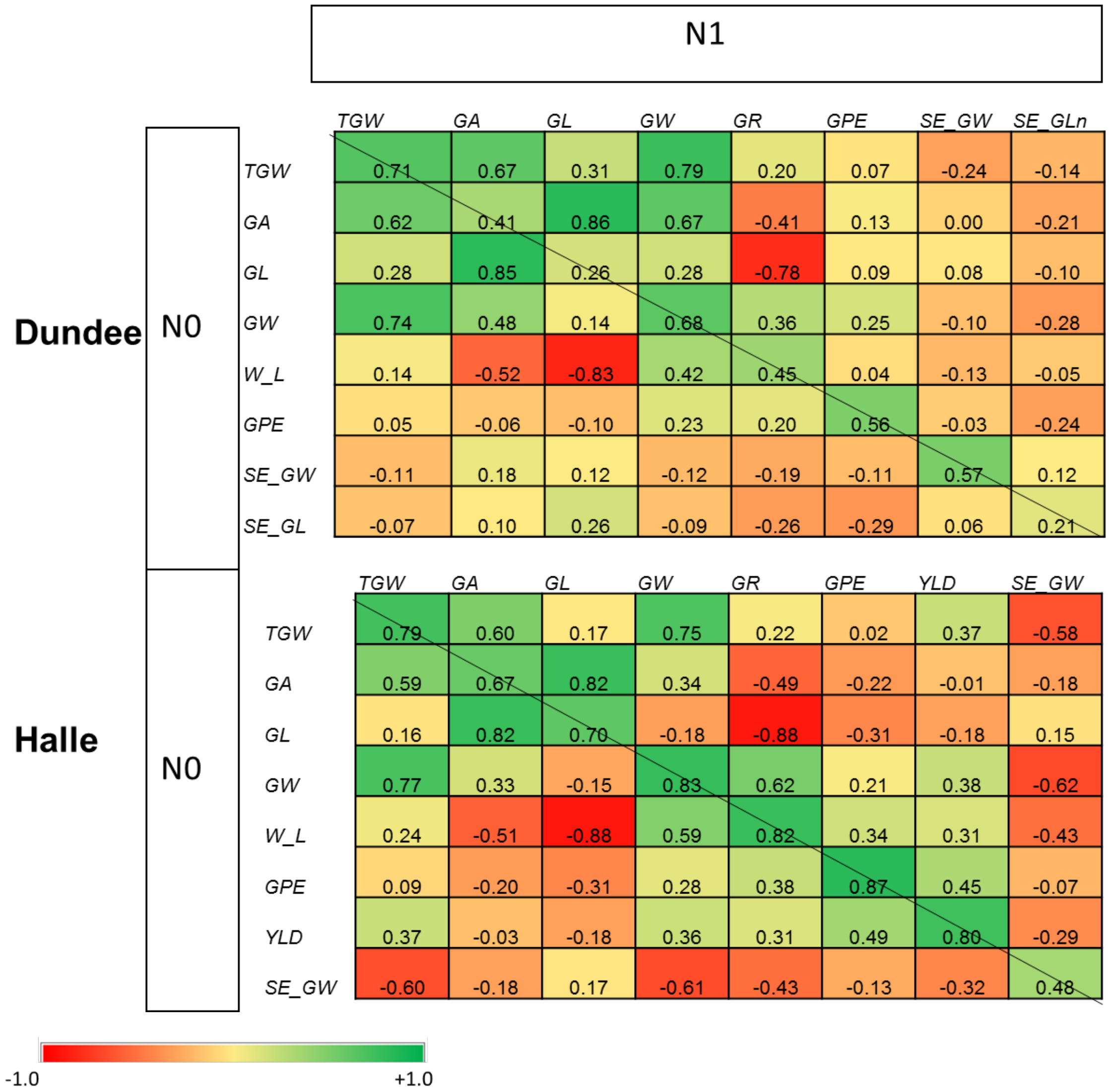


N1

Dundee N0

	TGW	GA	GL	GW	GR	GPE	SE_GW	SE_GLn
TGW	0.71	0.67	0.31	0.79	0.20	0.07	-0.24	-0.14
GA	0.62	0.41	0.86	0.67	-0.41	0.13	0.00	-0.21
GL	0.28	0.85	0.26	0.28	-0.78	0.09	0.08	-0.10
GW	0.74	0.48	0.14	0.68	0.36	0.25	-0.10	-0.28
W_L	0.14	-0.52	-0.83	0.42	0.45	0.04	-0.13	-0.05
GPE	0.05	-0.06	-0.10	0.23	0.20	0.56	-0.03	-0.24
SE_GW	-0.11	0.18	0.12	-0.12	-0.19	-0.11	0.57	0.12
SE_GL	-0.07	0.10	0.26	-0.09	-0.26	-0.29	0.06	0.21

Halle N0

	TGW	GA	GL	GW	GR	GPE	YLD	SE_GW
TGW	0.79	0.60	0.17	0.75	0.22	0.02	0.37	-0.58
GA	0.59	0.67	0.82	0.34	-0.49	-0.22	-0.01	-0.18
