_c116755_285	6B	168	0.00042	0.110	112	9	-13.66
RFL_Contig2024_600	6B	168	0.00042	0.110	112	9	-13.66
BS00035630_51	7B	172	0.00010	0.136	110	11	-11.80
Tdurum_contig14821_751	7B	344	0.00071	0.101	24	97	7.60

Table 36: Significant markers for DON values (DON) at a-LOG(p-value) threshold of 2,5 with position on chromosome (cM) and allele effects for spring wheat lines in 2015 where n number of 'a' lines are indicated by a positive effect and 'b' by a negative effect.

Marker	Chr	Pos	p-value	R^2	n=a	n=b	Effect
Ex_c27351_850	1A	216	0.0027	0.077	114	9	-13.90
wsnp_BE495786A_Ta_2_1	1A	240	0.0025	0.078	22	101	9.02
Kukri_c20062_389	1D	133	0.0005	0.106	10	113	16.62
CAP12_rep_c6956_169	2A	385	0.0019	0.083	21	102	-9.87
Kukri_c25843_669	2B	258	0.0024	0.079	8	115	16.15
Ku_c68678_924	2B	262	0.0002	0.123	10	113	18.93
BS00030497_51	2B	263	0.0002	0.123	10	113	18.93
Excalibur_rep_c68899_191	2B	264	0.0002	0.123	10	113	18.93
IAAV1101	2B	264	0.0002	0.123	10	113	18.93
JD_c11869_1297	2B	264	0.0002	0.123	113	10	-18.93
Tdurum_contig47202_1699	2B	264	0.0002	0.123	10	113	18.93
Tdurum_contig62458_179	2B	264	0.0012	0.090	11	112	15.48
RFL_Contig996_818	2B	264	0.0013	0.089	12	111	14.40
Tdurum_contig30989_79	2B	269	0.0012	0.090	11	112	15.48
Excalibur_c7964_1290	2B	458	0.0009	0.096	19	104	-10.33
Tdurum_contig57254_254	2B	458	0.0009	0.096	19	104	-10.33
D_contig17313_245	2D	6	0.0008	0.098	26	97	11.10
BS00067499_51	3A	218	0.0005	0.104	13	110	17.02
RAC875_rep_c109554_198	3A	604	0.0003	0.115	116	7	-19.99
Excalibur_c17654_166	3A	617	0.0003	0.115	116	7	-19.99
D_GBF1XID02GHPCU_167	3D	264	0.0030	0.075	19	104	11.72
Excalibur_c13811_1086	4A	556	0.0026	0.077	96	27	8.56
BobWhite_c20382_117	4A	591	0.0029	0.076	81	42	-8.51
Rht-B1	4B	159	0.0008	0.097	78	45	-8.84
Tdurum_contig10466_87	4B	226	0.0028	0.077	113	10	-15.85
RAC875_c67417_275	4B	230	0.0028	0.077	10	113	15.85
Ku_c102710_1055	5A	212	0.0014	0.087	16	107	14.25
wsnp_Ex_c19519_28487099	5A	344	0.0003	0.114	101	22	-17.05
Tdurum_contig17712_200	5A	344	0.0003	0.112	24	99	16.31
CAP11_c1740_41	5A	345	0.0004	0.110	21	102	18.74
wsnp_CAP11_c1740_947838	5A	345	0.0004	0.110	21	102	18.74
wsnp_Ex_c7487_12808011	5A	345	0.0004	0.110	21	102	18.74
wsnp_Ku_c3397_6300446	5A	345	0.0004	0.110	21	102	18.74
RAC875_c79649_197	5B	36	0.0026	0.077	113	10	14.82
wsnp_Ex_c56629_58677561	5B	36	0.0026	0.077	113	10	14.82
JD_c6222_563	5B	40	0.0026	0.077	10	113	-14.82
RAC875_rep_c111720_149	5B	195	0.0010	0.093	24	99	12.62
Kukri_c82296_367	5B	195	0.0025	0.079	21	102	13.94
BobWhite_c18121_478	5B	214	0.0014	0.088	22	101	13.86
BS00010909_51	5B	214	0.0025	0.079	21	102	13.94
BS00063099_51	5B	214	0.0025	0.079	21	102	13.94
BS00065996_51	5B	214	0.0025	0.079	21	102	13.94
BS00088558_51	5B	214	0.0025	0.079	21	102	13.94
BobWhite_c16398_128	5B	214	0.0025	0.079	21	102	13.94

BobWhite_c17735_131	5B	214	0.0025	0.079	21	102	13.94
BobWhite_c17735_254	5B	214	0.0025	0.079	21	102	13.94
BobWhite_c7070_196	5B	214	0.0025	0.079	21	102	13.94
BobWhite_c756_886	5B	214	0.0025	0.079	21	102	13.94
Excalibur_c18941_603	5B	214	0.0025	0.079	21	102	13.94
Excalibur_c21847_53	5B	214	0.0025	0.079	21	102	13.94
Excalibur_c28850_166	5B	214	0.0025	0.079	21	102	13.94
Excalibur_c30606_424	5B	214	0.0025	0.079	21	102	13.94
Excalibur_c560_180	5B	214	0.0025	0.079	21	102	13.94
GENE-3318_637	5B	214	0.0025	0.079	21	102	13.94
IAAV5029	5B	214	0.0025	0.079	21	102	13.94
IAAV6818	5B	214	0.0025	0.079	21	102	13.94
IAAV8929	5B	214	0.0025	0.079	21	102	13.94
IACX8282	5B	214	0.0025	0.079	21	102	13.94
Jagger_c1791_133	5B	214	0.0025	0.079	21	102	13.94
Kukri_c65301_127	5B	214	0.0025	0.079	21	102	13.94
RAC875_c38382_625	5B	214	0.0025	0.079	21	102	13.94
RAC875_c98401_90	5B	214	0.0025	0.079	21	102	13.94
RAC875_s114930_80	5B	214	0.0025	0.079	21	102	13.94
RFL_Contig4472_2387	5B	214	0.0025	0.079	21	102	13.94
wsnp_Ex_rep_c70120_69069699	5B	214	0.0025	0.079	21	102	13.94
wsnp_Ex_rep_c70120_69069885	5B	214	0.0025	0.079	21	102	13.94
wsnp_JD_c46203_31643976	5B	214	0.0025	0.079	21	102	13.94
BobWhite_c30583_75	5B	220	0.0025	0.079	21	102	13.94
TA002629-0128	5B	220	0.0025	0.079	21	102	13.94
BS00098227_51	5B	221	0.0025	0.079	21	102	13.94
BobWhite_c46203_1055	5B	221	0.0025	0.079	21	102	13.94
Excalibur_c2727_124	5B	221	0.0025	0.079	21	102	13.94
GENE-4297_86	5B	221	0.0025	0.079	21	102	13.94
Jagger_c4318_79	5B	221	0.0025	0.079	21	102	13.94
Jagger_c6210_187	5B	221	0.0025	0.079	21	102	13.94
Kukri_c66814_100	5B	221	0.0025	0.079	21	102	13.94
RAC875_c66955_439	5B	221	0.0025	0.079	21	102	13.94
RAC875_rep_c87796_168	5B	221	0.0025	0.079	21	102	13.94
RAC875_s116485_298	5B	221	0.0025	0.079	21	102	13.94
RFL_Contig2357_185	5B	221	0.0025	0.079	21	102	13.94
RFL_Contig3939_1276	5B	221	0.0025	0.079	21	102	13.94
BS00022068_51	5B	222	0.0025	0.079	21	102	13.94
BS00098228_51	5B	222	0.0025	0.079	21	102	13.94
BobWhite_c8422_189	5B	222	0.0025	0.079	21	102	13.94
wsnp_Ex_c33327_41834973	5D	151	0.0013	0.090	24	99	12.03
wsnp_JD_rep_c62958_40146122	5D	224	0.0005	0.107	19	104	14.71
BobWhite_c23224_196	5D	311	0.0014	0.087	24	99	13.71
BS00099074_51	6A	287	0.0011	0.092	20	103	10.35
RAC875_c27781_591	6A	329	0.0005	0.105	17	106	-13.76
Excalibur_c30571_346	6D	335	0.0010	0.093	110	13	-14.49
Excalibur_c2991_320	6D	335	0.0016	0.086	16	107	12.03
Excalibur_c63506_512	6D	335	0.0016	0.086	16	107	12.03

cfd56_271	SSR	133	0.0019	0.083	100	23	-11.22
gwm148_184	SSR	284	0.0016	0.086	109	14	-11.49
gwm410_372	SSR	487	0.0002	0.125	115	8	-20.87

Table 37: Significant markers for DON values after regression (DON_reg) at a-LOG(p-value) threshold of 2,5 with position on chromosome (cM) and allele effects for spring wheat lines in 2015 where n number of 'a' lines are indicated by a positive effect and 'b' by a negative effect.

Marker	Chr	Pos	p-value	R^2	n=a	n=b	Effect
CAP12_rep_c6956_169	2A	385	0.0011	0.093	20	101	-9.89
Kukri_c44_1704	2B	257	0.0030	0.076	112	9	-13.76
RAC875_rep_c99492_65	2B	257	0.0030	0.076	9	112	13.76
Kukri_c62277_80	2B	259	0.0030	0.076	9	112	13.76
Ku_c68678_924	2B	262	0.0002	0.122	10	111	17.68
Kukri_c44_1476	2B	262	0.0030	0.076	9	112	13.76
RAC875_c6751_609	2B	262	0.0030	0.076	9	112	13.76
BS00030497_51	2B	263	0.0002	0.122	10	111	17.68
Excalibur_rep_c68899_191	2B	264	0.0002	0.122	10	111	17.68
IAAV1101	2B	264	0.0002	0.122	10	111	17.68
JD_c11869_1297	2B	264	0.0002	0.122	111	10	-17.68
Tdurum_contig47202_1699	2B	264	0.0002	0.122	10	111	17.68
Tdurum_contig62458_179	2B	264	0.0009	0.096	11	110	14.99
RFL_Contig996_818	2B	264	0.0030	0.076	12	109	12.50
Tdurum_contig60978_352	2B	267	0.0030	0.076	12	109	13.23
Tdurum_contig30989_79	2B	269	0.0009	0.096	11	110	14.99
Jagger_c36_213	2B	269	0.0030	0.076	12	109	13.23
Excalibur_c7964_1290	2B	458	0.0018	0.085	19	102	-9.15
Tdurum_contig57254_254	2B	458	0.0018	0.085	19	102	-9.15
RAC875_c95081_166	2B	458	0.0030	0.077	13	108	-9.37
BS00067499_51	3A	218	0.0029	0.077	13	108	13.68
RAC875_rep_c109554_198	3A	604	0.0004	0.109	114	7	-18.24
Excalibur_c17654_166	3A	617	0.0004	0.109	114	7	-18.24
Excalibur_c24391_321	3B	183	0.0021	0.082	39	82	-7.24
Tdurum_contig56661_291	3B	292	0.0020	0.083	56	65	7.90
IAAV792	3B	292	0.0020	0.083	67	54	-7.89
RAC875_c106500_413	3B	292	0.0026	0.079	57	64	7.74
Ra_c9061_2115	3B	292	0.0026	0.079	57	64	7.74
wsnp_Ex_c7291_12517871	3B	292	0.0026	0.079	57	64	7.74
BobWhite_c20382_117	4A	591	0.0018	0.085	80	41	-8.44
Excalibur_rep_c69170_425	4A	591	0.0022	0.082	43	78	8.09
wsnp_Ex_c13953_21832185	4A	591	0.0022	0.082	43	78	8.09
RAC875_c4965_1523	4A	591	0.0024	0.080	81	40	-7.66
BS00040305_51	4B	176	0.0025	0.080	37	84	7.59
Tdurum_contig86933_317	4B	206	0.0021	0.082	39	82	-8.22
Tdurum_contig47552_957	4B	206	0.0030	0.077	41	80	-7.81
Kukri_c17224_278	4B	208	0.0029	0.077	97	24	-8.53
Ku_c102710_1055	5A	212	0.0019	0.084	15	106	13.06
Tdurum_contig17712_200	5A	344	0.0023	0.081	23	98	12.97

Kukri_c16864_398	5B	521	0.0028	0.078	110	11	-11.28
Tdurum_contig65330_190	5B	521	0.0028	0.078	110	11	-11.28
wsnp_JD_rep_c62958_40146122	5D	224	0.0005	0.105	18	103	13.72
Excalibur_c58410_729	6B	327	0.0022	0.082	21	100	10.18
wsnp_Ex_rep_c70036_68988728	6B	327	0.0022	0.082	21	100	10.18
Excalibur_c30571_346	6D	335	0.0023	0.081	108	13	-12.71
wsnp_Ex_c10430_17064001	7D	263	0.0031	0.076	66	55	-6.81
gwm148_184	SSR	284	0.0003	0.118	107	14	-12.69
gwm410_372	SSR	487	0.0008	0.098	113	8	-17.23

Winter wheat 2015

Table 38: Significant markers for anther extrusion (AE) at a-LOG(p-value) threshold of 2,5 with position on chromosome (cM) and allele effects for winter wheat lines in 2015 where n number of 'a' lines are indicated by a positive effect and 'b' by a negative effect.

Marker	Chr	Pos	p-value	R^2	n=a	n=b	Effect
BobWhite_c20902_177	1A	66	0.0031	0.208	23	25	-1.48
BS00080318_51	2B	424	0.0020	0.228	25	23	1.70
BS00084417_51	2B	431	0.0020	0.228	25	23	1.70
Excalibur_c224_1383	2B	431	0.0020	0.228	25	23	1.70
GENE-1355_265	2B	431	0.0020	0.228	25	23	1.70
IACX8947	2B	431	0.0020	0.228	25	23	1.70
Kukri_c21087_79	2B	431	0.0020	0.228	25	23	1.70
Kukri_c25702_948	2B	431	0.0020	0.228	25	23	1.70
Excalibur_c63327_110	2B	431	0.0022	0.223	26	22	1.63
Excalibur_c8314_405	3B	80	0.0021	0.227	42	6	1.93
tplb0028p23_691	3B	204	0.0026	0.215	13	35	-1.45
Kukri_c49752_254	3B	56	0.0030	0.210	41	7	2.44
RAC875_rep_c118229_56	3B	56	0.0030	0.210	41	7	2.44
Tdurum_contig96830_155	5A	290	0.0004	0.306	9	39	2.15
Ex_c9327_1198	5A	278	0.0020	0.228	40	8	-1.95
Ex_c9327_1907	5A	278	0.0020	0.228	8	40	1.95
IAAV6488	5A	278	0.0020	0.228	8	40	1.95
Tdurum_contig59338_1902	5A	278	0.0020	0.228	8	40	1.95
Tdurum_contig76136_404	5A	278	0.0020	0.228	8	40	1.95
Excalibur_s102388_276	6A	50	0.0007	0.280	13	35	1.90
wsnp_Ex_c9779_16145653	6A	50	0.0007	0.280	13	35	1.90
Kukri_c25244_199	6A	61	0.0007	0.280	13	35	1.90
Excalibur_c9779_465	6A	61	0.0021	0.227	15	33	1.57
Kukri_rep_c101615_148	6A	61	0.0021	0.227	15	33	1.57
RAC875_c24285_1049	6D	341	0.0008	0.275	39	9	-2.29
cfd018b_207	SSR	105	0.0006	0.290	36	12	-1.86

Table 39: Significant markers for days to heading (DH) at a-LOG(p-value) threshold of 2,5 with position on chromosome (cM) and allele effects for winter wheat lines in 2015 where n number of 'a' lines are indicated by a positive effect and 'b' by a negative effect.

Marker	Chr	Pos	p-value	R^2	n=a	n=b	Effect
RAC875_c14066_452	1A	182	0.0024	0.218	42	6	4.44
Excalibur_c7237_1084	1A	184	0.0024	0.218	6	42	-4.44
RAC875_c10090_963	1A	184	0.0024	0.218	6	42	-4.44
RAC875_rep_c111911_116	1A	184	0.0024	0.218	6	42	-4.44
CAP11_c6014_160	1A	216	0.0009	0.266	31	17	2.71
TA013367-0455	1A	216	0.0009	0.266	31	17	2.71
wsnp_Ex_rep_c101746_87053634	1A	216	0.0009	0.266	31	17	2.71
Excalibur_c17872_137	1A	216	0.0018	0.232	15	33	-2.26
Excalibur_c33881_618	1A	216	0.0018	0.232	15	33	-2.26
RAC875_c15998_53	1A	216	0.0018	0.232	15	33	-2.26
wsnp_Ex_c33831_42253707	1A	216	0.0018	0.232	15	33	-2.26
Ex_c6765_2118	1A	216	0.0027	0.214	13	35	-2.31
RAC875_c38417_246	1A	216	0.0027	0.214	13	35	-2.31
RAC875_c55052_604	1A	216	0.0028	0.212	35	13	2.35
wsnp_Ex_c8885_14842394	1A	216	0.0028	0.212	35	13	2.35
wsnp_Ku_c18611_27943266	1A	216	0.0028	0.212	35	13	2.35
wsnp_Ex_c5634_9906981	1A	218	0.0011	0.256	17	31	-2.34
wsnp_Ex_c5634_9907829	1A	218	0.0011	0.256	17	31	-2.34
wsnp_Ex_c44049_50205457	1A	219	0.0005	0.295	39	9	3.58
RAC875_c41113_144	1A	219	0.0008	0.272	16	32	-2.43
BobWhite_c1488_504	1A	219	0.0009	0.266	17	31	-2.71
Kukri_rep_c101316_375	1A	219	0.0009	0.266	17	31	-2.71
wsnp_Ra_c6182_10833256	1A	219	0.0009	0.266	17	31	-2.71
wsnp_Ex_c44049_50205904	1A	219	0.0010	0.261	10	38	-2.95
CAP12_c6266_339	1A	219	0.0018	0.232	15	33	-2.26
Ex_c12763_662	1A	219	0.0018	0.232	15	33	-2.26
Excalibur_c11273_284	1A	219	0.0018	0.232	15	33	-2.26
IAAV7131	1A	219	0.0018	0.232	15	33	-2.26
Ku_c6979_182	1A	219	0.0018	0.232	15	33	-2.26
RAC875_c33300_141	1A	219	0.0018	0.232	15	33	-2.26
RAC875_c68797_400	1A	219	0.0018	0.232	15	33	-2.26
RFL_Contig5001_1099	1A	219	0.0018	0.232	15	33	-2.26
wsnp_Ex_c1374_2630830	1A	219	0.0018	0.232	15	33	-2.26
wsnp_Ex_c34260_42602746	1A	219	0.0018	0.232	15	33	-2.26
wsnp_Ex_c3572_6531810	1A	219	0.0018	0.232	15	33	-2.26
wsnp_Ex_rep_c105541_89932598	1A	219	0.0018	0.232	15	33	-2.26
wsnp_Ra_c18045_27024765	1A	219	0.0018	0.232	15	33	-2.26
Excalibur_rep_c68424_255	1A	219	0.0020	0.228	17	31	-2.07
wsnp_JD_c40990_29127031	1A	219	0.0020	0.227	14	34	-2.12
CAP8_c2843_226	1A	219	0.0027	0.214	13	35	-2.31
Excalibur_c14943_695	1A	219	0.0027	0.214	13	35	-2.31
IACX2325	1A	219	0.0027	0.214	13	35	-2.31
Kukri_rep_c103147_745	1A	219	0.0027	0.214	13	35	-2.31

CAP12_c6266_187	1A	219	0.0028	0.212	35	13	2.35
CAP12_c6266_298	1A	219	0.0028	0.212	35	13	2.35
wsnp_Ex_c21592_30743513	1A	220	0.0018	0.232	15	33	-2.26
wsnp_Ex_c21592_30743815	1A	220	0.0018	0.232	15	33	-2.26
wsnp_Ex_c34260_42602649	1A	220	0.0018	0.232	15	33	-2.26
Tdurum_contig48416_335	1A	220	0.0027	0.214	13	35	-2.31
wsnp_Ex_c34821_43076533	1A	220	0.0028	0.212	35	13	2.35
Ra_c11023_679	1A	230	0.0009	0.266	17	31	-2.71
RAC875_c18539_1159	1A	230	0.0018	0.232	15	33	-2.26
wsnp_JD_c24506_20670773	1A	230	0.0018	0.232	15	33	-2.26
wsnp_Ex_c3906_7086294	1A	230	0.0029	0.210	12	36	-2.16
wsnp_Ex_rep_c105443_89868548	1A	245	0.0029	0.210	43	5	-3.16
Kukri_c40121_373	2A	388	0.0012	0.253	35	13	2.19
Excalibur_c28325_140	2A	391	0.0012	0.253	35	13	2.19
Excalibur_c96_619	2A	402	0.0026	0.214	16	32	2.45
RAC875_c58006_352	2A	402	0.0026	0.214	16	32	2.45
BobWhite_c15773_166	2A	483	0.0028	0.211	6	42	-2.72
BobWhite_c18256_158	3A	43	0.0020	0.227	41	7	3.50
Kukri_c13830_601	3A	107	0.0011	0.259	8	40	-2.57
BobWhite_c37325_92	3A	107	0.0011	0.255	10	38	-2.51
Kukri_c13830_556	3A	107	0.0015	0.243	7	41	-2.75
TA001702-0608	3A	107	0.0015	0.243	7	41	-2.75
TA001885-0568	3A	113	0.0015	0.243	7	41	-2.75
Tdurum_contig52302_649	3A	113	0.0015	0.240	42	6	3.00
Tdurum_contig52302_92	3A	113	0.0015	0.240	42	6	3.00
wsnp_JD_c2722_3653988	3A	113	0.0015	0.240	42	6	3.00
BS00082982_51	3A	279	0.0020	0.228	4	44	-3.99
BS00110266_51	3A	279	0.0020	0.228	4	44	-3.99
Tdurum_contig61299_55	3A	280	0.0003	0.333	8	40	-4.46
tplb0050h15_1287	3A	280	0.0003	0.333	8	40	-4.46
wsnp_Ex_c2148_4035913	3A	280	0.0004	0.309	6	42	-4.53
wsnp_Ex_c32003_40728918	3A	280	0.0004	0.309	6	42	-4.53
BS00040798_51	3A	284	0.0003	0.333	8	40	-4.46
Excalibur_rep_c105085_102	3A	284	0.0003	0.333	8	40	-4.46
Kukri_c82097_197	3A	284	0.0003	0.333	8	40	-4.46
wsnp_Ex_c10667_17387885	3A	284	0.0003	0.333	8	40	-4.46
wsnp_Ex_c9468_15696542	3A	284	0.0003	0.333	8	40	-4.46
wsnp_Ra_c29280_38672141	3A	284	0.0003	0.333	8	40	-4.46
wsnp_Ex_c15269_23491104	3A	284	0.0004	0.305	5	43	-4.73
wsnp_Ex_c15269_23492289	3A	284	0.0004	0.305	5	43	-4.73
Excalibur_c29205_537	3A	284	0.0015	0.240	7	41	-3.39
IAAV4286	3A	284	0.0017	0.236	9	39	-3.15
IAAV5821	3A	285	0.0003	0.333	8	40	-4.46
Tdurum_contig50392_1355	3A	285	0.0003	0.333	8	40	-4.46
Ku_c73010_143	3A	288	0.0020	0.228	4	44	-3.99
IACX3871	3B	284	0.0008	0.276	32	16	2.38
BS00066357_51	3B	284	0.0024	0.219	33	15	2.12
Ra_c60252_1733	4A	497	0.0025	0.217	41	7	3.17