GL	0.16	0.82	0.70	-0.18	-0.88	-0.31	-0.18	0.15
GW	0.77	0.33	-0.15	0.83	0.62	0.21	0.38	-0.62
W_L	0.24	-0.51	-0.88	0.59	0.82	0.34	0.31	-0.43
GPE	0.09	-0.20	-0.31	0.28	0.38	0.87	0.45	-0.07
YLD	0.37	-0.03	-0.18	0.36	0.31	0.49	0.80	-0.29
SE_GW	-0.60	-0.18	0.17	-0.61	-0.43	-0.13	-0.32	0.48

Figure S1: Correlation matrix of the yield traits across locations and treatments. Red = negative correlation, green = positive correlation. Correlations between the treatments are shown diagonally.

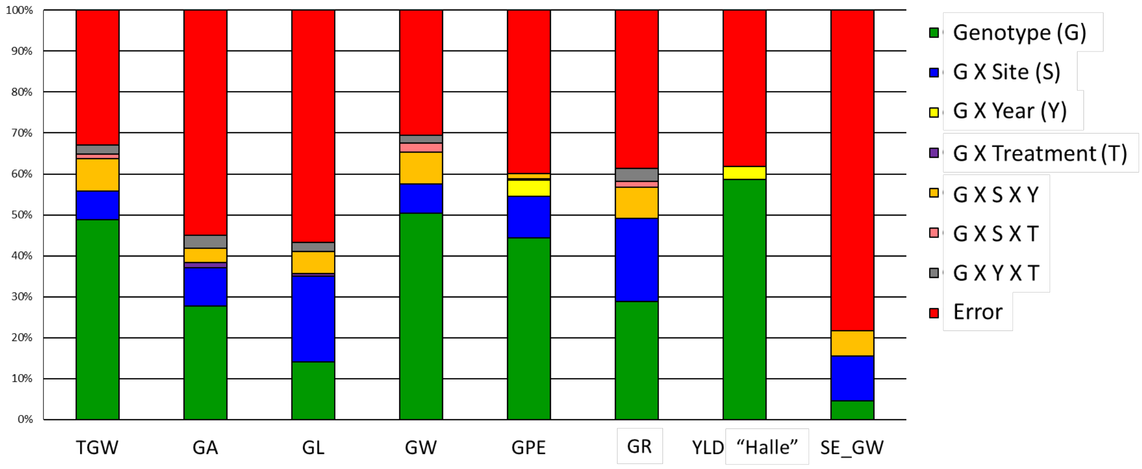


Figure S2: Variance components of the yield traits displayed in percentages.

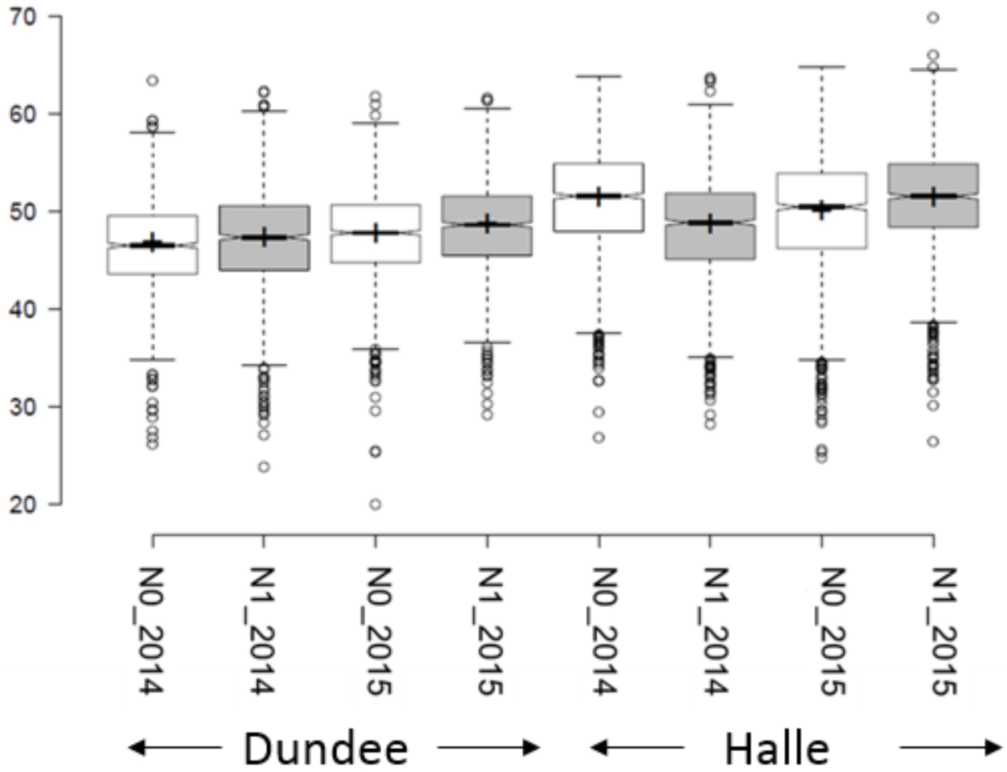


Figure S3: Box plot of thousand grain weight (TGW in grams).