Ra_c60252_743	4A	497	0.0025	0.217	7	41	-3.17
BobWhite_c2236_111	5A	248	0.0004	0.305	43	5	4.73
BS00109052_51	5A	249	0.0004	0.305	43	5	4.73
GENE-2344_73	5A	496	0.0022	0.223	6	42	-4.30
BobWhite_rep_c64315_180	5A	496	0.0026	0.216	5	43	-4.47
GENE-4826_86	6A	81	0.0011	0.256	9	39	-3.70
IAAV1234	6A	175	0.0020	0.227	41	7	-2.81
Excalibur_c30324_564	6A	175	0.0026	0.215	8	40	2.97
Ku_c14907_456	6A	175	0.0026	0.215	8	40	2.97
Ku_c97015_209	6A	175	0.0026	0.215	8	40	2.97
IAAV5188	6A	177	0.0026	0.215	8	40	2.97
Excalibur_rep_c69189_235	6B	250	0.0026	0.214	12	36	-2.52
RAC875_c19631_269	7A	153	0.0021	0.226	42	6	3.04
Kukri_rep_c74538_62	7A	435	0.0018	0.233	43	5	3.38
wsnp_Ex_rep_c68047_66792559	7A	435	0.0018	0.233	43	5	3.38
Kukri_c22450_963	7B	178	0.0008	0.270	6	42	-4.87
GENE-4826_641	7B	182	0.0011	0.256	9	39	-3.70
Tdurum_contig10932_375	7B	182	0.0011	0.256	9	39	-3.70
Tdurum_contig81683_217	7B	186	0.0008	0.270	6	42	-4.87
wsnp_Ex_c6590_11419735	7B	186	0.0008	0.270	6	42	-4.87
Kukri_rep_c109239_223	7D	294	0.0008	0.270	41	7	3.25
wsnp_Ex_rep_c68671_67525179	7D	297	0.0008	0.270	41	7	3.25
IAAV4133	7D	299	0.0007	0.280	42	6	3.74
BS00009457_51	7D	300	0.0008	0.270	7	41	-3.25
IACX7714	7D	300	0.0008	0.270	7	41	-3.25
wsnp_Ex_rep_c66483_64738995	7D	300	0.0008	0.270	41	7	3.25
wsnp_cd454041D_Ta_2_1	7D	300	0.0008	0.270	7	41	-3.25

Table 40: Significant markers for plant height (PH) at a-LOG(p-value) threshold of 2,0 with position on chromosome (cM) and allele effects for winter wheat lines in 2015 where n number of 'a' lines are indicated by a positive effect and 'b' by a negative effect.

Marker	Chr	Pos	p-value	R^2	n=a	n=b	Effect
Excalibur_c105151_200	1A	117	0.0071	0.169	13	35	-10.52
BS00022977_51	1A	117	0.0091	0.158	33	15	7.49
BS00100287_51	1A	117	0.0091	0.158	33	15	7.49
Kukri_rep_c108031_378	1A	117	0.0091	0.158	33	15	7.49
Tdurum_contig50845_215	1A	117	0.0091	0.158	33	15	7.49
Tdurum_contig50845_82	1A	117	0.0091	0.158	33	15	7.49
BS00026453_51	1A	134	0.0091	0.158	33	15	7.49
BS00089031_51	1B	273	0.0007	0.282	22	26	12.57
GENE-0487_795	1B	276	0.0026	0.217	18	30	14.60
BS00055866_51	1B	276	0.0026	0.216	34	14	-12.22
GENE-0487_644	1B	276	0.0026	0.216	34	14	-12.22
IACX11274	1B	276	0.0026	0.216	34	14	-12.22
RAC875_c87950_333	1B	276	0.0026	0.216	34	14	-12.22
BS00055864_51	1B	276	0.0071	0.169	15	33	10.80
BS00073381_51	2A	219	0.0062	0.175	39	9	-14.68

Excalibur_c8009_325	2A	476	0.0093	0.157	43	5	-11.91
BobWhite_c17783_174	2A	479	0.0093	0.157	43	5	-11.91
RAC875_c76186_353	2B	362	0.0067	0.172	24	24	9.68
Excalibur_c7449_587	2B	363	0.0010	0.262	14	34	14.26
Tdurum_contig10219_295	2B	363	0.0010	0.262	14	34	14.26
Tdurum_contig96648_102	2B	363	0.0055	0.180	26	22	-10.05
RAC875_c3397_274	2B	363	0.0082	0.163	24	24	9.63
Kukri_c52356_96	2B	364	0.0008	0.273	14	34	14.19
Excalibur_c46178_303	2B	365	0.0010	0.262	14	34	14.26
RFL_Contig3044_346	2B	365	0.0010	0.262	14	34	14.26
Excalibur_c65341_303	2B	365	0.0082	0.163	24	24	9.63
Kukri_c84629_315	2B	365	0.0082	0.163	24	24	9.63
Excalibur_c36280_764	2B	365	0.0094	0.156	23	25	8.28
IAAV2917	2B	365	0.0094	0.156	23	25	8.28
IACX6309	2B	368	0.0082	0.163	24	24	9.63
Ra_c69196_575	2B	368	0.0082	0.163	24	24	9.63
Ku_c9369_1965	2B	374	0.0010	0.262	14	34	14.26
Ku_c9369_1726	2D	183	0.0018	0.233	13	35	13.48
RAC875_rep_c104403_524	3A	274	0.0059	0.177	17	31	9.83
wsnp_Ex_rep_c101340_86719115	3A	276	0.0036	0.201	34	14	-10.93
wsnp_Ex_rep_c101340_86719239	3A	276	0.0036	0.201	34	14	-10.93
JD_c1187_1398	3A	276	0.0091	0.158	16	32	9.32
wsnp_JD_c1187_1731186	3A	276	0.0091	0.158	16	32	9.32
Tdurum_contig67686_851	3A	578	0.0028	0.213	41	7	-13.55
RFL_Contig3008_1370	3B	34	0.0063	0.174	18	30	-8.66
wsnp_CAP8_c6899_3227098	3B	262	0.0081	0.163	8	40	15.67
BobWhite_c6016_214	3D	0	0.0013	0.248	9	39	19.38
wsnp_Ku_c13640_21686670	4A	200	0.0087	0.160	40	8	-15.89
wsnp_BF474615A_Ta_1_1	4A	202	0.0087	0.160	40	8	-15.89
Tdurum_contig9530_69	4A	603	0.0015	0.242	33	15	-14.52
RFL_Contig3621_947	4A	603	0.0092	0.157	13	35	12.09
wsnp_Ex_c5072_9006666	4A	641	0.0040	0.195	14	34	13.04
Kukri_c3866_1768	4A	641	0.0059	0.178	16	32	12.02
Tdurum_contig54776_1396	4A	641	0.0062	0.175	16	32	12.47
Excalibur_c28898_668	4A	641	0.0089	0.159	37	11	-13.93
Kukri_c44248_242	4A	641	0.0089	0.159	37	11	-13.93
TA004020-0357	4A	641	0.0089	0.159	37	11	-13.93
Ku_c71122_384	4B	107	0.0062	0.175	43	5	-19.19
RAC875_c27160_307	4B	107	0.0062	0.175	43	5	-19.19
wsnp_Ex_c16389_24884851	4B	107	0.0062	0.175	43	5	-19.19
wsnp_Ra_rep_c71114_69138821	4B	107	0.0062	0.175	43	5	-19.19
Rht-D1	4D	117	0.0082	0.162	27	21	9.91
Kukri_c2781_719	5A	252	0.0041	0.194	41	7	-19.70
Kukri_rep_c77459_316	5A	282	0.0047	0.188	23	25	-7.80
Kukri_c13590_344	5A	335	0.0068	0.171	33	15	-9.53
BS00066143_51	5A	335	0.0073	0.168	24	24	-8.42
BobWhite_c19155_246	5A	335	0.0073	0.168	24	24	-8.42
RFL_Contig5739_1542	5B	221	0.0048	0.187	41	7	9.02

RFL_Contig5739_641	5B	221	0.0048	0.187	41	7	9.02
Kukri_c5685_1066	5B	359	0.0037	0.199	10	38	10.56
IACX9238	5B	360	0.0083	0.162	32	16	-7.75
Tdurum_contig29967_456	5B	375	0.0092	0.157	8	40	-9.39
RFL_Contig5616_1779	5B	571	0.0095	0.156	33	15	-7.95
RAC875_rep_c106589_784	5B	659	0.0012	0.253	6	42	15.08
Tdurum_contig92922_58	5B	659	0.0012	0.253	6	42	15.08
Tdurum_contig28552_211	5B	659	0.0014	0.246	5	43	22.56
Tdurum_contig28552_88	5B	659	0.0045	0.190	7	41	12.26
wsnp_Ex_c19770_28768859	6A	185	0.0076	0.166	29	19	8.78
Ku_c8125_1049	6A	185	0.0084	0.161	28	20	8.54
RAC875_c75884_249	6A	185	0.0096	0.155	29	19	8.44
Ra_c4568_960	6A	338	0.0077	0.165	16	32	-6.50
BS00086173_51	6A	384	0.0087	0.160	17	31	-6.82
wmc044_282	SSR	730	0.0078	0.165	43	5	12.80

Table 41: Significant markers for fusarium head blight (FHB) at a-LOG(p-value) threshold of 2,0 with position on chromosome (cM) and allele effects for winter wheat lines in 2015 where n number of 'a' lines are indicated by a positive effect and 'b' by a negative effect.

Marker	Chr	Pos	p-value	R^2	n=a	n=b	Effect
BobWhite_c20902_177	1A	66	0.0072	0.168	23	25	12.44
wsnp_RFL_Contig4735_5673999	1A	75	0.0067	0.172	14	34	-14.65
wsnp_BE637864B_Ta_1_1	1B	200	0.0023	0.222	30	18	-15.54
BobWhite_c3771_441	1B	200	0.0037	0.200	19	29	14.91
BobWhite_c8218_162	1B	200	0.0037	0.200	19	29	14.91
BS00099465_51	2B	54	0.0015	0.243	8	40	21.65
tplb0028p23_852	3B	204	0.0073	0.168	36	12	-14.00
TA002019-0994	4B	35	0.0086	0.160	14	34	19.60
BS00022466_51	4B	253	0.0051	0.184	31	17	-13.33
BobWhite_c8115_648	4B	260	0.0075	0.167	30	18	-12.29
IAAV2725	4B	260	0.0075	0.167	30	18	-12.29
RAC875_c24515_602	4B	260	0.0075	0.167	30	18	-12.29
Tdurum_contig62286_271	4B	260	0.0075	0.167	30	18	-12.29
BS00068178_51	5A	351	0.0054	0.182	31	17	-15.56
BS00098207_51	5A	351	0.0054	0.182	17	31	15.56
GENE-3189_377	5A	351	0.0054	0.182	31	17	-15.56
GENE-3318_556	5A	351	0.0054	0.182	31	17	-15.56
Kukri_c14889_1086	5A	351	0.0054	0.182	31	17	-15.56
Kukri_c14889_116	5A	351	0.0054	0.182	31	17	-15.56
tplb0053c01_1628	5B	359	0.0080	0.163	11	37	14.77
TA002565-0478	5D	173	0.0022	0.225	26	22	14.67
wsnp_Ex_rep_c67164_65655648	5D	173	0.0022	0.225	26	22	14.67
BS00021901_51	5D	179	0.0056	0.180	21	27	-12.30
wsnp_Ex_c65985_64188864	5D	179	0.0056	0.180	21	27	-12.30
wsnp_Ku_rep_c72922_72561803	5D	179	0.0056	0.180	21	27	-12.30
BS00090253_51	6A	32	0.0060	0.177	38	10	-15.07
Kukri_c7458_1132	6A	99	0.0094	0.156	26	22	-12.18

BS00023080_51	6B	317	0.0097	0.155	17	31	12.49
Tdurum_contig17421_310	6B	317	0.0097	0.155	17	31	12.49
BS00010282_51	7A	304	0.0059	0.177	7	41	18.50
wsnp_JD_c1219_1766041	7A	708	0.0079	0.164	24	24	-11.83
BS00067599_51	7B	206	0.0055	0.180	25	23	-13.64
Tdurum_contig9934_104	7B	207	0.0055	0.180	25	23	-13.64
wsnp_Ex_rep_c69954_68913284	7B	213	0.0050	0.185	27	21	-14.99
BS00022522_51	7B	427	0.0089	0.159	8	40	17.65
BS00083578_51	7B	427	0.0089	0.159	40	8	-17.66
Tdurum_contig8719_370	7B	456	0.0051	0.184	24	24	-12.66
Excalibur_c16245_801	7B	456	0.0058	0.178	42	6	-19.74
Kukri_rep_c105704_342	7B	456	0.0058	0.178	42	6	-19.74
Ku_c22990_969	7B	457	0.0058	0.178	42	6	-19.74
BS00101348_51	7B	458	0.0092	0.158	32	16	11.96
gwm644_164	SSR	550	0.0038	0.198	39	9	-16.88

Table 42: Significant markers for fusarium head blight after regression (FHB_reg) at a-LOG(p-value) threshold of 2,0 with position on chromosome (cM) and allele effects for winter wheat lines in 2015 where n number of 'a' lines are indicated by a positive effect and 'b' by a negativ effect.

Marker	Chr	Pos	p-value	R^2	n=a	n=b	Effect
BobWhite_c20902_177	1A	66	0.0028	0.213	23	25	12.86
wsnp_RFL_Contig4735_5673999	1A	75	0.0053	0.182	14	34	-13.46
wsnp_BE637864B_Ta_1_1	1B	200	0.0059	0.177	30	18	-12.47
BS00066305_51	1B	502	0.0094	0.156	15	33	-11.23
BobWhite_c20073_382	1B	509	0.0081	0.163	18	30	-10.96
BS00099465_51	2B	54	0.0026	0.216	8	40	18.42
Excalibur_c30167_243	2B	87	0.0076	0.166	22	26	-11.71
BS00059315_51	2B	283	0.0054	0.182	41	7	-17.30
Excalibur_c37239_916	2B	283	0.0084	0.161	39	9	-14.66
RAC875_rep_c112008_519	2B	291	0.0058	0.179	7	41	16.48
Ra_c11529_647	5A	655	0.0029	0.210	30	18	-13.76
Tdurum_contig16032_330	5B	222	0.0064	0.174	29	19	12.97
CAP7_c591_515	7A	615	0.0097	0.155	18	30	-11.22
BS00081132_51	7B	129	0.0051	0.184	23	25	-12.91
BS00039502_51	7B	330	0.0072	0.169	11	37	13.49
wsnp_Ku_c1455_2890228	7B	420	0.0074	0.167	25	23	11.42
wsnp_Ex_c13064_20670748	7B	429	0.0074	0.167	25	23	11.42
Excalibur_c16245_801	7B	456	0.0085	0.161	42	6	-16.95
Kukri_rep_c105704_342	7B	456	0.0085	0.161	42	6	-16.95
Tdurum_contig8719_370	7B	456	0.0088	0.159	24	24	-11.04
Ku_c22990_969	7B	457	0.0085	0.161	42	6	-16.95
gwm644_164	SSR	550	0.0032	0.206	39	9	-15.85

Appendix 2

Spring wheat 2013-2015

Table 43: Significant markers for anther extrusion (AE) at a-LOG(p-value) threshold of 2,5 with position on chromosome (cM) and allele effects for spring wheat lines from 2013-2015 where n number of 'a' lines are indicated by a positive effect and 'b' by a negative effect.

					2013	2014	2015	Mean 2013-2015		
Marker	Chr	Pos	n=a	n=b	R^2	R^2	R^2	p-value	Effect	R^2
BS00066338_51	1B	287	6	117	0.035	0.034	0.044	0,0004	-1,88	0.106
BS00069125_51	1B	287	6	117	0.035	0.034	0.044	0,0004	-1,88	0.106
IACX2852	1B	287	6	117	0.035	0.034	0.044	0,0004	-1,88	0.106
Kukri_c11547_1526	1B	287	6	117	0.035	0.034	0.044	0,0004	-1,88	0.106
RFL_Contig7_380	1B	287	6	117	0.035	0.034	0.044	0,0004	-1,88	0.106
BobWhite_c11460_291	1B	216	31	92	0.095	0.096	0.043	0.0018	1,05	0.083
BS00022581_51	1B	216	30	93	0.104	0.105	0.049	0.0020	1,04	0.081
BS00060270_51	1B	216	30	93	0.104	0.105	0.049	0.0020	1,04	0.081
BS00071555_51	1B	216	30	93	0.104	0.105	0.049	0.0020	1,04	0.081
Excalibur_c57972_116	1B	216	30	93	0.104	0.105	0.049	0.0020	1,04	0.081
Tdurum_contig8081_2331	1B	216	30	93	0.104	0.105	0.049	0.0020	1,04	0.081
Tdurum_contig28899_127	1B	215	93	30	0.104	0.105	0.049	0.0020	-1,04	0.081
Tdurum_contig20299_508	1B	243	50	73	0.019	0.019	0.028	0.0026	0,89	0.078
Kukri_c5357_323	1B	352	78	45	0.034	0.036	0.010	0.0028	-0,96	0.076
Excalibur_c7964_1290	2B	458	19	104	0.105	0.106	0.043	0.0011	1,05	0.091
Tdurum_contig57254_254	2B	458	19	104	0.105	0.106	0.043	0.0011	1,05	0.091
Excalibur_rep_c109101_94	2D	6	112	11	0.049	0.046	0.051	0.0027	1,28	0.077
wsnp_Ex_c18883_27772081	3A	169	97	26	0.105	0.105	0.035	0,0004	-1,04	0.108
Ku_c10913_2542	4A	293	97	26	0.073	0.072	0.054	0.0017	1,12	0.084
RFL_Contig3621_947	4A	603	26	97	0.039	0.037	0.034	0.0028	-1,05	0.076
RAC875_c107130_384	4B	265	61	62	0.057	0.057	0.041	0.0017	0,80	0.084
GENE-1584_692	4B	264	60	63	0.039	0.040	0.044	0.0020	0,75	0.081
Kukri_rep_c102608_599	5A	530	32	91	0.018	0.018	0.030	0.0023	0,91	0.080
Kukri_rep_c103150_398	5B	88	68	55	0.101	0.104	0.016	0.0026	-0.78	0.077
wsnp_Ex_c1011_1931797	6A	104	88	35	0.058	0.061	0.086	0,0004	1,17	0.124
Kukri_c35255_1312	6A	104	78	45	0.050	0.052	0.058	0,0004	1,05	0.099
Excalibur_c23748_1050	6A	103	78	45	0.050	0.052	0.058	0,0004	1,05	0.099
IACX7895	6A	103	51	72	0.060	0.062	0.067	0.0015	-0,93	0.086
BS00012023_51	6A	104	77	46	0.043	0.045	0.053	0.0018	0,96	0.083
IACX5772	6A	103	77	46	0.043	0.045	0.053	0.0018	0,96	0.083
wsnp_Ku_c7458_12842353	6A	103	77	46	0.043	0.045	0.053	0.0018	0,96	0.083
BS00023150_51	7D	332	103	20	0.079	0.079	0.034	0,0004	-1,21	0.119
RAC875_rep_c106588_205	7D	332	101	22	0.059	0.060	0.021	0.0011	-1.00	0.091
barc228_194	SSR		117	6	0.026	0.028	0.028	0.0012	1,85	0.089

Table 44: Significant markers for Fusarium head blight after regression (FHB_reg) at a-LOG(p-value) threshold of 2,5 with position on chromosome (cM) and allele effects for spring wheat lines from 2013-2015 where n number of 'a' lines are indicated by a positive effect and 'b' by a negative effect.

					2013	2014	2015	Mean 2013-2015		
Marker	Chr	Pos	n=a	n=b	R^2	R^2	R^2	Effect	p-value	R^2
BobWhite_c4743_63	2A	362	22	101	0.045	0.106	0.046	7.70	0.0016	0.086
BobWhite_c71_391	3A	349	12	111	0.062	0.051	0.074	-12.26	0.0006	0.102
Excalibur_c39002_242	3A	347	12	111	0.062	0.051	0.074	-12.26	0.0006	0.102
wsnp_BF292596A_Ta_1_3	3A	347	12	111	0.062	0.051	0.074	-12.26	0.0006	0.102
wsnp_Ku_c458_954940	3A	346	12	111	0.062	0.051	0.074	-12.26	0.0006	0.102
BS00022459_51	3A	439	83	40	0.070	0.002	0.031	7.20	0.0016	0.086
BS00110550_51	3A	414	83	40	0.070	0.002	0.031	7.20	0.0016	0.086
BS00110350_51	3A	439	85	38	0.061	0.008	0.026	6.98	0.0028	0.077
IAAV5302	3B	347	92	31	0.057	0.032	0.065	7.81	0.0015	0.086
Excalibur_c766_705	3B	558	46	77	0.079	0.089	0.041	5.70	0.0021	0.081
RFL_Contig3621_1295	4A	603	33	90	0.007	0.005	0.068	6.65	0.0030	0.075
Excalibur_c26997_272	5A	44	49	74	0.083	0.019	0.043	-8.37	0.0001	0.129
wsnp_Ex_c6209_10838456	5A	43	62	61	0.112	0.038	0.023	-6.57	0.0011	0.092
wsnp_Ex_c6209_10838852	5A	81	22	101	0.028	0.013	0.040	-7.14	0.0016	0.085
BobWhite_c41542_354	5A	33	21	102	0.025	0.014	0.032	-7.31	0.0024	0.079
RAC875_c28639_621	5A	30	21	102	0.025	0.014	0.032	-7.31	0.0024	0.079
JD_c20036_865	5A	314	7	116	0.0005	0.019	0.110	13.57	0.0027	0.077
Ra_c700_1024	5A	314	116	7	0.0005	0.019	0.110	-13.57	0.0027	0.077
Ra_c700_2210	5A	314	7	116	0.0005	0.019	0.110	13.57	0.0027	0.077
RFL_Contig3285_1009	5B	565	67	56	0.052	0.017	0.059	-6.12	0.0022	0.080
wsnp_Ex_c1011_1931797	6A	104	88	35	0.033	0.058	0.085	-6.93	0.0018	0.083
RAC875_c17011_373	6B	419	40	83	0.072	0.020	0.059	-7.22	0.0015	0.087
BS00090069_51	6B	134	20	103	0.080	0.012	0.048	7.48	0.0031	0.075
Tdurum_contig46334_832	7A	447	33	90	0.032	0.022	0.057	-7.27	0.0019	0.082
wsnp_Ku_c60707_6250905 1	7B	287	26	97	0.043	0.013	0.015	7.70	0.0016	0.086
D_contig12156_209	7D	250	106	17	0.081	0.044	0.048	-12.26	0.0006	0.102
Kukri_rep_c108604_137	7D	250	106	17	0.081	0.044	0.048	-12.26	0.0006	0.102

Table 45: Significant markers for DON values after regression (DON_reg) at a-LOG(p-value) threshold of 2,5 with position on chromosome (cM) and allele effects for spring wheat lines from 2013-2015 where n number of 'a' lines are indicated by a positive effect and 'b' by a negative effect.