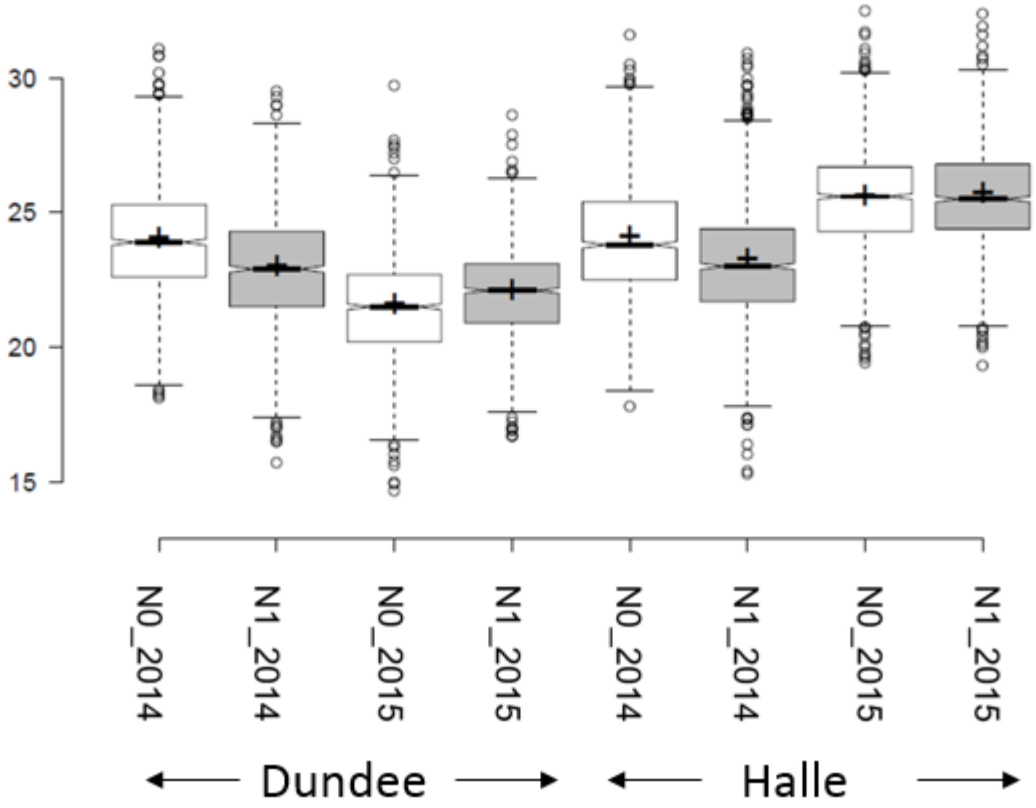


Figure S4: Box plot of grain area (GA in mm^2).