					2013	2014	2015	Mean 2013-2015		
Marker	Chr	Pos	n=a	n=b	R2	R2	R2	Effect	p-value	R2
BobWhite_c1027_1127	1A	462	15	108	0.059	0.039	0.073	5.09	0.0015	0.086
Excalibur_c27376_74	1A	462	108	15	0.059	0.039	0.073	-5.09	0.0015	0.086
BS00042197_51	1B	195	12	111	0.046	0.053	0.068	-4.45	0.0022	0.080
Ra_c7492_1229	2A	341	13	110	0.052	0.084	0.062	6.39	0.0030	0.075
BS00022896_51	2A	366	106	17	0.164	0.070	0.073	-6.83	0.0001	0.139
BS00012320_51	2A	368	19	104	0.160	0.060	0.037	6.52	0.0005	0.104
RAC875_c38018_278	2A	368	19	104	0.160	0.060	0.037	6.52	0.0005	0.104
RFL_Contig4517_1300	2A	368	104	19	0.160	0.060	0.037	-6.52	0.0005	0.104
RFL_Contig4517_1276	2A	368	20	103	0.132	0.056	0.027	5.77	0.0017	0.084
CAP12_rep_c6956_169	2A	385	21	102	0.071	0.046	0.093	-3.91	0.0004	0.110

wsnp_Ex_c21409_30544027	2A	390	101	22	0.104	0.120	0.048	-6.10	0.0003	0.113
Kukri_c29170_702	2A	419	96	27	0.067	0.060	0.065	-4.05	0.0008	0.098
wsnp_Ex_c7829_13320738	2A	419	96	27	0.067	0.060	0.065	-4.05	0.0008	0.098
Kukri_c44_1704	2B	257	114	9	0.020	0.067	0.076	-4.23	0.0026	0.077
RAC875_rep_c99492_65	2B	257	9	114	0.020	0.067	0.076	4.23	0.0026	0.077
Kukri_c62277_80	2B	259	9	114	0.020	0.067	0.076	4.23	0.0026	0.077
Ku_c68678_924	2B	262	10	113	0.018	0.032	0.122	3.42	0.0012	0.091
Kukri_c44_1476	2B	262	9	114	0.020	0.067	0.076	4.23	0.0026	0.077
RAC875_c6751_609	2B	262	9	114	0.020	0.067	0.076	4.23	0.0026	0.077
BS00030497_51	2B	263	10	113	0.018	0.032	0.122	3.42	0.0012	0.091
Excalibur_rep_c68899_191	2B	264	10	113	0.018	0.032	0.122	3.42	0.0012	0.091
IAAV1101	2B	264	10	113	0.018	0.032	0.122	3.42	0.0012	0.091
JD_c11869_1297	2B	264	113	10	0.018	0.032	0.122	-3.42	0.0012	0.091
Tdurum_contig47202_1699	2B	264	10	113	0.018	0.032	0.122	3.42	0.0012	0.091
Excalibur_c7964_1290	2B	458	19	104	0.046	0.009	0.085	-2.72	0.0031	0.075
Tdurum_contig57254_254	2B	458	19	104	0.046	0.009	0.085	-2.72	0.0031	0.075
D_contig17313_245	2D	6	26	97	0.071	0.081	0.065	4.44	0.0008	0.096
Excalibur_rep_c109101_94	2D	6	112	11	0.105	0.073	0.036	-5.97	0.0020	0.082
BS00081688_51	3A	362	117	6	0.059	0.033	0.057	-5.41	0.0031	0.074
Excalibur_c17655_467	3A	362	117	6	0.059	0.033	0.057	-5.41	0.0031	0.074
GENE-1981_131	3A	362	117	6	0.059	0.033	0.057	-5.41	0.0031	0.074
RAC875_rep_c109554_198	3A	604	116	7	0.090	0.042	0.109	-7.14	0.0001	0.128
Excalibur_c17654_166	3A	617	116	7	0.090	0.042	0.109	-7.14	0.0001	0.128
Kukri_rep_c114164_106	3D	416	105	18	0.055	0.031	0.060	3.46	0.0031	0.075
Ra_c30013_483	4A	191	12	111	0.073	0.246	0.015	8.06	0.0027	0.077
wsnp_BE398523A_Ta_2_1	4A	191	111	12	0.073	0.246	0.015	-8.06	0.0027	0.077
wsnp_Ex_c11663_18779609	4A	191	111	12	0.073	0.246	0.015	-8.06	0.0027	0.077
wsnp_Ex_c12_21212	4A	191	111	12	0.073	0.246	0.015	-8.06	0.0027	0.077
wsnp_Ex_c13623_21404172	4A	191	12	111	0.073	0.246	0.015	8.06	0.0027	0.077
wsnp_Ex_c3463_6348659	4A	191	12	111	0.073	0.246	0.015	8.06	0.0027	0.077
wsnp_Ex_c3463_6348808	4A	191	111	12	0.073	0.246	0.015	-8.06	0.0027	0.077
wsnp_Ex_rep_c101826_87124211	4A	191	111	12	0.073	0.246	0.015	-8.06	0.0027	0.077
RAC875_c5394_1052	4A	194	12	111	0.073	0.246	0.015	8.06	0.0027	0.077
wsnp_Ex_c5492_9691880	4A	194	111	12	0.073	0.246	0.015	-8.06	0.0027	0.077
wsnp_Ku_c10224_16965872	4A	194	12	111	0.073	0.246	0.015	8.06	0.0027	0.077
wsnp_Ex_c5492_9691241	4A	195	12	111	0.073	0.246	0.015	8.06	0.0027	0.077
BobWhite_c13322_215	4A	200	11	112	0.129	0.163	0.010	8.72	0.0030	0.075
wsnp_Ex_c1563_2986030	4A	200	11	112	0.129	0.163	0.010	8.72	0.0030	0.075
wsnp_Ex_rep_c101638_86971861	4A	200	11	112	0.129	0.163	0.010	8.72	0.0030	0.075
wsnp_Ex_rep_c66706_65037564	4A	200	112	11	0.129	0.163	0.010	-8.72	0.0030	0.075
BobWhite_c1593_539	4A	200	114	9	0.121	0.075	0.025	-8.16	0.0031	0.075
BobWhite_c4931_170	4A	200	114	9	0.121	0.075	0.025	-8.16	0.0031	0.075
Jagger_c2057_97	4A	200	114	9	0.121	0.075	0.025	-8.16	0.0031	0.075
wsnp_BG604678A_Ta_1_2	4A	200	114	9	0.121	0.075	0.025	-8.16	0.0031	0.075
wsnp_Ex_c12933_20488438	4A	200	114	9	0.121	0.075	0.025	-8.16	0.0031	0.075
wsnp_Ex_c2403_4502745	4A	200	9	114	0.121	0.075	0.025	8.16	0.0031	0.075
wsnp_Ex_c64593_63334637	4A	200	114	9	0.121	0.075	0.025	-8.16	0.0031	0.075
Kukri_c29625_198	4A	203	114	9	0.121	0.075	0.025	-8.16	0.0031	0.075

wsnp_Ex_c829_1620518	4A	203	114	9	0.121	0.075	0.025	-8.16	0.0031	0.075
Tdurum_contig47552_957	4B	206	42	81	0.026	0.068	0.077	-2.72	0.0018	0.084
Tdurum_contig86933_317	4B	206	40	83	0.020	0.063	0.082	-2.55	0.0019	0.082
BS00087144_51	4B	206	41	82	0.025	0.065	0.073	-2.70	0.0022	0.080
wsnp_Ku_rep_c104382_90867406	4B	206	41	82	0.025	0.065	0.073	-2.70	0.0022	0.080
Kukri_c17224_278	4B	208	99	24	0.025	0.044	0.077	-2.69	0.0031	0.075
Ku_c102710_1055	5A	212	16	107	0.063	0.046	0.084	5.10	0.0010	0.094
BobWhite_c18121_478	5B	214	22	101	0.031	0.064	0.069	4.33	0.0025	0.078
BobWhite_c6328_410	5D	178	12	111	0.056	0.195	0.041	6.98	0.0017	0.085
Excalibur_c49805_63	5D	270	101	22	0.070	0.083	0.067	-5.01	0.0009	0.095
GENE-3872_608	6B	115	69	54	0.042	0.057	0.060	-2.28	0.0031	0.075
Excalibur_c30571_346	6D	335	110	13	0.041	0.043	0.081	-4.25	0.0019	0.083
Excalibur_c1142_724	7A	555	6	117	0.107	0.012	0.069	6.36	0.0009	0.096
Kukri_c57593_79	7A	595	95	28	0.051	0.028	0.068	3.33	0.0020	0.082
wsnp_RFL_Contig2805_2579582	7A	595	31	92	0.037	0.034	0.075	-2.96	0.0020	0.082
Kukri_rep_c98227_390	7A	595	96	27	0.051	0.037	0.054	3.44	0.0030	0.075
wsnp_Ku_c44600_51841068	7B	502	111	12	0.073	0.246	0.015	-8.06	0.0027	0.077
wsnp_Ex_c10430_17064001	7D	263	67	56	0.042	0.075	0.076	-2.87	0.0008	0.096
gwm148_184	SSR	284	109	14	0.006	0.058	0.118	-2.31	0.0017	0.084

Spring wheat 2013-2014

Table 46: Significant markers for deoxynivalenol after regression (DON_reg) at a-LOG(p-value) threshold of 3,0 with position on chromosome (cM) and allele effects for spring wheat lines from 2013-2014 where n number of 'a' lines are indicated by a positive effect and 'b' by a negative effect.

					2013	2014	Mean 2013-2014		
Marker	Chr	Pos	n=a	n=b	R^2	R^2	Effect	p-value	R^2
RAC875_c140_872	1B	142	10	113	0.080	0.084	7.04	0.00048	0.106
wsnp_Ra_c2633_5017265	1D	39	27	96	0.076	0.099	4.59	0.00066	0.100
BS00012320_51	2A	368	19	104	0.160	0.060	6.29	0.00002	0.160
RAC875_c38018_278	2A	368	19	104	0.160	0.060	6.29	0.00002	0.160
RFL_Contig4517_1300	2A	368	104	19	0.160	0.060	-6.29	0.00002	0.160
wsnp_Ex_c21409_30544027	2A	390	101	22	0.104	0.120	-3.56	0.00003	0.155
BS00022896_51	2A	366	106	17	0.164	0.070	-6.83	0.00004	0.148
RFL_Contig4517_1276	2A	368	20	103	0.132	0.056	5.77	0.00008	0.138
BS00022903_51	2A	365	116	7	0.085	0.074	-7.52	0.00027	0.116
wsnp_JD_rep_c49438_33652645	2B	61	86	37	0.065	0.106	-3.82	0.00049	0.105
IAAV5743	2B	504	22	101	0.042	0.133	-4.75	0.00075	0.098
Excalibur_c17250_751	2B	61	85	38	0.058	0.104	-3.68	0.00076	0.098
RFL_Contig2324_729	2B	583	96	27	0.070	0.076	-4.19	0.00079	0.097
Excalibur_rep_c109101_94	2D	6	112	11	0.105	0.073	-5.97	0.00023	0.118
D_contig17313_245	2D	6	26	97	0.071	0.081	4.44	0.00094	0.094
BobWhite_c13322_215	4A	200	11	112	0.129	0.163	8.72	0.00001	0.178
wsnp_Ex_c1563_2986030	4A	200	11	112	0.129	0.163	8.72	0.00001	0.178
wsnp_Ex_rep_c101638_86971861	4A	200	11	112	0.129	0.163	8.72	0.00001	0.178
wsnp_Ex_rep_c66706_65037564	4A	200	112	11	0.129	0.163	-8.72	0.00001	0.178
wsnp_Ex_c5492_9691241	4A	195	12	111	0.073	0.246	8.06	0.00002	0.162
RAC875_c5394_1052	4A	194	12	111	0.073	0.246	8.06	0.00002	0.162
wsnp_Ex_c5492_9691880	4A	194	111	12	0.073	0.246	-8.06	0.00002	0.162
wsnp_Ku_c10224_16965872	4A	194	12	111	0.073	0.246	8.06	0.00002	0.162

Ra_c30013_483	4A	191	12	111	0.073	0.246	8.06	0.00002	0.162
wsnp_BE398523A_Ta_2_1	4A	191	111	12	0.073	0.246	-8.06	0.00002	0.162
wsnp_Ex_c11663_18779609	4A	191	111	12	0.073	0.246	-8.06	0.00002	0.162
wsnp_Ex_c12_21212	4A	191	111	12	0.073	0.246	-8.06	0.00002	0.162
wsnp_Ex_c13623_21404172	4A	191	12	111	0.073	0.246	8.06	0.00002	0.162
wsnp_Ex_c3463_6348659	4A	191	12	111	0.073	0.246	8.06	0.00002	0.162
wsnp_Ex_c3463_6348808	4A	191	111	12	0.073	0.246	-8.06	0.00002	0.162
wsnp_Ex_rep_c101826_87124211	4A	191	111	12	0.073	0.246	-8.06	0.00002	0.162
Excalibur_c31814_298	4A	191	10	113	0.090	0.180	8.60	0.00004	0.151
IAAV6223	4A	191	113	10	0.090	0.180	-8.60	0.00004	0.151
IAAV7636	4A	191	113	10	0.090	0.180	-8.60	0.00004	0.151
wsnp_Ex_rep_c67779_66463916	4A	191	10	113	0.090	0.180	8.60	0.00004	0.151
wsnp_Ex_rep_c70327_69270561	4A	191	113	10	0.090	0.180	-8.60	0.00004	0.151
wsnp_Ku_c5979_10559245	4A	191	113	10	0.090	0.180	-8.60	0.00004	0.151
wsnp_Ra_c33762_42584098	4A	191	113	10	0.090	0.180	-8.60	0.00004	0.151
Excalibur_c38000_595	4A	200	110	13	0.068	0.192	-7.19	0.00007	0.138
wsnp_Ex_c9464_15689857	4A	195	110	13	0.068	0.192	-7.19	0.00007	0.138
IAAV1461	4A	194	13	110	0.068	0.192	7.19	0.00007	0.138
wsnp_Ex_c2266_4247520	4A	194	110	13	0.068	0.192	-7.19	0.00007	0.138
wsnp_Ex_c30876_39741201	4A	194	110	13	0.068	0.192	-7.19	0.00007	0.138
wsnp_Ex_c8092_13695482	4A	194	110	13	0.068	0.192	-7.19	0.00007	0.138
wsnp_Ku_c48043_54334230	4A	194	110	13	0.068	0.192	-7.19	0.00007	0.138
CAP12_c5519_132	4A	191	13	110	0.068	0.192	7.19	0.00007	0.138
Kukri_c29625_198	4A	203	114	9	0.121	0.075	-8.16	0.00010	0.133
wsnp_Ex_c829_1620518	4A	203	114	9	0.121	0.075	-8.16	0.00010	0.133
BobWhite_c1593_539	4A	200	114	9	0.121	0.075	-8.16	0.00010	0.133
BobWhite_c4931_170	4A	200	114	9	0.121	0.075	-8.16	0.00010	0.133
Jagger_c2057_97	4A	200	114	9	0.121	0.075	-8.16	0.00010	0.133
wsnp_BG604678A_Ta_1_2	4A	200	114	9	0.121	0.075	-8.16	0.00010	0.133
wsnp_Ex_c12933_20488438	4A	200	114	9	0.121	0.075	-8.16	0.00010	0.133
wsnp_Ex_c2403_4502745	4A	200	9	114	0.121	0.075	8.16	0.00010	0.133
wsnp_Ex_c64593_63334637	4A	200	114	9	0.121	0.075	-8.16	0.00010	0.133
Kukri_c89772_150	4A	200	13	110	0.093	0.108	6.75	0.00015	0.125
RAC875_c4629_1344	4A	200	11	112	0.067	0.152	7.59	0.00021	0.120
wsnp_Ex_c1373_2628597	4A	200	11	112	0.067	0.152	7.59	0.00021	0.120
BobWhite_c17999_112	4A	191	11	112	0.082	0.115	7.53	0.00023	0.118
Excalibur_c4283_201	4A	191	11	112	0.082	0.115	7.53	0.00023	0.118
RAC875_c110384_153	4A	191	11	112	0.082	0.115	7.53	0.00023	0.118
RFL_Contig5998_745	4A	191	112	11	0.082	0.115	-7.53	0.00023	0.118
wsnp_CAP7_c2931_1395666	4A	191	11	112	0.082	0.115	7.53	0.00023	0.118
wsnp_Ex_c10186_16720660	4A	191	11	112	0.082	0.115	7.53	0.00023	0.118
wsnp_Ra_rep_c107017_90667618	4A	191	112	11	0.082	0.115	-7.53	0.00023	0.118
Ex_c67622_392	4A	200	109	14	0.051	0.175	-6.34	0.00026	0.116
wsnp_Ex_c7335_12579818	4A	200	113	10	0.092	0.066	-7.01	0.00042	0.108
Kukri_c80869_122	4A	160	78	45	0.069	0.072	-3.30	0.00062	0.101
BobWhite_c7235_365	4A	160	77	46	0.060	0.083	-3.34	0.00075	0.098
BS00011173_51	4A	160	77	46	0.060	0.083	-3.34	0.00075	0.098
Excalibur_c13276_1322	4A	160	77	46	0.060	0.083	-3.34	0.00075	0.098
wsnp_Ex_c55245_57821389	4A	160	77	46	0.060	0.083	-3.34	0.00075	0.098
wsnp_Ex_c55245_57821568	4A	160	77	46	0.060	0.083	-3.34	0.00075	0.098
Ex_c23792_486	4A	194	10	113	0.044	0.129	7.19	0.00080	0.097
BobWhite_c47401_491	5A	737	15	108	0.116	0.116	6.71	0.00005	0.144
wsnp_Ex_c20899_30011827	5A	737	108	15	0.116	0.116	-6.71	0.00005	0.144
Excalibur_c47920_249	5A	64	117	6	0.032	0.179	-8.04	0.00085	0.096
Tdurum_contig53796_360	5B	56	95	28	0.076	0.072	4.49	0.00050	0.105

IAAV731	5B	56	96	27	0.072	0.065	4.30	0.00079	0.097
Tdurum_contig8695_379	5B	56	96	27	0.072	0.065	4.30	0.00079	0.097
BobWhite_c6328_410	5D	178	12	111	0.056	0.195	6.98	0.00015	0.126
Excalibur_c49805_63	5D	270	101	22	0.070	0.083	-5.01	0.00079	0.097
BS00063175_51	6D	185	110	13	0.058	0.110	-5.64	0.00082	0.097
Kukri_rep_c70864_638	7A	256	14	109	0.092	0.070	5.94	0.00047	0.106
wsnp_Ex_c13248_20898211	7A	256	14	109	0.092	0.070	5.94	0.00047	0.106
wsnp_Ku_c44600_51841068	7B	502	111	12	0.073	0.246	-8.06	0.00002	0.162
Kukri_c77849_131	7B	540	16	107	0.044	0.168	5.66	0.00045	0.107
barc228_194	SSR	58	117	6	0.084	0.132	-9.32	0.00013	0.128
cfd47_213	SSR	124	111	12	0.046	0.144	-6.85	0.00080	0.097
csLV46G22_0	SSR	155	115	8	0.052	0.078	-6.18	0.00113	0.091

Winter wheat 2014-2015

Table 47: Significant markers for anther extrusion (AE) at a-LOG(p-value) threshold of 2,5 with position on chromosome (cM) and allele effects for winter wheat lines from 2014-2015 where n number of 'a' lines are indicated by a positive effect and 'b' by a negative effect.

					2014	2015	Mean 2014-2015		
Marker	Chr	Pos	n=a	n=b	R^2	R^2	Effect	p-value	R^2
BobWhite_c32938_264	2B	368	31	17	0.042	0.166	-1.56	0.0030	0.210
Excalibur_c3506_610	2B	368	31	17	0.042	0.166	-1.56	0.0030	0.210
BS00080318_51	2B	424	25	23	0.114	0.228	1.38	0.0021	0.227
BS00084417_51	2B	431	25	23	0.114	0.228	1.38	0.0021	0.227
Excalibur_c224_1383	2B	431	25	23	0.114	0.228	1.38	0.0021	0.227
GENE-1355_265	2B	431	25	23	0.114	0.228	1.38	0.0021	0.227
IACX8947	2B	431	25	23	0.114	0.228	1.38	0.0021	0.227
Kukri_c21087_79	2B	431	25	23	0.114	0.228	1.38	0.0021	0.227
Kukri_c25702_948	2B	431	25	23	0.114	0.228	1.38	0.0021	0.227
wsnp_Ku_c2249_4335279	3A	600	39	9	0.083	0.128	-1.60	0.0026	0.217
BS00111294_51	3B	56	10	38	0.200	0.192	-1.62	0.0026	0.217
TA006354-0937	3D	416	39	9	0.083	0.128	-1.60	0.0026	0.217
Excalibur_c4302_2208	3D	432	39	9	0.083	0.128	-1.60	0.0026	0.217
RFL_Contig148_359	3D	432	39	9	0.083	0.128	-1.60	0.0026	0.217
Tdurum_contig42257_4485	4A	278	5	43	0.182	0.082	1.91	0.0025	0.219
Tdurum_contig75584_1118	4A	603	11	37	0.301	0.134	1.72	0.0008	0.272
wsnp_Ex_c4942_8793029	6D	331	37	11	0.068	0.175	-1.46	0.0022	0.224
RAC875_c24285_1049	6D	341	39	9	0.136	0.275	-1.96	0.0002	0.344
GENE-3993_284	6D	341	11	37	0.068	0.175	1.46	0.0022	0.224
cfd018b_207	SSR	105	36	12	0.181	0.290	-1.65	0.0003	0.332
gwm301_239	SSR	423	43	5	0.313	0.108	-2.10	0.0014	0.246

Table 48: Significant markers for fusarium head blight after regression (FHB_reg) at a-LOG(p-value) threshold of 2,0 with position on chromosome (cM) and allele effects for winter wheat lines from 2014-2015 where n number of 'a' lines are indicated by a positive effect and 'b' by a negative effect.

					2014	2015	Mean 2014-2015		

Marker	Chr	Pos	n=a	n=b	R^2	R^2	Effect	p-value	R^2
BobWhite_c20902_177	1A	66	23	25	0.003	0.213	9.58	0.0078	0.165
wsnp_RFL_Contig4735_5673999	1A	75	14	34	0.007	0.182	-11.20	0.0060	0.176
wsnp_CAP11_c710_458019	1A	75	16	32	0.006	0.139	9.95	0.0093	0.157
BS00076668_51	1A	216	8	40	0.014	0.122	-12.98	0.0095	0.156
BobWhite_c24113_529	1A	216	8	40	0.014	0.122	-12.98	0.0095	0.156
CAP11_c2984_419	1A	216	8	40	0.014	0.122	-12.98	0.0095	0.156
IAAV7414	1A	216	8	40	0.014	0.122	-12.98	0.0095	0.156
RAC875_c9965_354	1A	216	8	40	0.014	0.122	-12.98	0.0095	0.156
RAC875_rep_c76047_63	1A	216	8	40	0.014	0.122	-12.98	0.0095	0.156
tplb0032d09_1393	1A	216	8	40	0.014	0.122	-12.98	0.0095	0.156
wsnp_Ex_c14733_22819350	1A	216	8	40	0.014	0.122	-12.98	0.0095	0.156
wsnp_Ex_c14733_22819625	1A	216	8	40	0.014	0.122	-12.98	0.0095	0.156
wsnp_Ex_c49829_54319220	1A	216	8	40	0.014	0.122	-12.98	0.0095	0.156
wsnp_Ex_c50235_54588957	1A	216	8	40	0.014	0.122	-12.98	0.0095	0.156
wsnp_RFL_Contig1736_858448	1A	216	8	40	0.014	0.122	-12.98	0.0095	0.156
BobWhite_c20073_382	1B	509	18	30	0.000	0.163	-10.04	0.0050	0.185
BS00099465_51	2B	54	8	40	0.007	0.216	14.65	0.0040	0.196
Excalibur_c30167_243	2B	87	22	26	0.066	0.166	-9.71	0.0086	0.161
GENE-1294_120	2B	465	25	23	0.004	0.116	-10.14	0.0068	0.171
wsnp_Ex_c12875_20407926	3A	47	27	21	0.029	0.076	9.44	0.0072	0.168
BS00084348_51	3A	66	42	6	0.011	0.114	-13.77	0.0098	0.154
RAC875_c68056_81	3A	574	28	20	0.000	0.111	10.08	0.0082	0.163
Excalibur_rep_c66331_1967	3B	45	34	14	0.068	0.073	-10.97	0.0080	0.164
tplb0028p23_852	3B	204	36	12	0.000	0.112	-10.59	0.0099	0.154
Kukri_c20236_209	4B	218	8	40	0.038	0.096	12.87	0.0092	0.157
BS00023196_51	6B	124	34	14	0.024	0.087	-11.07	0.0069	0.171
Ex_c20409_854	6B	160	20	28	0.000	0.135	-9.78	0.0096	0.156
Ku_c24158_1468	6B	358	27	21	0.141	0.090	10.30	0.0092	0.157
BS00048090_51	7B	236	16	32	0.012	0.128	-10.10	0.0080	0.164
wsnp_Ku_c1455_2890228	7B	420	25	23	0.016	0.167	10.93	0.0028	0.213
BS00022522_51	7B	427	8	40	0.027	0.110	13.67	0.0079	0.164
BS00083578_51	7B	427	40	8	0.027	0.110	-13.67	0.0079	0.164
wsnp_Ex_c13064_20670748	7B	429	25	23	0.016	0.167	10.93	0.0028	0.213
Excalibur_c16245_801	7B	456	42	6	0.040	0.161	-15.44	0.0052	0.183
Kukri_rep_c105704_342	7B	456	42	6	0.040	0.161	-15.44	0.0052	0.183
Ku_c22990_969	7B	457	42	6	0.040	0.161	-15.44	0.0052	0.183
IAAV4542	7B	547	43	5	0.000	0.119	-17.06	0.0041	0.195
RAC875_c1329_225	7B	547	41	7	0.121	0.136	-13.91	0.0056	0.180
BS00004171_51	7B	547	34	14	0.075	0.144	-10.73	0.0095	0.156
cfd018b_207	SSR	105	36	12	0.078	0.117	10.68	0.0078	0.165
gwm427_232	SSR	493	42	6	0.045	0.104	-14.86	0.0061	0.176
gwm617a_146	SSR	527	41	7	0.021	0.114	-15.96	0.0020	0.228

Appendix 3

Table 49: Significant markers after validation on new MASBASIS lines with p-values, allele frequency and allele effect. Green area shows trials and traits where markers shows a p-value below 0,5 in an ANOVA test.

Marker	DH_2013				PH_2013			
	p value	X/Y	X-mean	Y-mean	p value	X/Y	X-mean	Y-mean
BS00069125_51	0.255	92/2	53.95	55.78	0.484	92/2	78.48	75.10
BS00063175_51	0.269	95/2	53.94	55.72	0.653	95/2	78.55	80.71
BS00022459_51	0.479	81/16	54.09	53.66	0.611	81/16	78.43	79.36
BS00023150_51	0.038	7/50	55.15	53.47	0.397	7/50	80.22	77.72
BS00110550_51	0.376	81/15	54.06	53.50	0.519	81/15	78.45	79.67
BobWhite_c13322_215	0.28	8/90	54.81	53.92	0.983	8/90	78.58	78.53
BobWhite_c6328_410	0.232	95/3	53.94	55.51	0.871	95/3	78.52	79.15
BobWhite_c47401_491	0.852	2/95	53.67	53.97	0.271	2/95	73.41	78.68
Excalibur_c49805_63	0.012	8/90	55.87	53.82	0.95	8/90	78.68	78.52
Excalibur_rep_c109101_94	0.558	10/87	53.62	54.06	0.726	10/87	79.24	78.45
Excalibur_c39002_242	0	83/3	53.60	58.79	0.738	83/3	78.67	80.00
Excalibur_c766_705	0.39	45/53	53.78	54.17	0.007	45/53	76.60	80.18
Excalibur_c17250_751	0.456	70/21	53.88	54.29	0.816	70/21	78.49	78.10
GENE-1584_692	0.66	34/62	54.10	53.89	0.26	34/62	77.50	79.11
IAAV5302	0.071	78/20	53.78	54.79	0.288	78/20	78.17	79.95
Kukri_c80869_122	0.976	77/19	53.98	53.96	0.269	77/19	78.95	77.05
Ku_c10913_2542	0.475	66/30	53.88	54.24	0.067	66/30	79.29	76.61
Kukri_rep_c70864_638	0.254	4/94	55.24	53.94	0.188	4/94	74.23	78.72
RAC875_c38018_278	0.508	87/11	53.94	54.41	0.143	87/11	78.18	81.31
RAC875_c107130_384	0.868	60/35	53.95	54.03	0.349	60/35	79.03	77.69
RAC875_c140_872	0.759	1/93	53.16	53.79	0.629	1/93	75.30	78.58
RFL_Contig3285_1009	0.666	34/59	54.09	53.89	0.469	34/59	78.98	77.94
RFL_Contig4517_1300	0.73	88/10	53.96	54.22	0.117	88/10	78.18	81.67
Tdurum_contig46334_832	0.012	9/84	55.52	53.69	0.079	9/84	82.28	78.17
wsnp_Ex_c1563_2986030	0.345	8/77	54.81	54.01	0.97	8/77	78.58	78.48
wsnp_Ku_c44600_51841068	0.87	72/7	54.11	54.26	0.858	72/7	78.92	79.41
wsnp_Ra_c2633_5017265	0.595	83/9	53.99	53.58	0.936	83/9	78.59	78.78
wsnp_JD_rep_c49438_33652645	0.427	18/62	54.27	53.79	0.854	18/62	78.34	78.68
wsnp_Ex_c1011_1931797	0.954	71/20	53.81	53.84	0.19	71/20	78.89	76.65
wsnp_Ex_c20899_30011827	0.173	89/1	53.93	50.88	0.467	89/1	78.84	73.85
wsnp_Ex_c6209_10838852	0.017	13/76	55.23	53.67	0.054	13/76	82.11	78.18
wsnp_Ex_rep_c101638_86971861	0.28	8/90	54.81	53.92	0.983	8/90	78.58	78.53
wsnp_BF292596A_Ta_1_3	0.001	5/93	57.03	53.83	0.429	5/93	80.84	78.41

Table 50: Significant markers after validation on new MASBASIS lines with p-values, allele frequency and allele effect. Green area shows trials and traits where markers shows a p-value below 0,5 in an ANOVA test.

Marker	FHB_2013				DON_2013			
	p value	X/Y	X-mean	Y-mean	p value	X/Y	X-mean	Y-mean
BS00069125_51	0.371	92/2	25.70	15.65	0.912	92/2	10.02	9.49
BS00063175_51	0.979	95/2	25.77	25.50	0.041	95/2	9.68	19.30
BS00022459_51	0.173	81/16	26.57	20.75	0.89	81/16	9.87	10.12
BS00023150_51	0.063	7/50	33.53	22.25	0	7/50	16.37	8.50
BS00110550_51	0.25	81/15	26.54	21.49	0.86	81/15	9.94	10.27
BobWhite_c13322_215	0.057	8/90	35.63	24.76	0	8/90	21.93	8.86
BobWhite_c6328_410	0.033	95/3	25.05	44.36	0	95/3	9.26	31.10
BobWhite_c47401_491	0.409	2/95	34.81	25.62	0.003	2/95	23.40	9.67
Excalibur_c49805_63	0.028	8/90	37.13	24.62	0	8/90	23.40	8.73
Excalibur_rep_c109101_94	0.158	10/87	32.32	24.95	0.267	10/87	12.16	9.70
Excalibur_c39002_242	0.233	83/3	26.81	15.73	0.901	83/3	10.11	9.60
Excalibur_c766_705	0.636	45/53	26.45	24.95	0.415	45/53	10.52	9.43
Excalibur_c17250_751	0.839	70/21	25.57	24.78	0.634	70/21	9.44	8.82
GENE-1584_692	0.818	34/62	25.28	26.05	0.972	34/62	9.89	9.94
IAAV5302	0.399	78/20	26.32	23.02	0.185	78/20	10.38	8.18
Kukri_c80869_122	0.265	77/19	24.61	29.08	0.777	77/19	9.60	10.05
Ku_c10913_2542	0.013	66/30	28.17	19.91	0.359	66/30	10.36	9.01
Kukri_rep_c70864_638	0.444	4/94	31.49	25.39	0.077	4/94	15.63	9.69
RAC875_c38018_278	0.081	87/11	24.67	33.33	0.305	87/11	9.69	11.85
RAC875_c107130_384	0.853	60/35	25.61	26.24	0.326	60/35	9.42	10.82
RAC875_c140_872	0.861	1/93	28.82	26.04	0.27	1/93	17.28	9.83
RFL_Contig3285_1009	0.151	34/59	28.56	23.85	0.065	34/59	10.97	8.72
RFL_Contig4517_1300	0.046	88/10	24.59	34.89	0.179	88/10	9.63	12.58
Tdurum_contig46334_832	0.971	9/84	26.31	26.51	0.742	9/84	9.26	10.04
wsnp_Ex_c1563_2986030	0.038	8/77	35.63	23.92	0	8/77	21.93	8.99
wsnp_Ku_c44600_51841068	0.028	72/7	24.76	38.55	0	72/7	9.13	23.20
wsnp_Ra_c2633_5017265	0.966	83/9	25.33	25.56	0.321	83/9	9.24	11.04
wsnp_JD_rep_c49438_33652645	0.558	18/62	27.40	24.90	0.338	18/62	10.97	9.29
wsnp_Ex_c1011_1931797	0.259	71/20	27.56	23.07	0.602	71/20	10.26	9.36
wsnp_Ex_c20899_30011827	0.837	89/1	25.40	28.65	0.792	89/1	9.61	11.28
wsnp_Ex_c6209_10838852	0.364	13/76	21.90	26.27	0.097	13/76	12.23	9.12
wsnp_Ex_rep_c101638_86971861	0.057	8/90	35.63	24.76	0	8/90	21.93	8.86
wsnp_BF292596A_Ta_1_3	0.157	5/93	16.06	26.16	0.432	5/93	7.66	10.05

Table 51: Significant markers after validation on new MASBASIS lines with p-values, allele frequency and allele effect. Green area shows trials and traits where markers shows a p-value below 0,5 in an ANOVA test.

Marker	DH_2014				PH_2014			
	p value	X/Y	X-mean	Y-mean	p value	X/Y	X-mean	Y-mean
BS00069125_51	0.473	92/2	54.91	56.13	0.024	92/2	78.37	87.95
BS00063175_51	0.375	95/3	54.87	56.06	0.859	95/3	78.69	78.07
BS00022459_51	0.304	83/14	55.12	54.44	0.737	83/14	78.76	79.33
BS00023150_51	0.244	13/60	55.56	54.75	0.455	13/60	77.67	79.00
BS00110550_51	0.396	84/14	55.02	54.44	0.704	84/14	78.69	79.33
BobWhite_c13322_215	0.188	10/89	54.03	55.06	0.002	10/89	73.35	79.33
BobWhite_c6328_410	0.686	95/4	54.94	55.42	0.183	95/4	78.89	74.90
BobWhite_c47401_491	0.503	3/96	54.06	54.99	0.114	3/96	73.47	78.89
Excalibur_c49805_63	0.281	8/89	55.84	54.90	0.015	8/89	73.91	79.18
Excalibur_rep_c109101_94	0.329	9/88	54.32	55.11	0.168	9/88	76.08	78.87
Excalibur_c39002_242	0.167	90/2	54.90	57.22	0.014	90/2	78.79	68.48
Excalibur_c766_705	0.302	45/54	54.69	55.18	0.749	45/54	78.94	78.56
Excalibur_c17250_751	0.117	61/30	55.25	54.43	0.827	61/30	78.60	78.88
GENE-1584_692	0.518	30/66	55.15	54.82	0.61	30/66	78.17	78.84
IAAV5302	0.279	76/16	55.07	54.37	0.675	76/16	78.83	78.15
Kukri_c80869_122	0.393	78/18	55.04	54.51	0.094	78/18	79.18	76.61
Ku_c10913_2542	0.468	73/25	54.87	55.26	0.704	73/25	78.56	79.08
Kukri_rep_c70864_638	0.664	3/95	54.38	54.98	0.002	3/95	68.64	79.08
RAC875_c38018_278	0.259	82/16	55.10	54.37	0.919	82/16	78.76	78.60
RAC875_c107130_384	0.677	64/32	54.86	55.07	0.348	64/32	78.99	77.80
RAC875_c140_872	0.38	2/94	56.31	54.85	0.373	2/94	75.41	79.06
RFL_Contig3285_1009	0.44	36/59	54.73	55.11	0.499	36/59	78.25	79.07
RFL_Contig4517_1300	0.274	83/16	55.07	54.37	0.922	83/16	78.75	78.60
Tdurum_contig46334_832	0.255	8/87	55.86	54.87	0.603	8/87	79.89	78.76
wsnp_Ex_c1563_2986030	0.176	10/85	54.03	55.10	0.002	10/85	73.35	79.39
wsnp_Ku_c44600_51841068	0.076	79/9	55.08	53.58	0.002	79/9	79.59	73.15
wsnp_Ra_c2633_5017265	0.104	85/8	55.11	53.69	0.972	85/8	79.03	78.96
wsnp_JD_rep_c49438_33652645	0.094	28/60	54.27	55.17	0.918	28/60	78.72	78.87
wsnp_Ex_c1011_1931797	0.773	71/20	54.87	55.04	0.838	71/20	78.97	78.67
wsnp_Ex_c20899_30011827	0.073	90/2	54.95	51.96	0.274	90/2	78.98	74.32
wsnp_Ex_c6209_10838852	0.506	8/79	55.35	54.77	0.839	8/79	79.06	78.62
wsnp_Ex_rep_c101638_86971861	0.188	10/89	54.03	55.06	0.002	10/89	73.35	79.33
wsnp_BF292596A_Ta_1_3	0.617	3/95	55.63	54.94	0.106	3/95	73.36	78.93

Table 52: Significant markers after validation on new MASBASIS lines with p-values, allele frequency and allele effect. Green area shows trials and traits where markers shows a p-value below 0,5 in an ANOVA test.

Marker	FHB_2014				DON_2014			
	p value	X/Y	X-mean	Y-mean	p value	X/Y	X-mean	Y-mean
BS00069125_51	0.796	92/2	4.93	4.09	0.255	92/2	2.77	5.36
BS00063175_51	0.671	95/3	5.00	3.85	0	95/3	2.52	10.14
BS00022459_51	0.793	83/14	5.01	4.66	0.66	83/14	2.75	3.15
BS00023150_51	0.241	13/60	3.62	5.19	0.116	13/60	3.01	2.30
BS00110550_51	0.841	84/14	4.93	4.66	0.661	84/14	2.75	3.15
BobWhite_c13322_215	0.582	10/89	5.68	4.84	0	10/89	7.09	2.32
BobWhite_c6328_410	0.223	95/4	4.81	7.66	0	95/4	2.48	10.40
BobWhite_c47401_491	0.587	3/96	3.51	4.97	0	3/96	9.77	2.58
Excalibur_c49805_63	0.084	8/89	7.65	4.72	0	8/89	8.67	2.27
Excalibur_rep_c109101_94	0.3	9/88	6.46	4.79	0.485	9/88	3.50	2.73
Excalibur_c39002_242	0.356	90/2	5.00	2.01	0.814	90/2	2.85	2.31
Excalibur_c766_705	0.112	45/54	5.73	4.26	0.297	45/54	3.16	2.50
Excalibur_c17250_751	0.52	61/30	4.97	4.34	0.811	61/30	2.38	2.45
GENE-1584_692	0.328	30/66	5.68	4.68	0.767	30/66	2.68	2.89
IAAV5302	0.849	76/16	5.05	4.80	0.233	76/16	2.97	1.94
Kukri_c80869_122	0.864	78/18	4.92	5.13	0.329	78/18	2.49	3.07
Ku_c10913_2542	0.122	73/25	4.55	6.19	0.305	73/25	2.98	2.24
Kukri_rep_c70864_638	0.581	3/95	3.48	4.98	0	3/95	9.46	2.59
RAC875_c38018_278	0.233	82/16	5.22	3.72	0.767	82/16	2.85	2.60
RAC875_c107130_384	0.109	64/32	4.41	6.00	0.401	64/32	2.67	3.24
RAC875_c140_872	0.971	2/94	5.14	5.02	0.749	2/94	2.10	2.83
RFL_Contig3285_1009	0.425	36/59	5.39	4.64	0.076	36/59	3.23	2.26
RFL_Contig4517_1300	0.251	83/16	5.16	3.72	0.775	83/16	2.84	2.60
Tdurum_contig46334_832	0.291	8/87	3.28	4.97	0.659	8/87	2.32	2.84
wsnp_Ex_c1563_2986030	0.612	10/85	5.68	4.89	0	10/85	7.09	2.33
wsnp_Ku_c44600_51841068	0.315	79/9	4.55	6.10	0	79/9	2.36	7.58
wsnp_Ra_c2633_5017265	0.135	85/8	4.64	7.14	0.954	85/8	2.41	2.38
wsnp_JD_rep_c49438_33652645	0.91	28/60	4.85	4.97	0.126	28/60	3.14	2.32
wsnp_Ex_c1011_1931797	0.454	71/20	4.81	5.68	0.434	71/20	2.70	3.32
wsnp_Ex_c20899_30011827	0.567	90/2	4.94	3.08	0.984	90/2	2.59	2.63
wsnp_Ex_c6209_10838852	0.865	8/79	4.62	4.91	0.055	8/79	4.10	2.43
wsnp_Ex_rep_c101638_86971861	0.582	10/89	5.68	4.84	0	10/89	7.09	2.32
wsnp_BF292596A_Ta_1_3	0.273	3/95	2.06	5.02	0.635	3/95	1.95	2.82

Table 53: Significant markers after validation on new MASBASIS lines with p-values, allele frequency and allele effect. Green area shows trials and traits where markers shows a p-value below 0,5 in an ANOVA test.