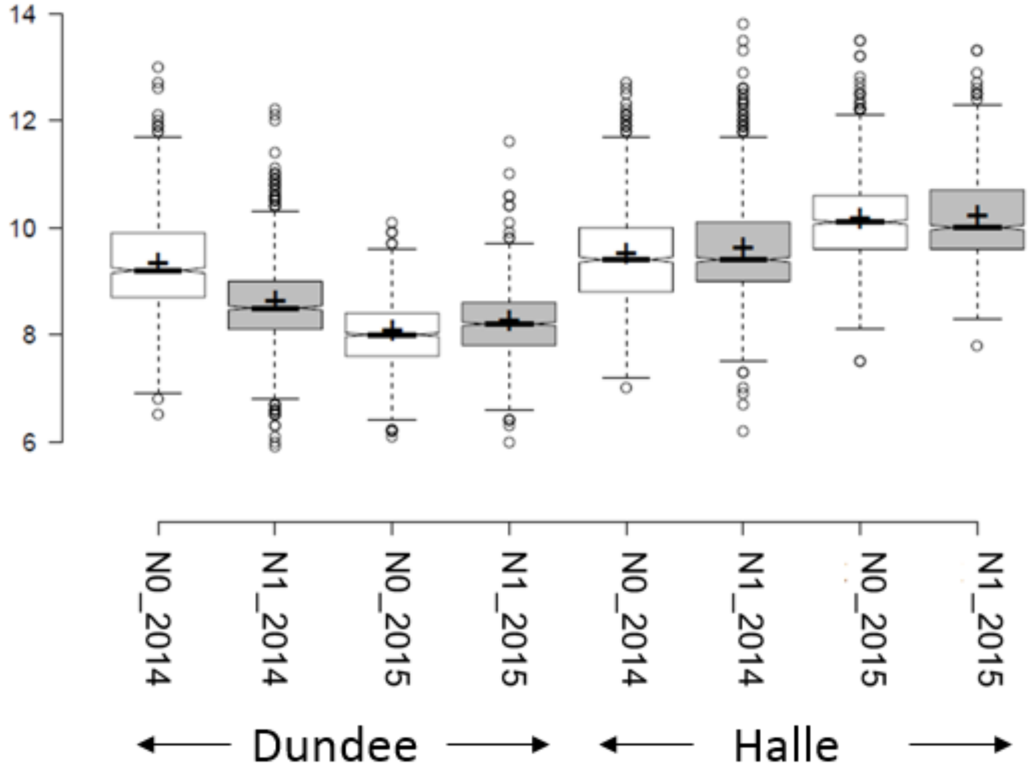


Figure S5: **Box plot of grain length (GL in mm).**

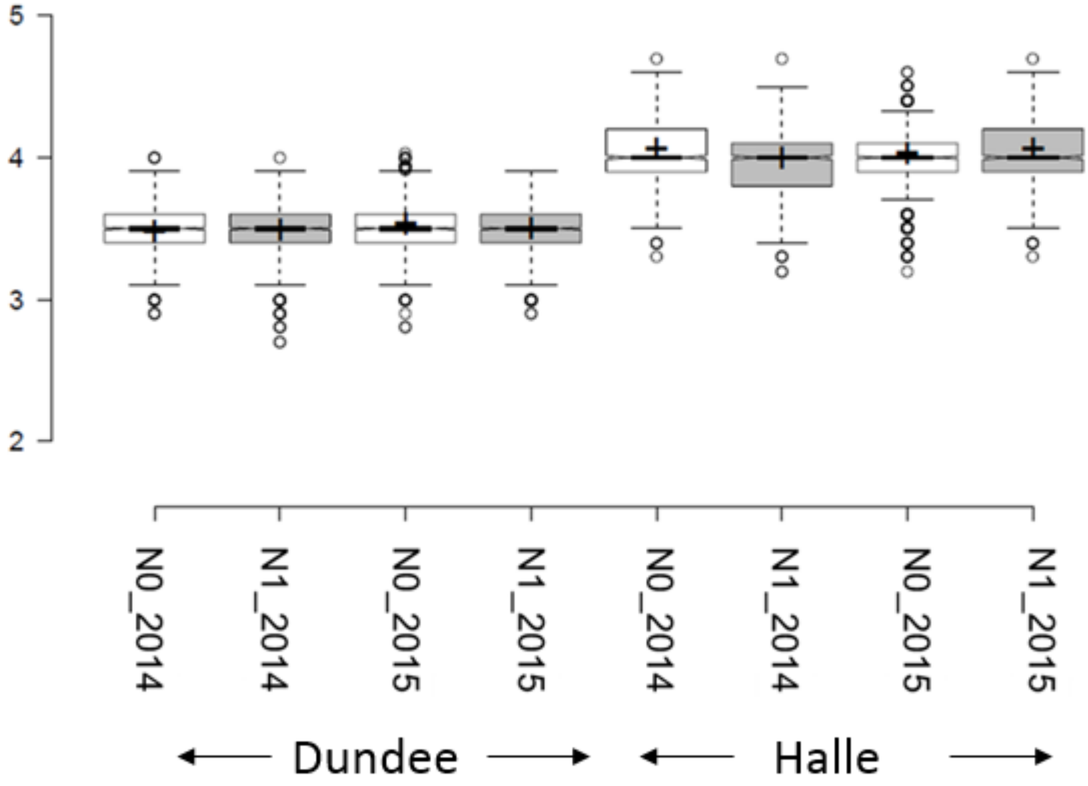


Figure S6: **Box plot of grain width (GW in mm).**