Marker	AE_2014 Vollebekk				AE_2014 Staur			
	p-value	X/Y	X-mean	Y-mean	p-value	X/Y	X-mean	Y-mean
BS00069125_51		73/0				73/0		
BS00063175_51	0.61	74/1	6.07	7.00	0.93	74/1	6.57	6.71
BS00022459_51	0.128	62/12	5.97	6.83	0.355	62/12	6.49	6.97
BS00023150_51	0.248	9/54	6.72	5.97	0.502	9/54	6.36	6.75
BS00110550_51	0.113	62/12	5.93	6.83	0.386	62/12	6.52	6.97
BobWhite_c13322_215	0.127	2/73	8.00	6.03	0.428	2/73	7.48	6.54
BobWhite_c6328_410		75/0				75/0		
BobWhite_c47401_491		0/75				0/75		
Excalibur_c49805_63	0.817	1/71	6.50	6.08	0.27	1/71	4.71	6.54
Excalibur_rep_c109101_94	0.212	5/70	5.10	6.15	0.312	5/70	5.85	6.62
Excalibur_c39002_242		71/0				71/0		
Excalibur_c766_705	0.601	35/40	6.20	5.98	0.127	35/40	6.26	6.84
Excalibur_c17250_751	0.058	48/18	5.81	6.78	0.16	48/18	6.77	6.13
GENE-1584_692	0.529	23/50	6.28	6.00	0.604	23/50	6.44	6.66
IAAV5302	0.637	63/9	6.03	6.33	0.116	63/9	6.68	5.76
Kukri_c80869_122	0.509	64/8	5.98	6.44	0.067	64/8	6.44	7.57
Ku_c10913_2542	0.448	58/16	5.97	6.37	0.682	58/16	6.53	6.73
Kukri_rep_c70864_638		0/74				0/74		
RAC875_c38018_278	0.706	64/9	6.04	6.28	0.71	64/9	6.54	6.33
RAC875_c107130_384	0.641	49/24	5.96	6.17	0.728	49/24	6.60	6.46
RAC875_c140_872	0.395	2/73	5.00	6.11	0.651	2/73	6.05	6.58
RFL_Contig3285_1009	0.626	22/51	5.89	6.11	0.135	22/51	6.21	6.81
RFL_Contig4517_1300	0.725	66/9	6.05	6.28	0.639	66/9	6.60	6.33
Tdurum_contig46334_832	0.68	3/71	6.50	6.05	0.062	3/71	8.29	6.49
wsnp_Ex_c1563_2986030	0.132	2/67	8.00	6.06	0.419	2/67	7.48	6.51
wsnp_Ku_c44600_51841068	0.128	61/2	6.04	8.00	0.464	61/2	6.61	7.48
wsnp_Ra_c2633_5017265	0.259	72/1	6.08	4.00	0.169	72/1	6.60	8.79
wsnp_JD_rep_c49438_33652645	0.016	18/50	7.06	5.87	0.155	18/50	6.07	6.72
wsnp_Ex_c1011_1931797	0.589	56/16	6.14	5.87	0.617	56/16	6.56	6.33
wsnp_Ex_c20899_30011827		74/0				74/0		
wsnp_Ex_c6209_10838852	0.085	3/68	4.33	6.16	0.878	3/68	6.71	6.56
wsnp_Ex_rep_c101638_86971861	0.132	2/72	8.00	6.05	0.425	2/72	7.48	6.53
wsnp_BF292596A_Ta_1_3		0/74				0/74		

Table 54: Significant markers after validation on new MASBASIS lines with p-values, allele frequency and allele effect. Green area shows trials and traits where markers shows a p-value below 0,5 in an ANOVA test.

Marker	AE_2015 Staur				DH_2015			
	p-value	X/Y	X-mean	Y-mean	p value	X/Y	X-mean	Y-mean
BS00069125_51		63/0			0.769	97/2	53.4	53.7
BS00063175_51	0.446	62/2	6.49	7.38	0.771	98/4	53.3	53.5
BS00022459_51	0.026	48/15	6.26	7.32	0.73	81/20	53.4	53.3
BS00023150_51	0.956	5/46	6.38	6.34	0.085	9/65	53.9	53.1
BS00110550_51	0.028	48/15	6.27	7.32	0.852	82/20	53.4	53.3
BobWhite_c13322_215	0.475	1/63	7.68	6.50	0.775	9/94	53.2	53.4
BobWhite_c6328_410		64/0			0.326	99/4	53.3	54.1
BobWhite_c47401_491		0/63			0.787	3/99	53.1	53.4
Excalibur_c49805_63	0.817	1/61	6.18	6.56	0.004	9/91	54.7	53.2
Excalibur_rep_c109101_94	0.812	4/60	6.70	6.50	0.757	8/93	53.2	53.4
Excalibur_c39002_242		61/0			0	90/3	53.2	56.2
Excalibur_c766_705	0.009	29/35	5.94	6.99	0.363	42/61	53.2	53.5
Excalibur_c17250_751	0.974	42/16	6.50	6.52	0.014	66/28	53.6	52.8
GENE-1584_692	0.135	20/42	6.03	6.70	0.897	33/67	53.3	53.4
IAAV5302	0.275	57/5	6.60	5.76	0.885	84/16	53.3	53.4
Kukri_c80869_122	0.782	58/5	6.56	6.34	0.544	86/15	53.4	53.1
Ku_c10913_2542	0.762	50/14	6.55	6.40	0.479	76/27	53.3	53.5
Kukri_rep_c70864_638		0/63			0.77	3/99	53.6	53.4
RAC875_c38018_278	0.246	57/6	6.39	7.18	0.296	89/13	53.4	53.0
RAC875_c107130_384	0.228	41/22	6.69	6.16	0.737	65/36	53.4	53.3
RAC875_c140_872	0.054	2/62	4.35	6.58	0.638	3/96	52.9	53.3
RFL_Contig3285_1009	0.208	20/44	6.13	6.69	0.515	37/64	53.2	53.4
RFL_Contig4517_1300	0.294	58/6	6.45	7.18	0.3	90/13	53.4	53.0
Tdurum_contig46334_832	0.019	1/61	2.71	6.54	0.024	7/89	54.5	53.2
wsnp_Ex_c1563_2986030	0.454	1/51	7.68	6.41	0.683	9/82	53.2	53.4
wsnp_Ku_c44600_51841068	0.517	57/1	6.66	7.68	0.551	86/8	53.4	53.1
wsnp_Ra_c2633_5017265	0.273	62/1	6.52	4.71	0.338	91/8	53.4	52.9
wsnp_JD_rep_c49438_33652645	0.687	12/42	6.29	6.51	0.026	22/63	52.8	53.6
wsnp_Ex_c1011_1931797	0.128	46/16	6.69	5.96	0.731	74/22	53.2	53.4
wsnp_Ex_c20899_30011827		63/0			0.289	94/2	53.4	52.2
wsnp_Ex_c6209_10838852	0.619	1/61	5.68	6.51	0.012	9/84	54.5	53.2
wsnp_Ex_rep_c101638_86971861	0.445	1/62	7.68	6.44	0.769	9/93	53.2	53.4
wsnp_BF292596A_Ta_1_3		0/63			0.076	5/97	54.5	53.3

Table 55: Significant markers after validation on new MASBASIS lines with p-values, allele frequency and allele effect. Green area shows trials and traits where markers shows a p-value below 0,5 in an ANOVA test.

Marker	FHB_2015				DON_2015			
	p value	X/Y	X-mean	Y-mean	p-value	X/Y	X-mean	Y-mean
BS00069125_51	0.002	97/2	41.67	75.64	0.338	97/2	21.88	28.57
BS00063175_51	0.826	98/4	42.18	43.98	0.036	98/4	21.51	31.85
BS00022459_51	0.072	81/20	43.47	36.41	0.749	81/20	22.22	21.44
BS00023150_51	0.538	9/65	44.58	41.28	0.037	9/65	26.50	19.96
BS00110550_51	0.055	82/20	44.12	36.41	0.753	82/20	22.21	21.44
BobWhite_c13322_215	0.001	9/94	58.98	40.94	0.000	9/94	34.28	20.79
BobWhite_c6328_410	0.003	99/4	41.57	65.86	0.000	99/4	20.90	48.41
BobWhite_c47401_491	0.019	3/99	64.1	41.96	0.008	3/99	36.40	21.51
Excalibur_c49805_63	0.001	9/91	58.93	41.09	0.000	9/91	40.54	20.29
Excalibur_rep_c109101_94	0.089	8/93	51.26	41.37	0.056	8/93	28.26	21.44
Excalibur_c39002_242	0.666	90/3	42.91	38.88	0.579	90/3	21.85	24.94
Excalibur_c766_705	0.108	42/61	45.59	40.4	0.552	42/61	21.28	22.44
Excalibur_c17250_751	0.509	66/28	41.54	43.75	0.253	66/28	22.40	20.11
GENE-1584_692	0.270	33/67	39.94	43.79	0.634	33/67	21.21	22.19
IAAV5302	0.035	84/16	43.92	34.57	0.766	84/16	21.69	22.48
Kukri_c80869_122	0.153	86/15	41.58	47.92	0.146	86/15	21.21	24.93
Ku_c10913_2542	0.960	76/27	42.47	42.65	0.598	76/27	21.67	22.82
Kukri_rep_c70864_638	0.008	3/99	66.5	41.72	0.170	3/99	29.60	21.77
RAC875_c38018_278	0.427	89/13	42.26	46.05	0.341	89/13	21.71	24.46
RAC875_c107130_384	0.613	65/36	43.35	41.65	0.915	65/36	21.93	21.72
RAC875_c140_872	0.743	3/96	45.72	42.56	0.949	3/96	21.31	21.68
RFL_Contig3285_1009	0.101	37/64	45.28	40.06	0.138	37/64	23.33	20.50
RFL_Contig4517_1300	0.399	90/13	42.01	46.05	0.323	90/13	21.61	24.46
Tdurum_contig46334_832	0.869	7/89	41.76	42.83	0.558	7/89	23.84	21.68
wsnp_Ex_c1563_2986030	0.002	9/82	58.98	41.49	0.000	9/82	34.28	20.96
wsnp_Ku_c44600_51841068	0.000	86/8	40.84	61.36	0.001	86/8	21.32	33.14
wsnp_Ra_c2633_5017265	0.115	91/8	41.07	49.99	0.153	91/8	21.06	25.77
wsnp_JD_rep_c49438_33652645	0.085	22/63	48.01	41.18	0.963	22/63	22.00	21.89
wsnp_Ex_c1011_1931797	0.317	74/22	41.93	45.94	0.736	74/22	21.55	22.34
wsnp_Ex_c20899_30011827	0.068	94/2	41.44	62	0.363	94/2	21.26	27.10
wsnp_Ex_c6209_10838852	0.349	9/84	46.07	40.98	0.001	9/84	30.80	20.32
wsnp_Ex_rep_c101638_86971861	0.001	9/93	58.98	41.17	0.000	9/93	34.28	20.88
wsnp_BF292596A_Ta_1_3	0.155	5/97	32.43	42.97	0.372	5/97	18.20	22.19

Table 56: Validation test of SSR markers genotyped on new MASBASIS.

Marker	DH_2013				PH_2013			
	p value	0/1	0-mean	1-mean	p value	0/1	0-mean	1-mean
barc228_190	0.4100	81/8	53.94	54.65	0.5550	81/8	78.56	80.06

barc228_192	0.7780	17/70	54.17	54.00	0.3050	17/70	80.19	78.29
barc228_194	0.9380	80/9	54.01	53.95	0.9640	80/9	78.71	78.60
cfd47_192	0.2840	92/3	54.02	52.64	0.5700	92/3	78.48	76.24
cfd47_194	0.4430	70/25	54.08	53.69	0.0080	70/25	79.48	75.41
cfd47_209	0.0910	91/3	53.88	56.05	0.6740	91/3	78.40	76.74
cfd47_211	0.6350	30/63	54.06	53.84	0.0090	30/63	75.73	79.59
cfd47_213		95/0				95/0		
cfd47_215	0.2140	89/6	53.91	55.06	0.9640	89/6	78.40	78.53
cfd47_218		95/0				95/0		
	FHB_2013				DON_2013			
	p value	0/1	0-mean	1-mean	p value	0/1	0-mean	1-mean
barc228_190	0.2850	81/8	24.44	30.68	0.4420	81/8	9.81	11.72
barc228_192	0.4620	17/70	27.40	24.32	0.0770	17/70	12.61	9.41
barc228_194	0.3550	80/9	25.52	20.39	0.7860	80/9	10.05	9.41
cfd47_192	0.8190	92/3	25.46	23.35	0.7390	92/3	9.81	8.53
cfd47_194	0.8080	70/25	25.16	26.04	0.4630	70/25	10.06	8.94
cfd47_209	0.6850	91/3	25.34	21.60	0.2820	91/3	9.39	13.24
cfd47_211	0.4920	30/63	23.62	25.98	0.9900	30/63	9.71	9.73
cfd47_213		95/0				95/0		
cfd47_215	0.8680	89/6	25.46	24.40	0.3520	89/6	9.61	12.18
cfd47_218		95/0				95/0		
	DH_2014				PH_2014			
	p value	0/1	0-mean	1-mean	p value	0/1	0-mean	1-mean
barc228_190	0.6650	74/14	54.90	54.60	0.1520	74/14	78.27	80.74
barc228_192	0.1930	21/66	54.29	55.07	0.2970	21/66	79.86	78.30
barc228_194	0.3800	81/7	54.92	54.09	0.8870	81/7	78.64	78.97
cfd47_192	0.1170	94/2	54.94	52.40	0.8910	94/2	78.65	79.20
cfd47_194	0.8520	66/30	54.92	54.82	0.5000	66/30	78.39	79.26
cfd47_209	0.0030	92/3	54.78	58.61	0.8100	92/3	78.64	77.80
cfd47_211	0.9120	36/60	54.92	54.87	0.6340	36/60	79.03	78.44
cfd47_213	0.9220	95/1	54.88	55.11	0.9170	95/1	78.67	78.05
cfd47_215	0.3980	91/5	54.84	55.72	0.9340	91/5	78.67	78.45
cfd47_218		96/0				96/0		
	FHB_2014				DON_2014			
	p value	0/1	0-mean	1-mean	p value	0/1	0-mean	1-mean
barc228_190	0.1610	74/14	5.32	3.38	0.9010	74/14	2.92	2.80
barc228_192	0.9840	21/66	4.82	4.80	0.3310	21/66	3.51	2.70
barc228_194	0.7470	81/7	4.96	5.57	0.6420	81/7	2.95	2.35
cfd47_192	0.0470	94/2	4.83	11.37	0.7240	94/2	2.82	2.02
cfd47_194	0.8610	66/30	4.91	5.09	0.1430	66/30	3.12	2.10
cfd47_209	0.1930	92/3	5.02	1.51	0.8870	92/3	2.71	2.96
cfd47_211	0.1700	36/60	5.81	4.47	0.7120	36/60	2.95	2.71
cfd47_213	0.8020	95/1	4.98	3.81	0.7930	95/1	2.79	3.63
cfd47_215	0.2910	91/5	4.85	7.10	0.0020	91/5	2.57	7.06
cfd47_218		96/0				96/0		
	AE_2014 Vollebekk				AE_2014 Staur			
	p-value	0/1	0-mean	1-mean	p-value	0/1	0-mean	1-mean

barc228_190	0.0030	52/13	5.80	7.42	0.5580	52/13	6.61	6.30
barc228_192	0.0260	16/49	7.00	5.84	0.8690	16/49	6.49	6.57
barc228_194	0.3970	61/4	6.18	5.38	0.4510	61/4	6.51	7.15
cfd47_192	0.6150	72/1	6.09	7.00	0.0080	72/1	6.58	2.28
cfd47_194	0.8680	47/26	6.07	6.15	0.3200	47/26	6.67	6.27
cfd47_209	0.7500	71/2	6.09	6.50	0.8650	71/2	6.53	6.33
cfd47_211	0.8800	27/46	6.14	6.08	0.1630	27/46	6.17	6.73
cfd47_213		73/0				73/0		
cfd47_215	0.7800	71/2	6.11	5.75	0.0430	71/2	6.59	4.23
cfd47_218		73/0				73/0		
	AE_2015 Staur				DH_2015			
	p-value	0/1	0-mean	1-mean	p value	0/1	0-mean	1-mean
barc228_190	0.9410	47/9	6.69	6.65	0.4270	81/11	53.37	52.98
barc228_192	0.3290	12/44	7.08	6.58	0.9030	18/73	53.37	53.32
barc228_194	0.1100	53/3	6.60	8.08	0.2670	86/6	53.28	54.00
cfd47_192	0.7130	60/1	6.58	5.98	0.5610	96/2	53.33	52.72
cfd47_194	0.1830	45/16	6.73	6.11	0.4850	78/20	53.37	53.12
cfd47_209	0.4140	59/2	6.54	7.48	0.0260	93/4	53.25	54.91
cfd47_211	0.2780	18/42	6.20	6.69	0.8730	29/67	53.31	53.26
cfd47_213		61/0			0.3490	97/1	53.31	54.69
cfd47_215	0.3760	59/2	6.60	5.58	0.7260	91/7	53.31	53.51
cfd47_218		61/0				98/0		
	FHB_2015				DON_2015			
	p value	0/1	0-mean	1-mean	p-value	0/1	0-mean	1-mean
barc228_190	0.6510	81/11	42.61	40.28	0.9200	81/11	21.99	21.69
barc228_192	0.8620	18/73	41.36	42.07	0.3780	18/73	23.41	21.30
barc228_194	0.4820	86/6	42.64	37.89	0.6860	86/6	22.06	20.47
cfd47_192	0.9110	96/2	42.12	43.43	0.7560	96/2	21.74	19.54
cfd47_194	0.4680	78/20	41.54	44.53	0.3670	78/20	22.15	19.92
cfd47_209	0.4320	93/4	41.83	48.45	0.2740	93/4	21.22	26.58
cfd47_211	0.3080	29/67	44.89	41.18	0.8220	29/67	22.08	21.59
cfd47_213	0.9490	97/1	42.14	43.20	0.0690	97/1	21.51	39.41
cfd47_215	0.6730	91/7	41.96	44.68	0.2360	91/7	21.36	25.94
cfd47_218		98/0				98/0		

Appendix 4

Spring wheat 2015

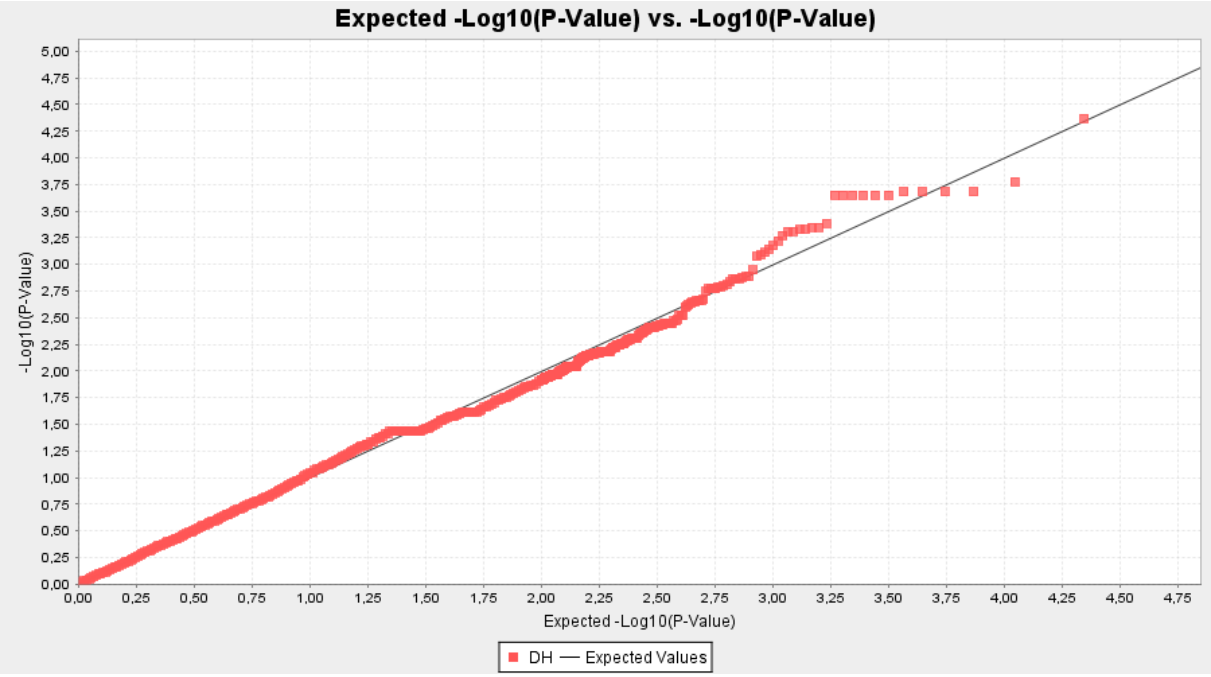

Figure 53: QQ-plot for p-values of the mixed linear model for DH in 2015 in spring wheat.

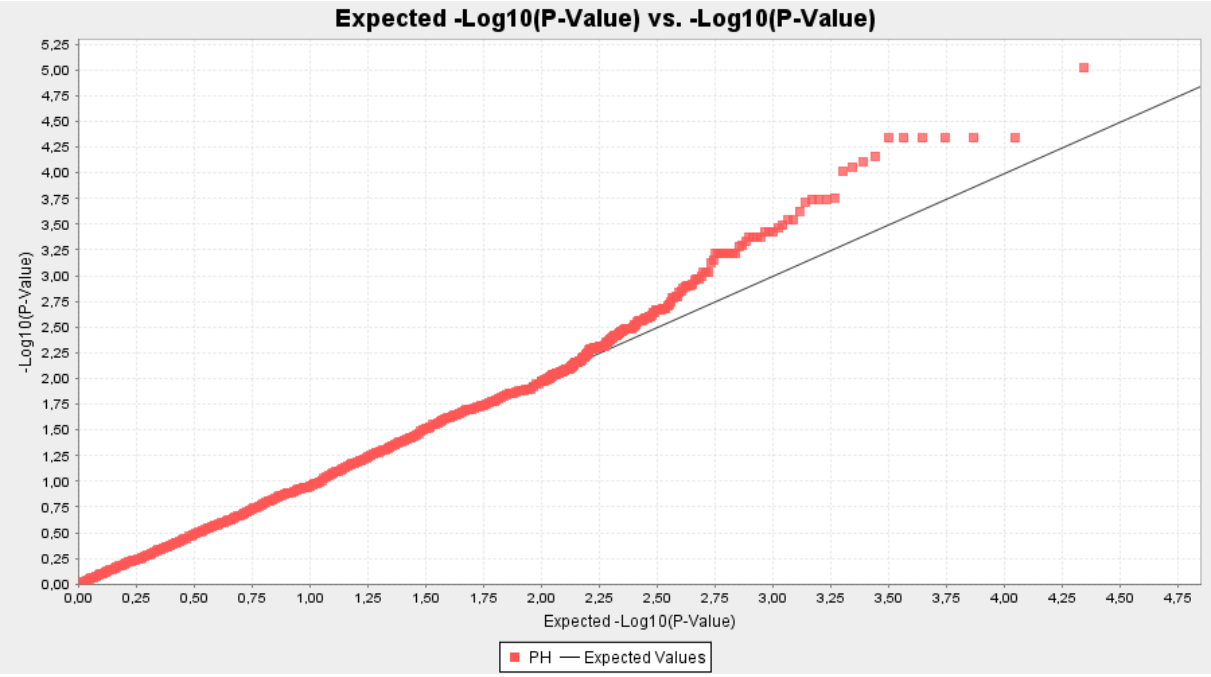

Figure 54: QQ-plot for p-values of the mixed linear model for PH in 2015 in spring wheat.

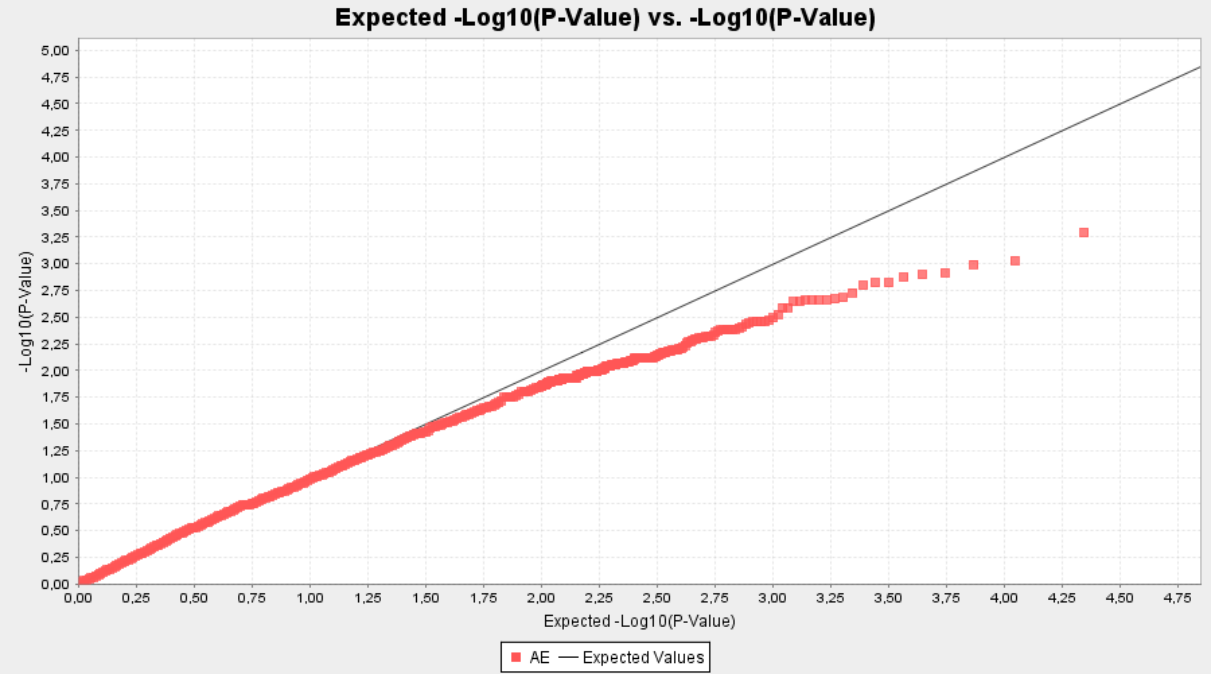

Figure 55: QQ-plot for p-values of the mixed linear model for AE in 2015 in spring wheat.

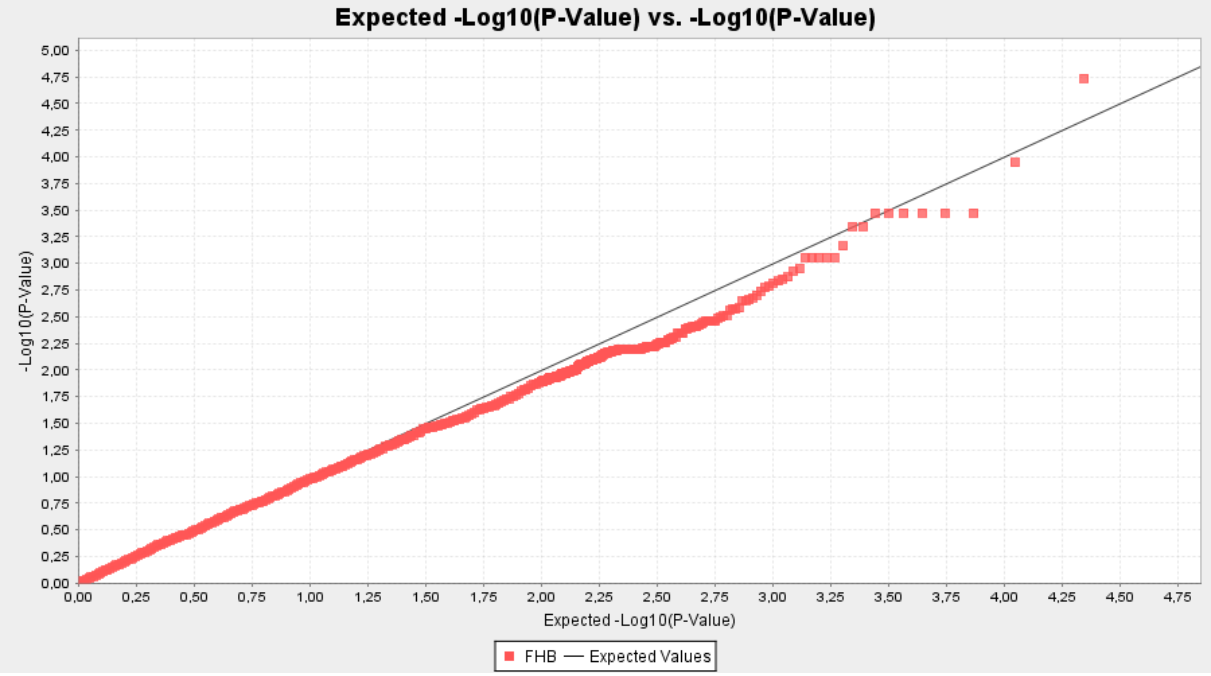

Figure 56: QQ-plot for p-values of the mixed linear model for FHB in 2015 in spring wheat.

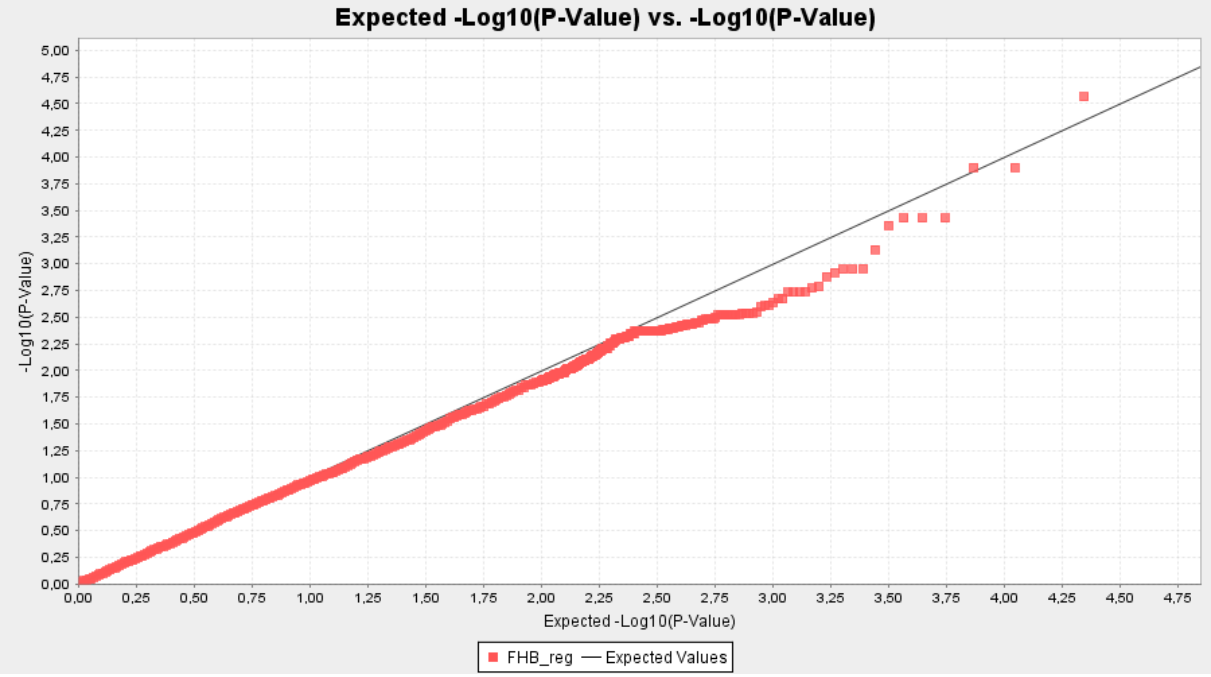

Figure 57: QQ-plot for p-values of the mixed linear model for FHB after regression in 2015 in spring wheat.

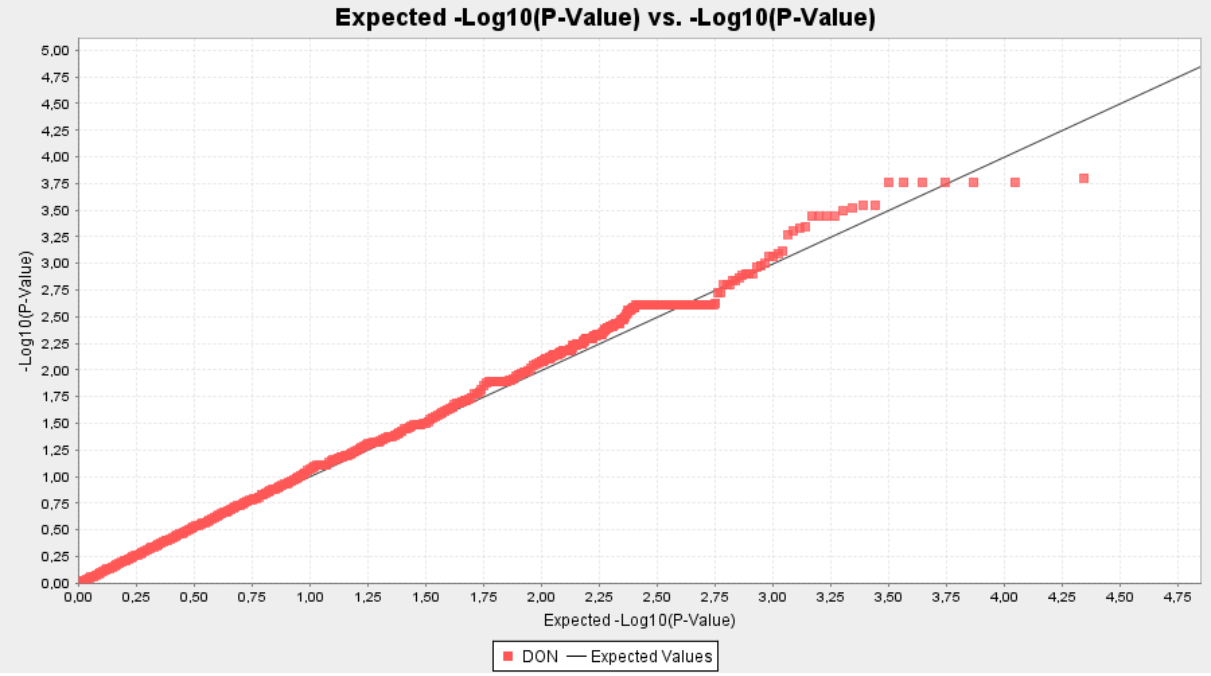

Figure 58: QQ-plot for p-values of the mixed linear model for DON values in 2015 in spring wheat.

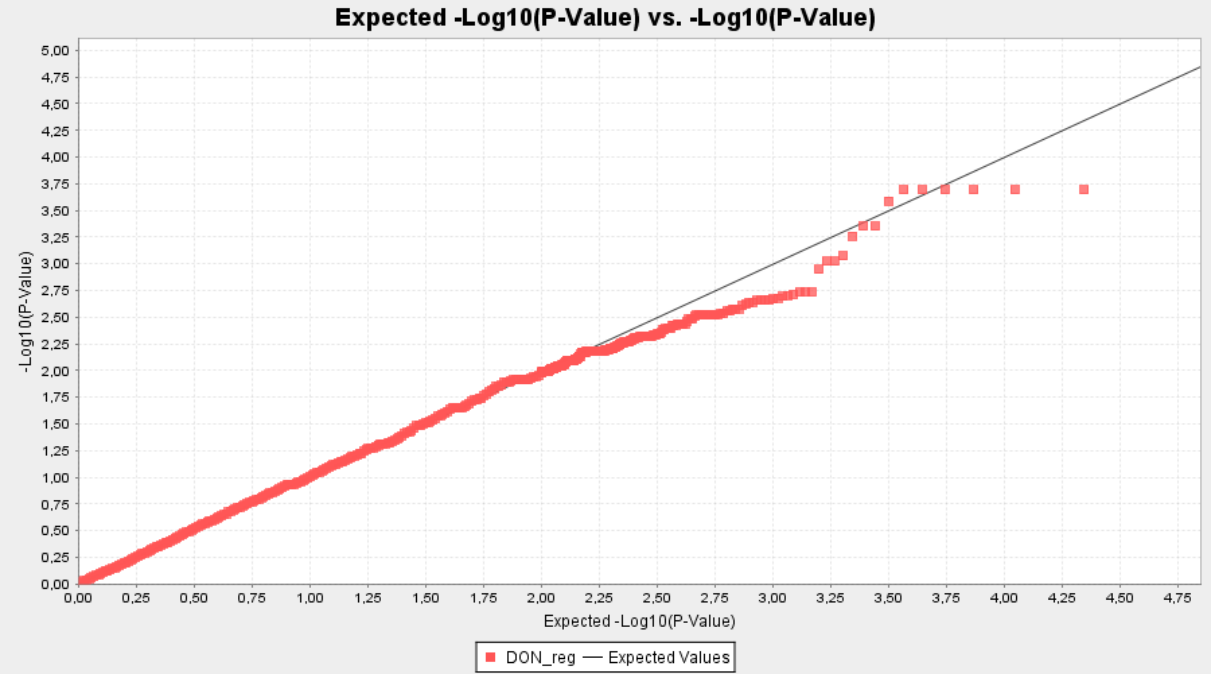

Figure 59: QQ-plot for p-values of the mixed linear model for DON values after regression in 2015 in spring wheat.

Spring wheat 2013-2015

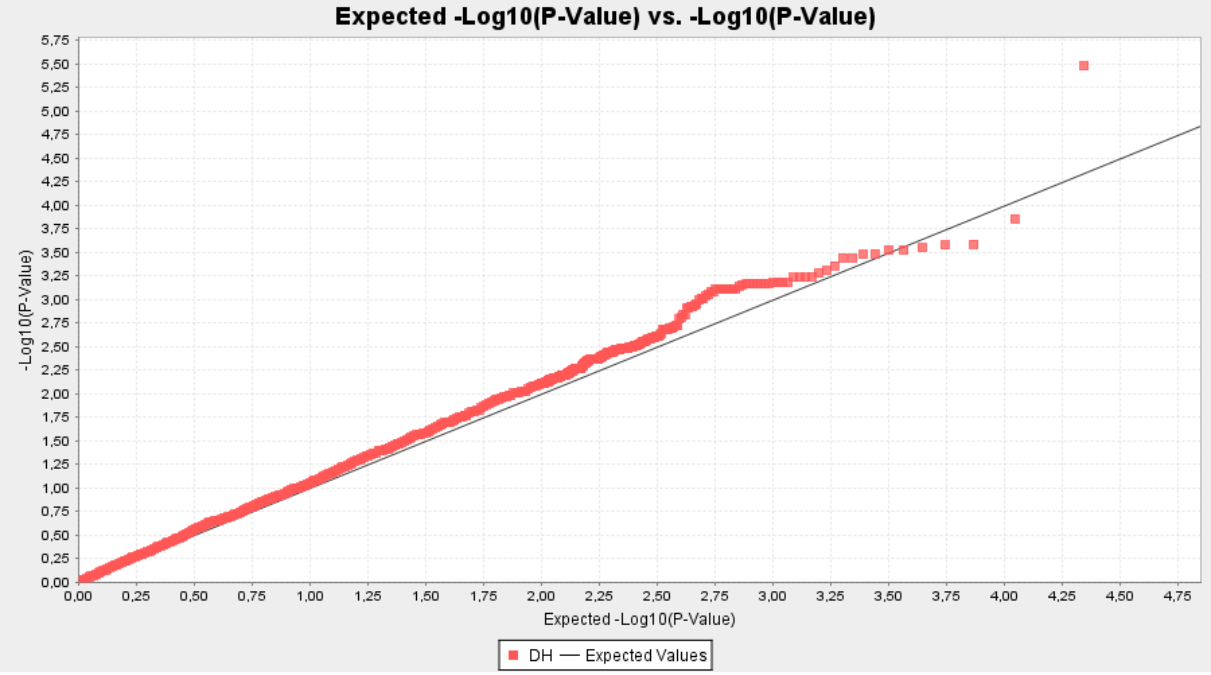

Figure 60: QQ-plot for p-values of the mixed linear model for DH from 2013-2015 in spring wheat

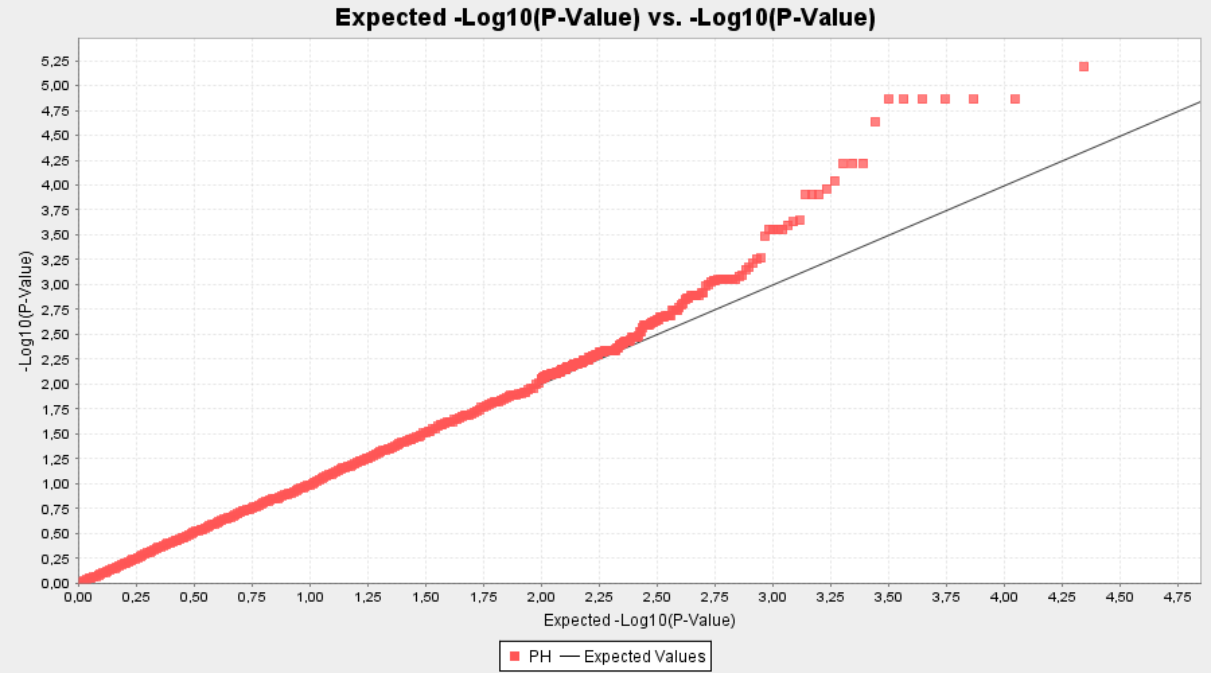

Figure 61: QQ-plot for p-values of the mixed linear model for PH from 2013-2015 in spring wheat.

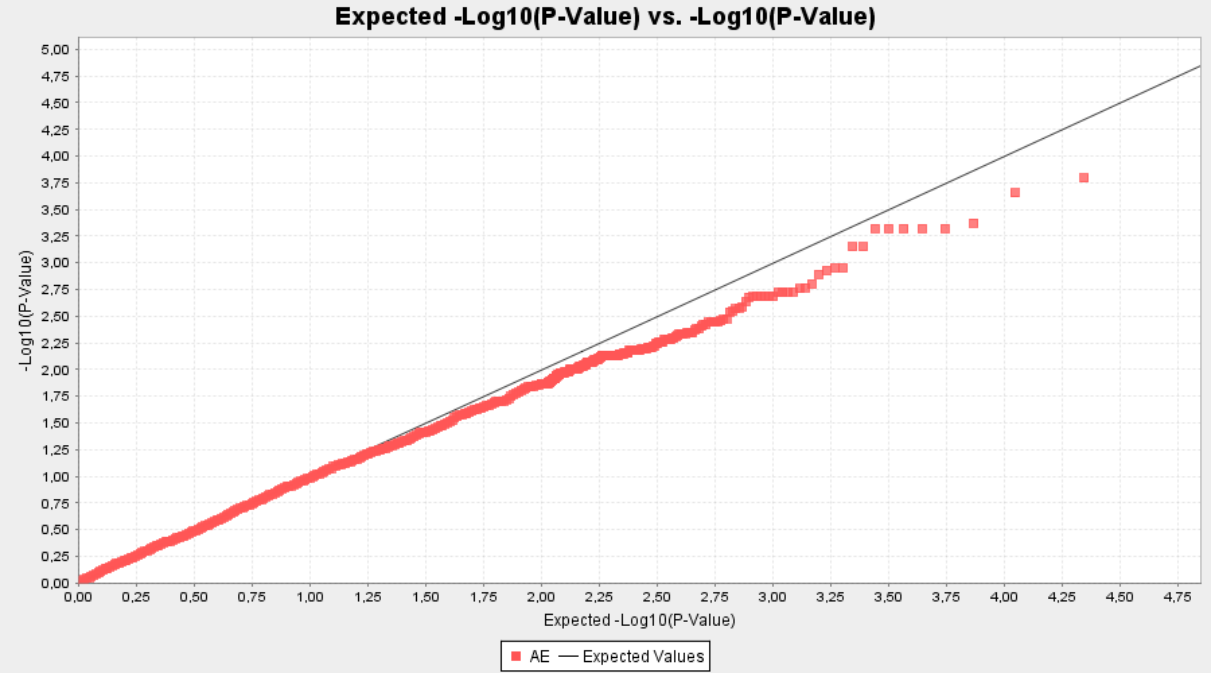

Figure 62: QQ-plot for p-values of the mixed linear model for AE from 2013-2015 in spring wheat.

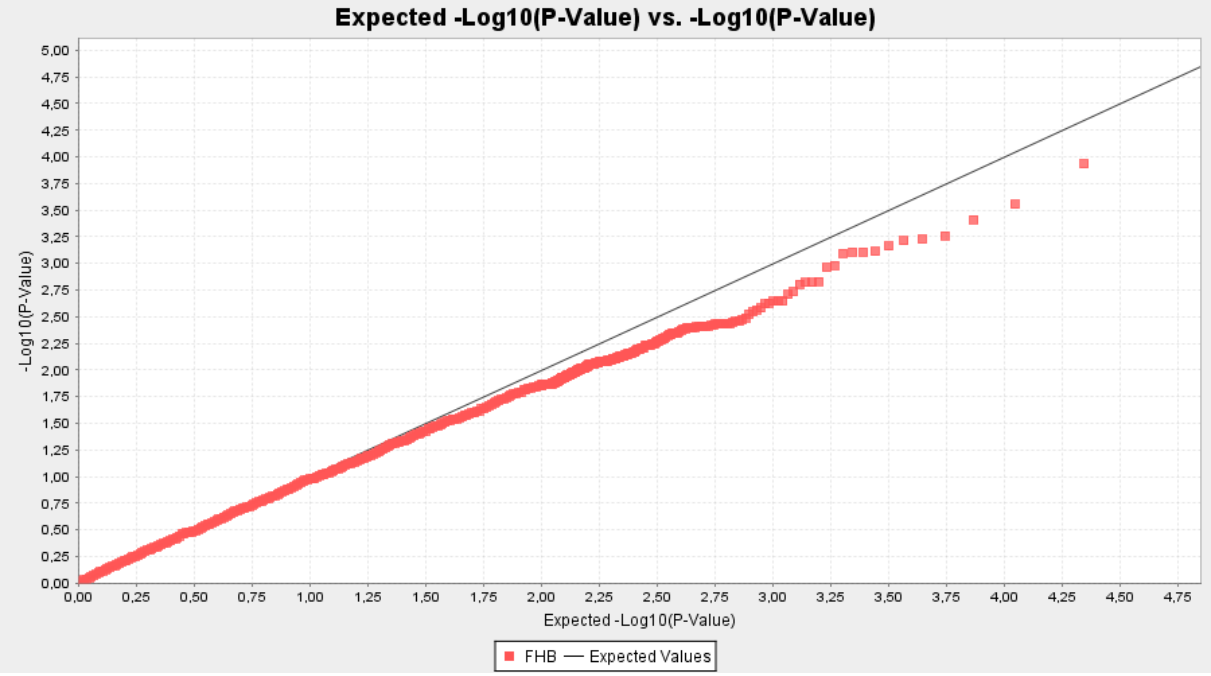

Figure 63: QQ-plot for p-values of the mixed linear model for FHB from 2013-2015 in spring wheat.

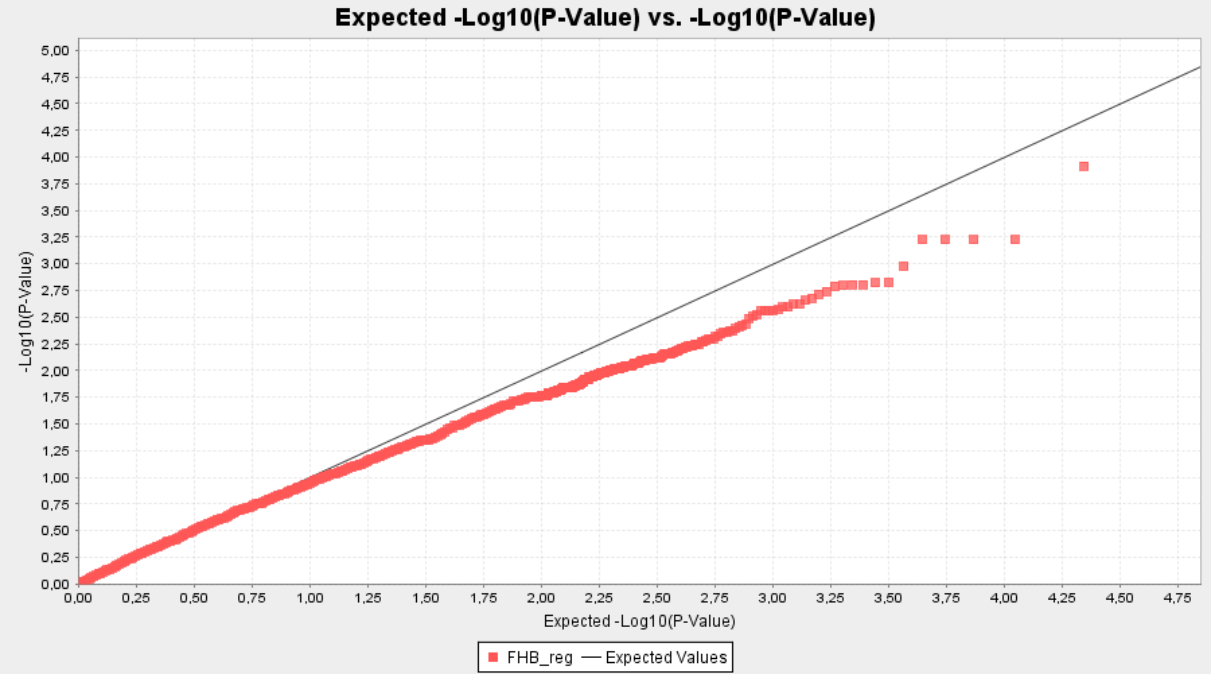

Figure 64: QQ-plot for p-values of the mixed linear model for FHB after regression from 2013-2015 in spring wheat.

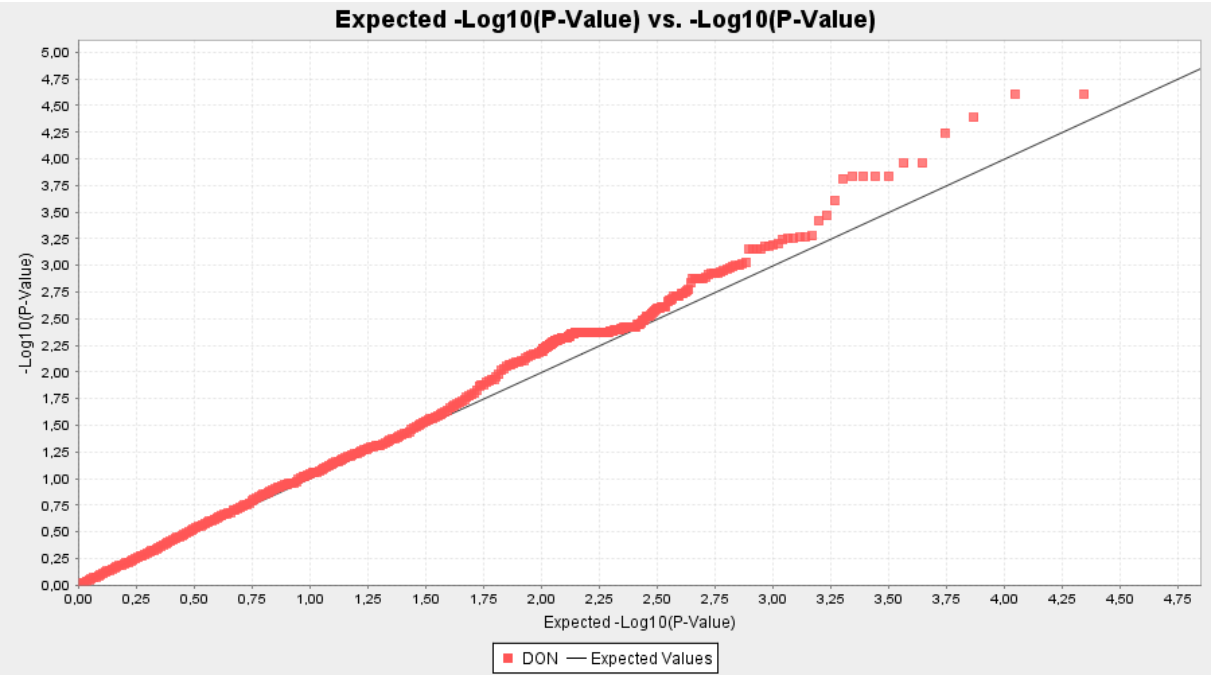

Figure 65: QQ-plot for p-values of the mixed linear model for DON from 2013-2015 in spring wheat.

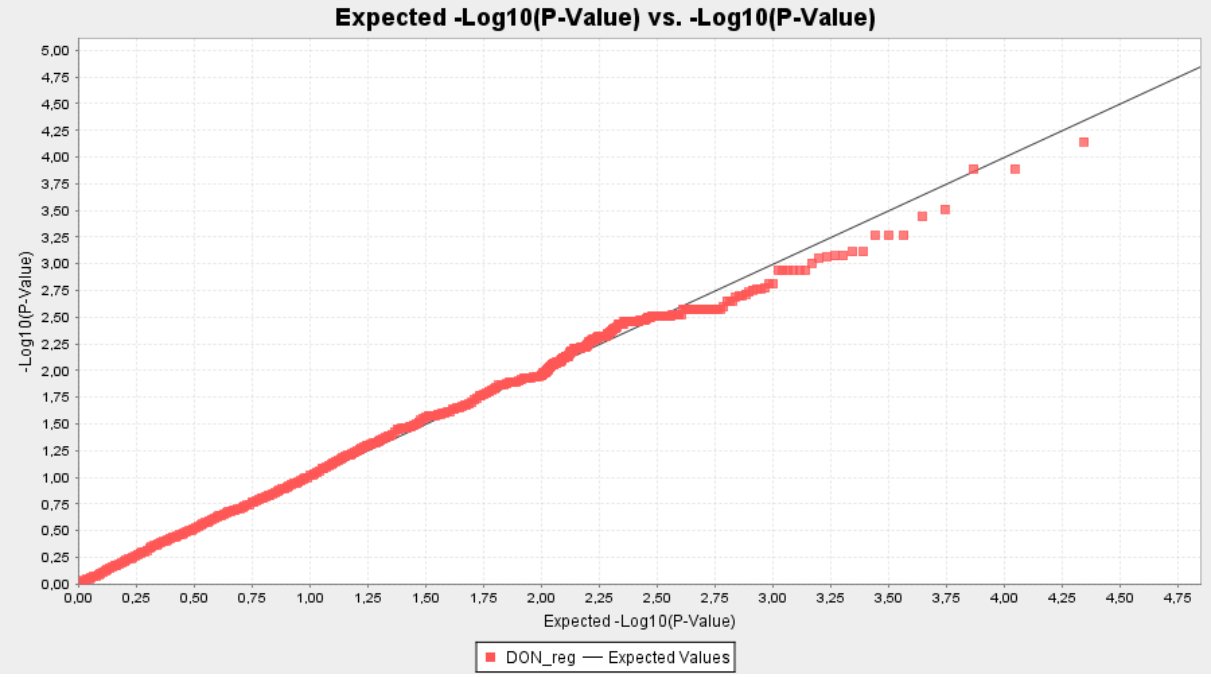

Figure 66: QQ-plot for p-values of the mixed linear model for DON_reg from 2013-2015 in spring wheat.

Spring wheat 2013-2014

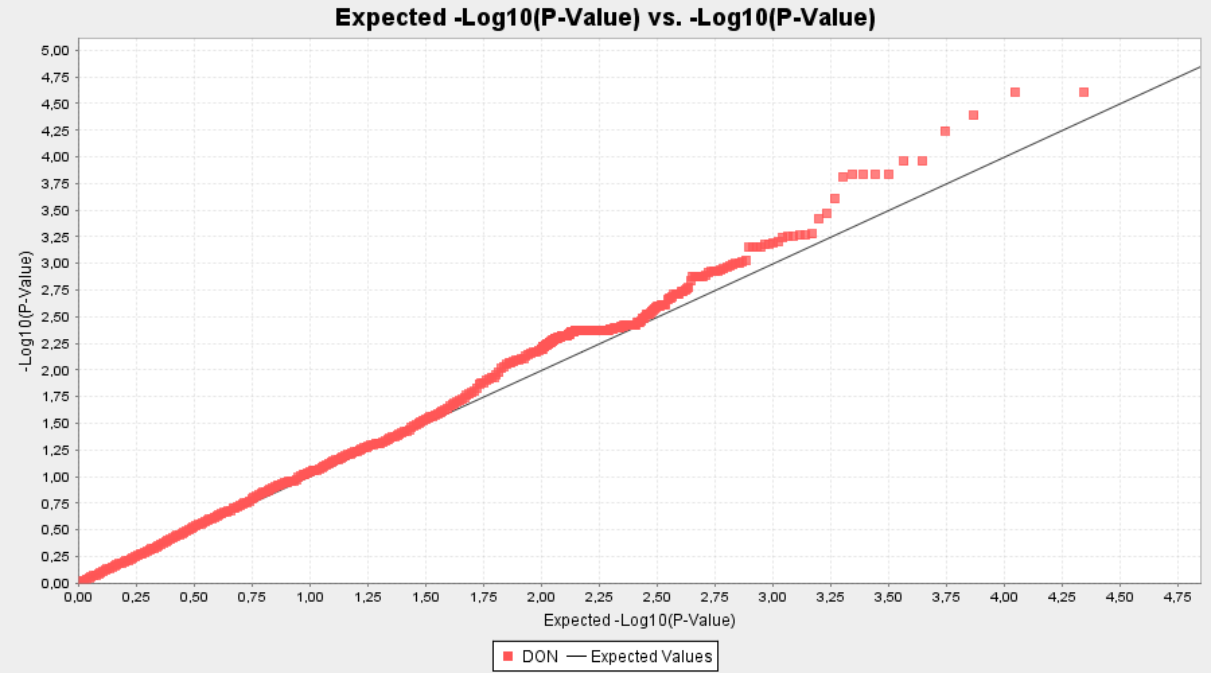

Figure 67: QQ-plot for p-values of the mixed linear model for DON values from 2013-2014 in spring wheat.

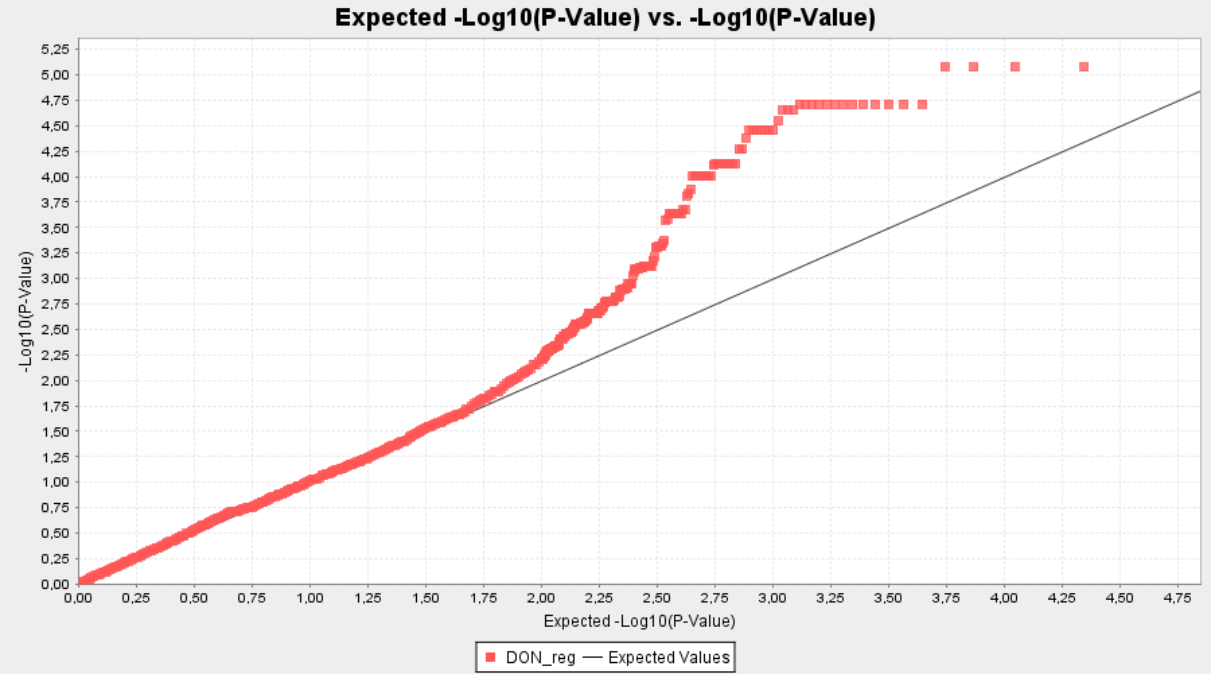

Figure 68: QQ-plot for p-values of the mixed linear model for DON values after regression from 2013-2014 in spring wheat.

Winter wheat 2015

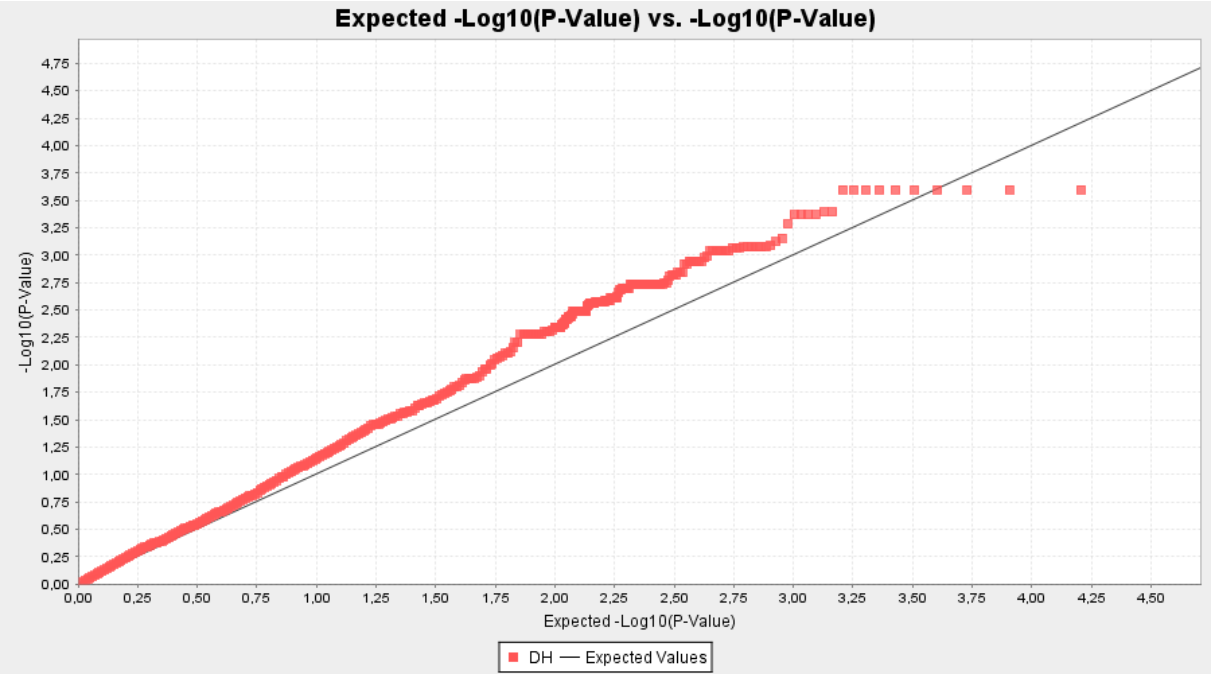

Figure 69: QQ-plot for p-values of the mixed linear model for DH in 2015 in winter wheat.

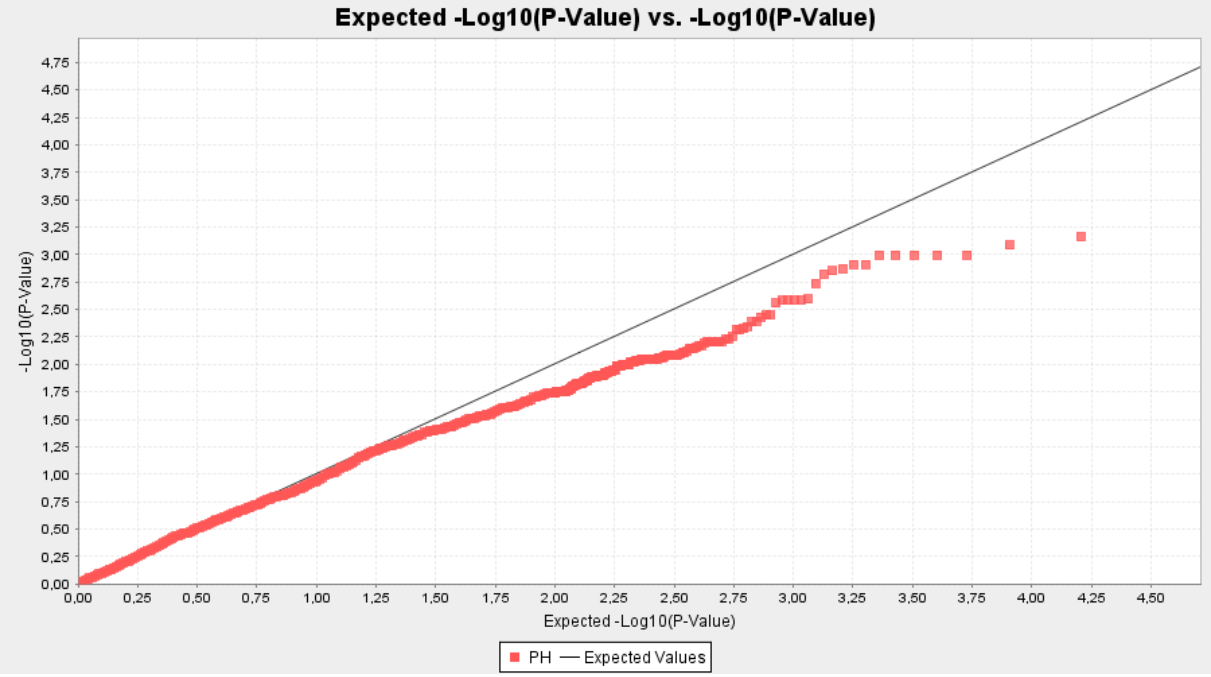

Figure 70: QQ-plot for p-values of the mixed linear model for PH in 2015 in winter wheat.

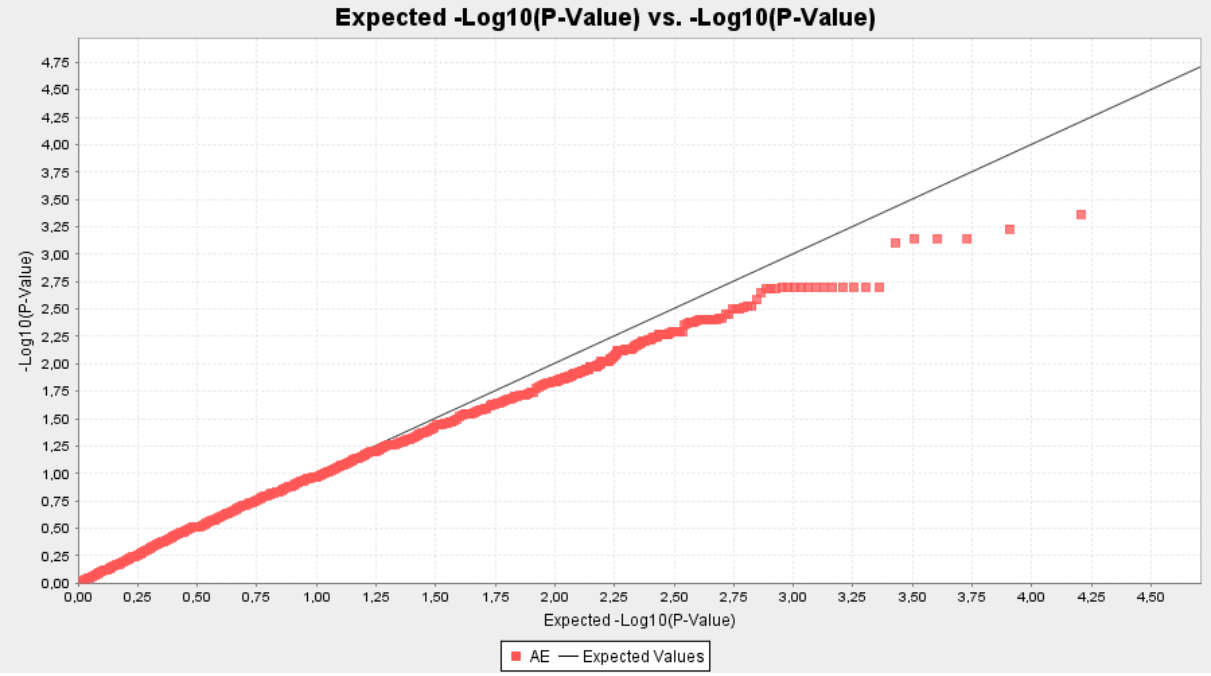

Figure 71: QQ-plot for p-values of the mixed linear model for AE in 2015 in winter wheat.

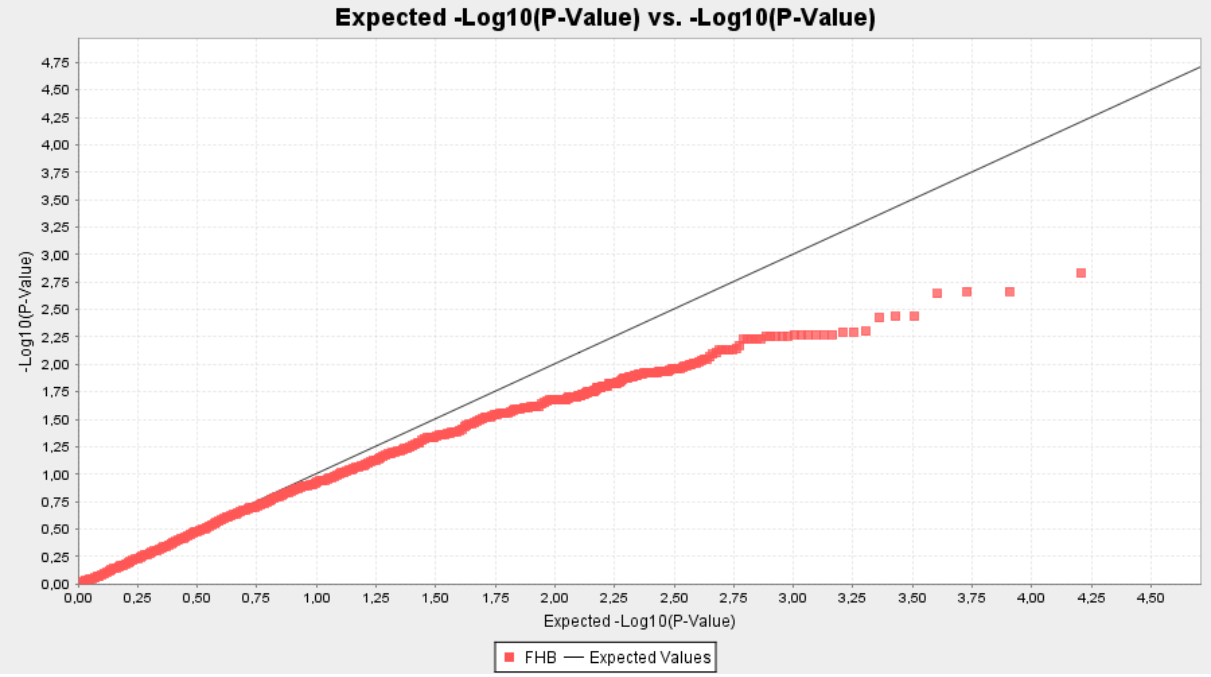

Figure 72: QQ-plot for p-values of the mixed linear model for FHB in 2015 in winter wheat.

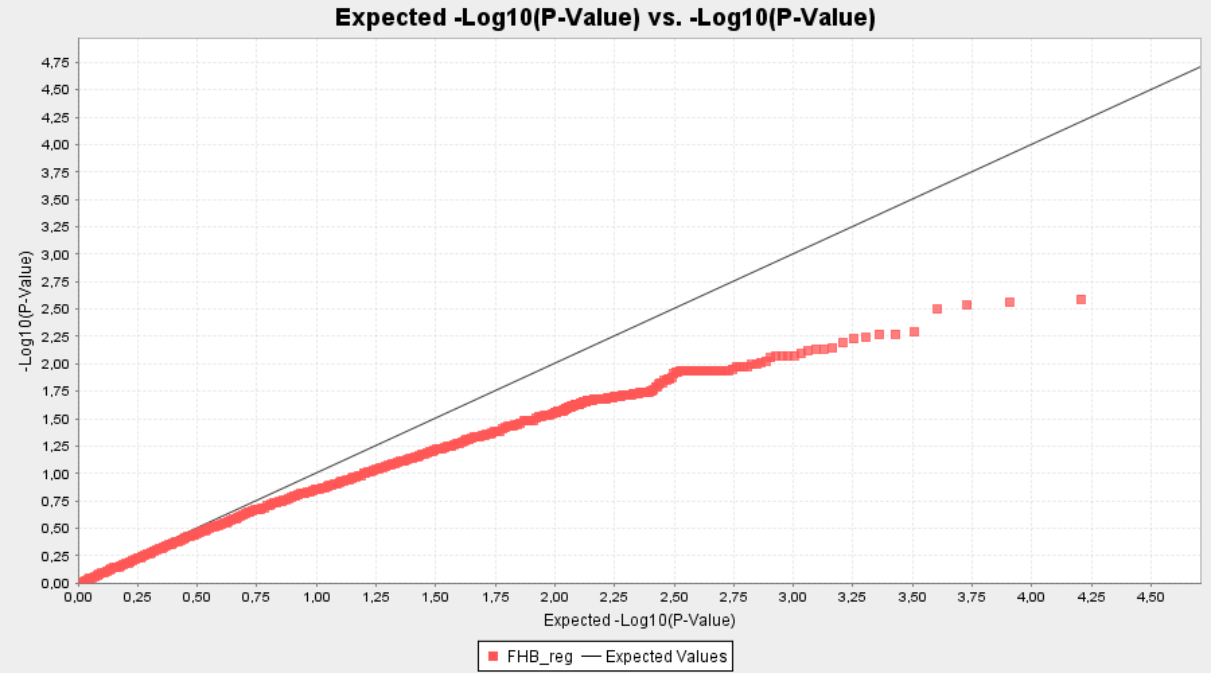

Figure 73: QQ-plot for p-values of the mixed linear model for FHB after regression in 2015 in winter wheat.

Winter wheat 2013-2015

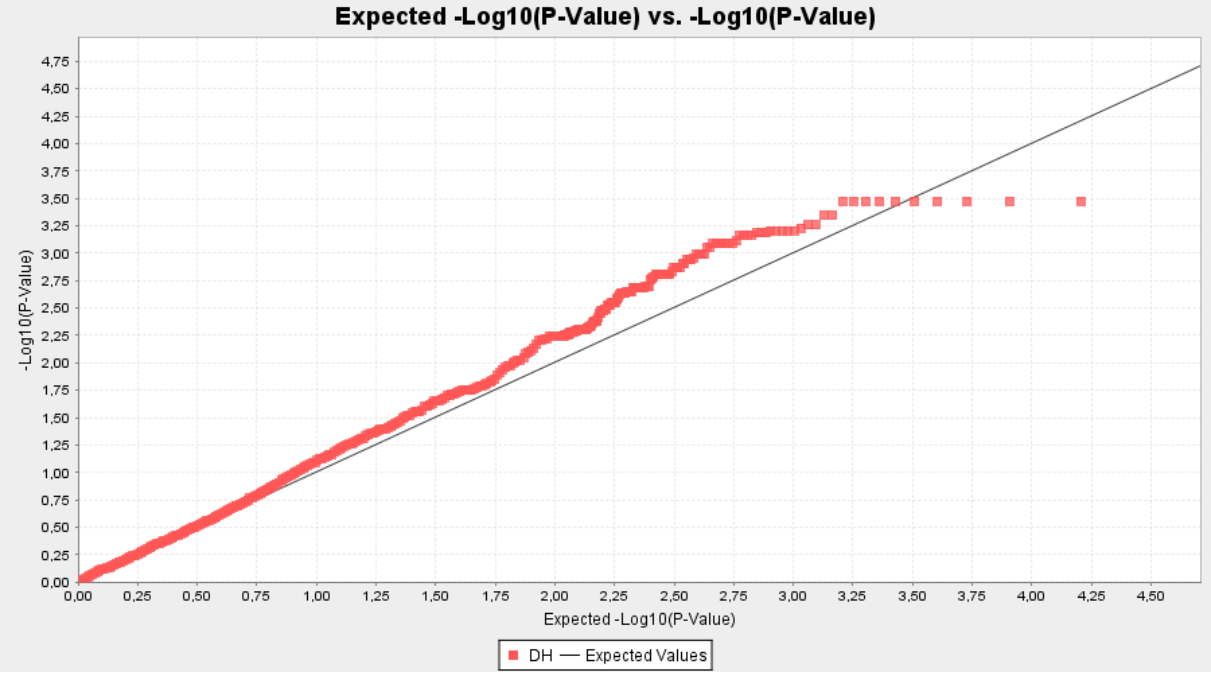

Figure 74: QQ-plot for p-values of the mixed linear model for DH from 2013-2015 in winter wheat.

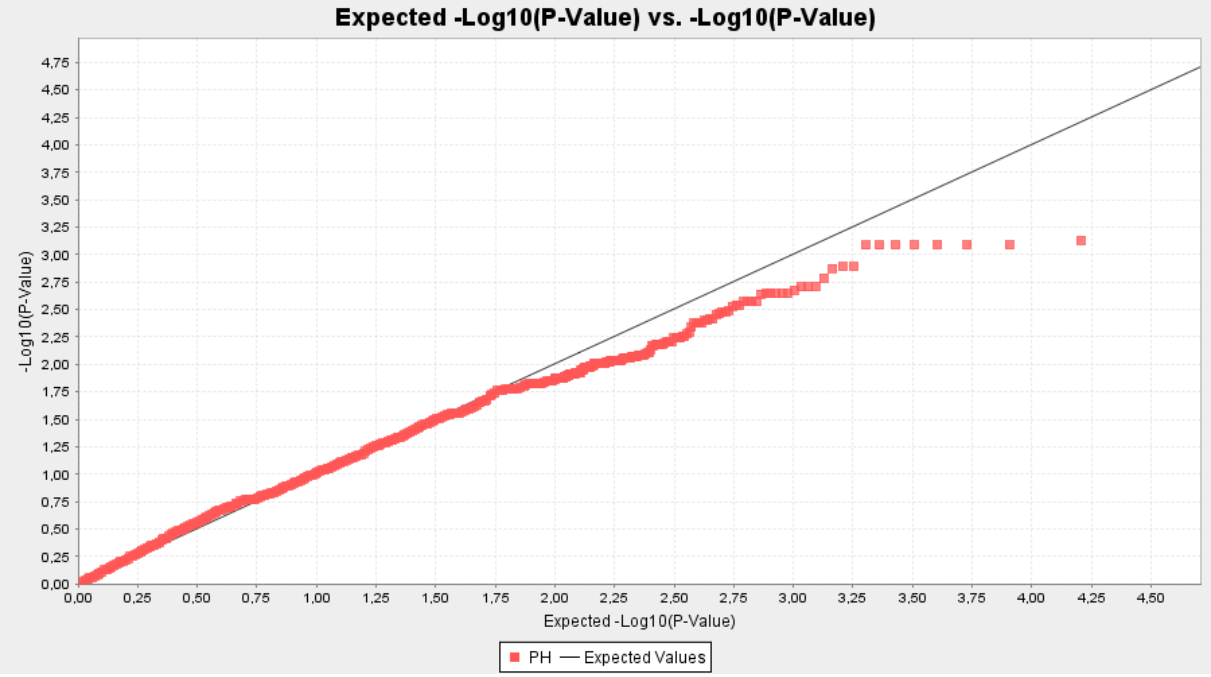

Figure 75: QQ-plot for p-values of the mixed linear model for PH from 2013-2015 in winter wheat.

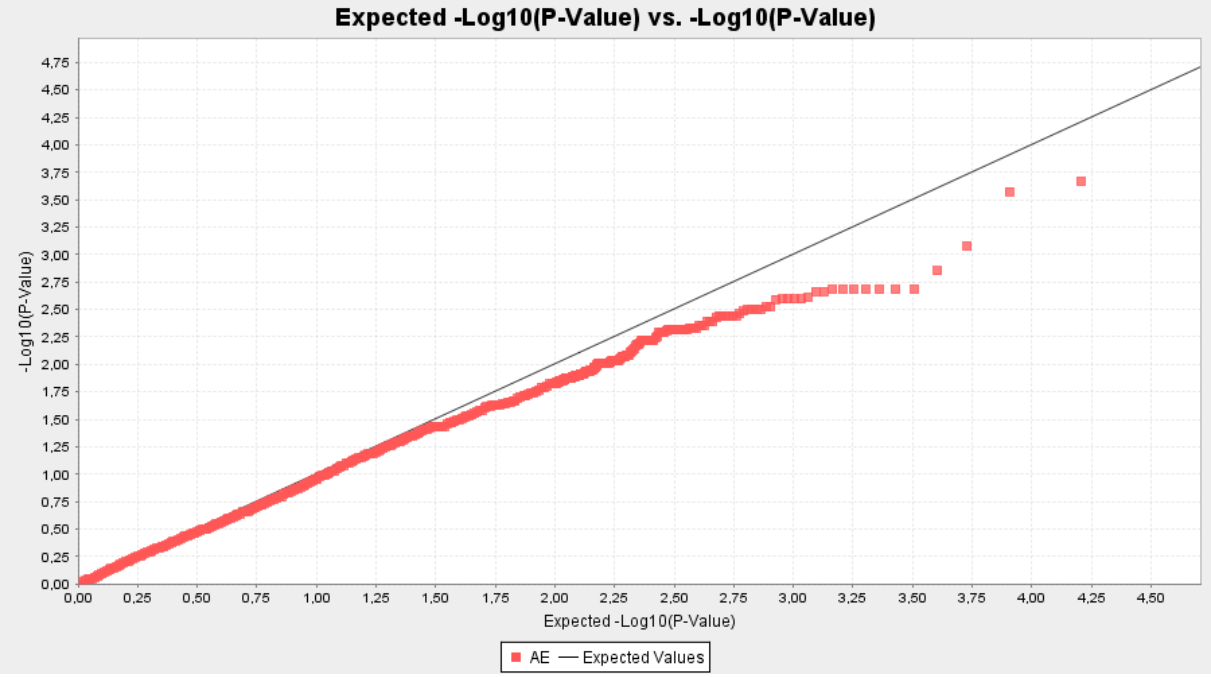

Figure 76: QQ-plot for p-values of the mixed linear model for AE from 2013-2015 in winter wheat.

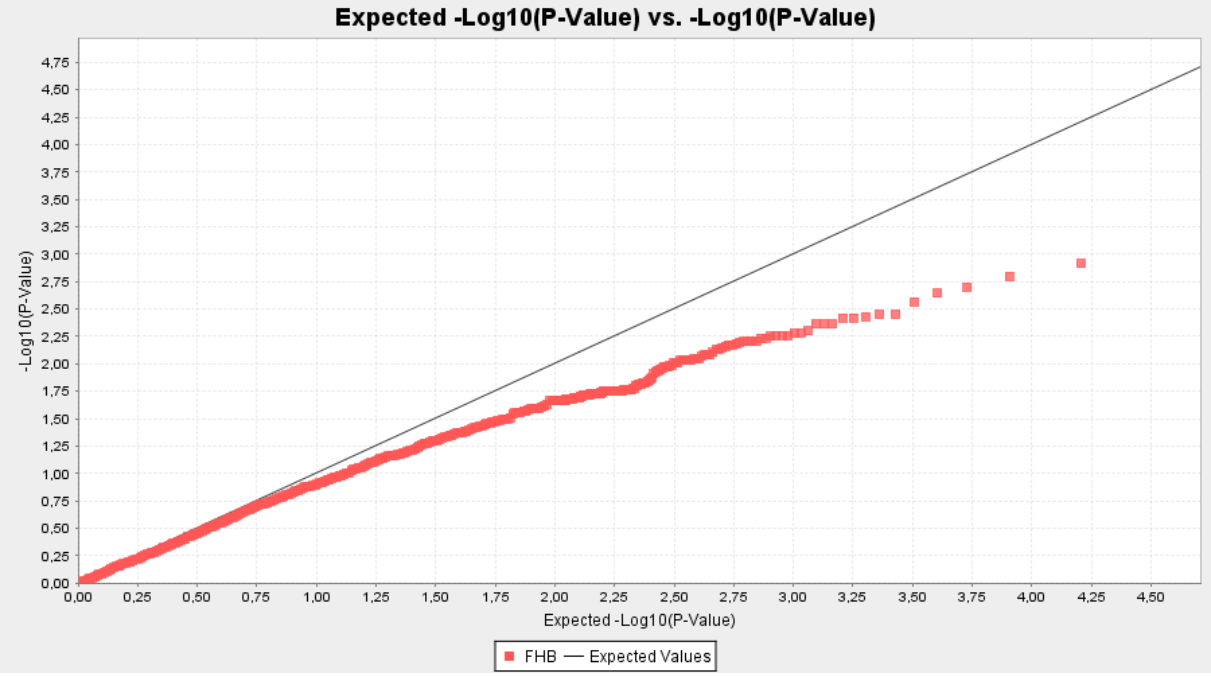

Figure 77: QQ-plot for p-values of the mixed linear model for FHB from 2013-2015 in winter wheat.

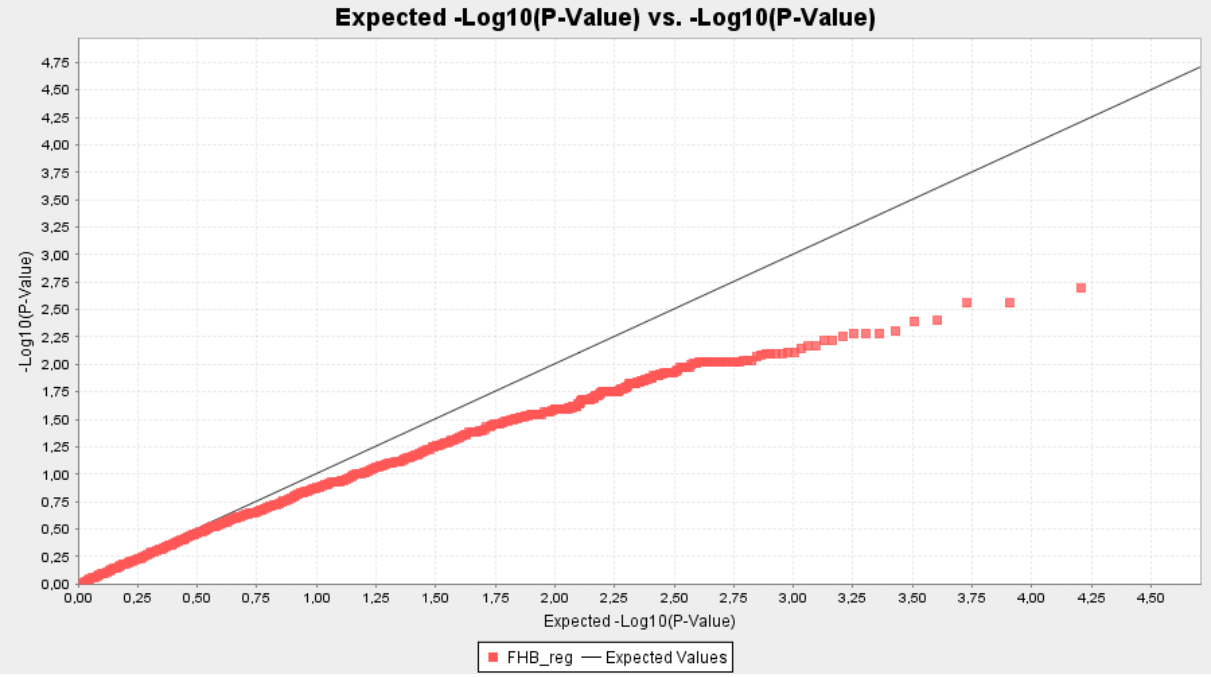

Figure 78: QQ-plot for p-values of the mixed linear model for FHB after regression from 2013-2015 in winter wheat.

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