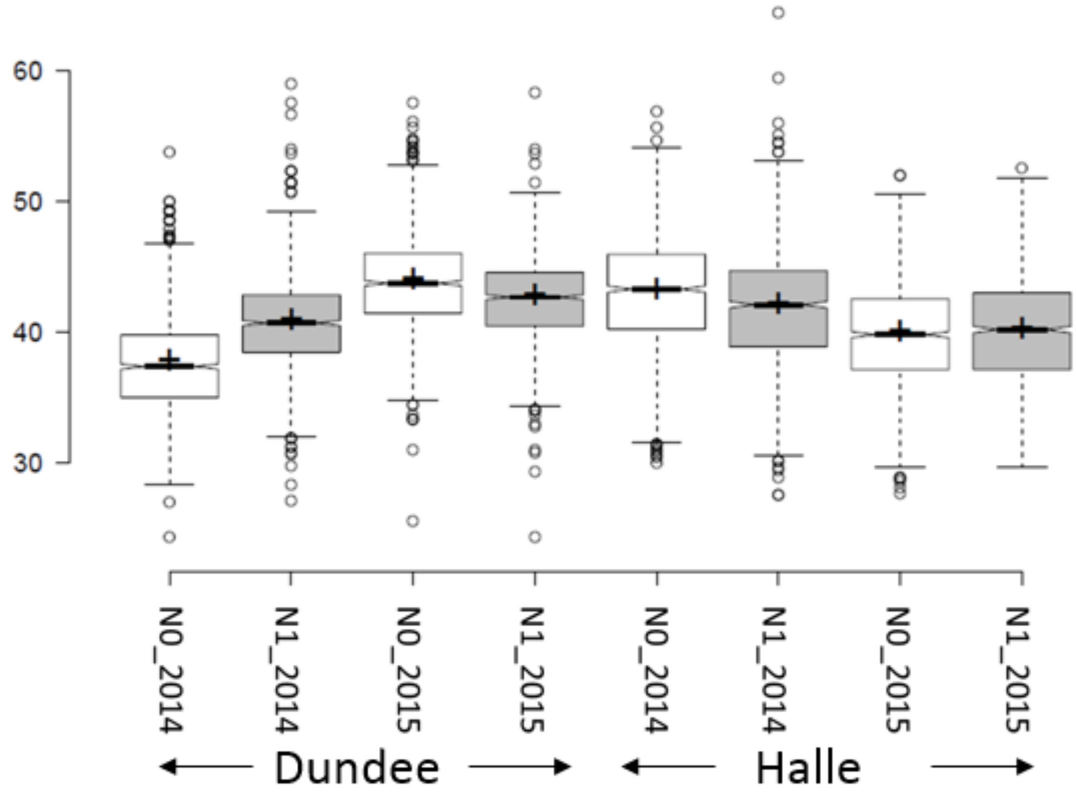


Figure S7: Box plot of grain roundness (width and grain length ratio in %) (GR).

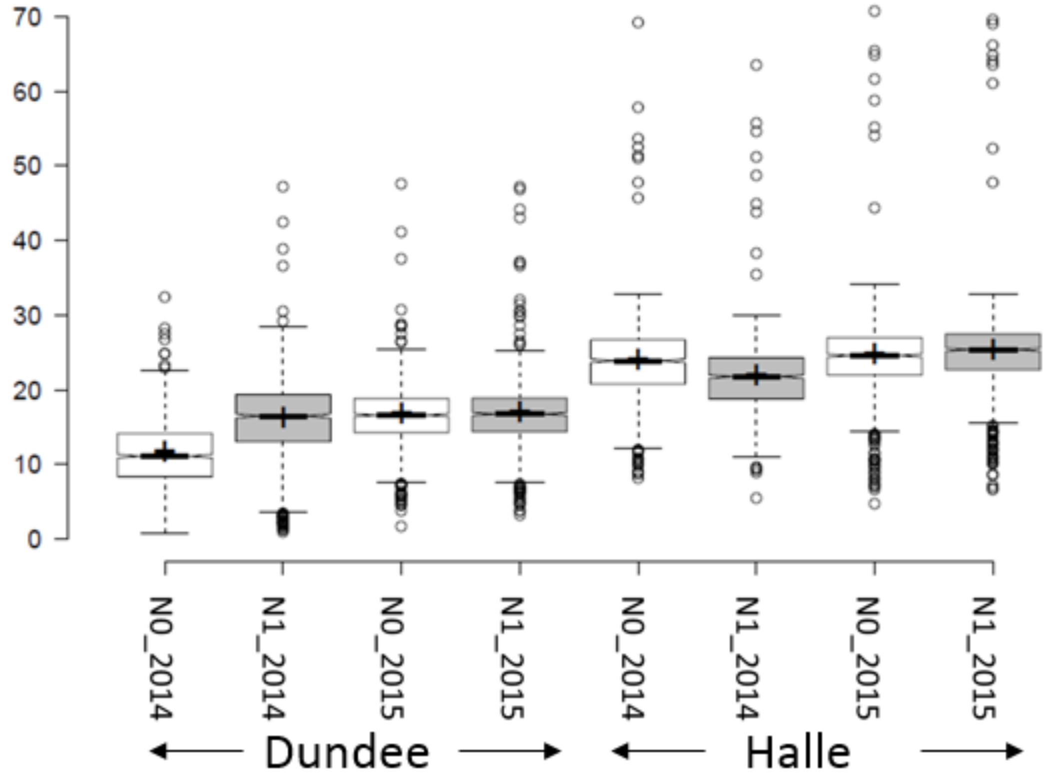


Figure S8: Box plot of grains per ear (GPE in number).

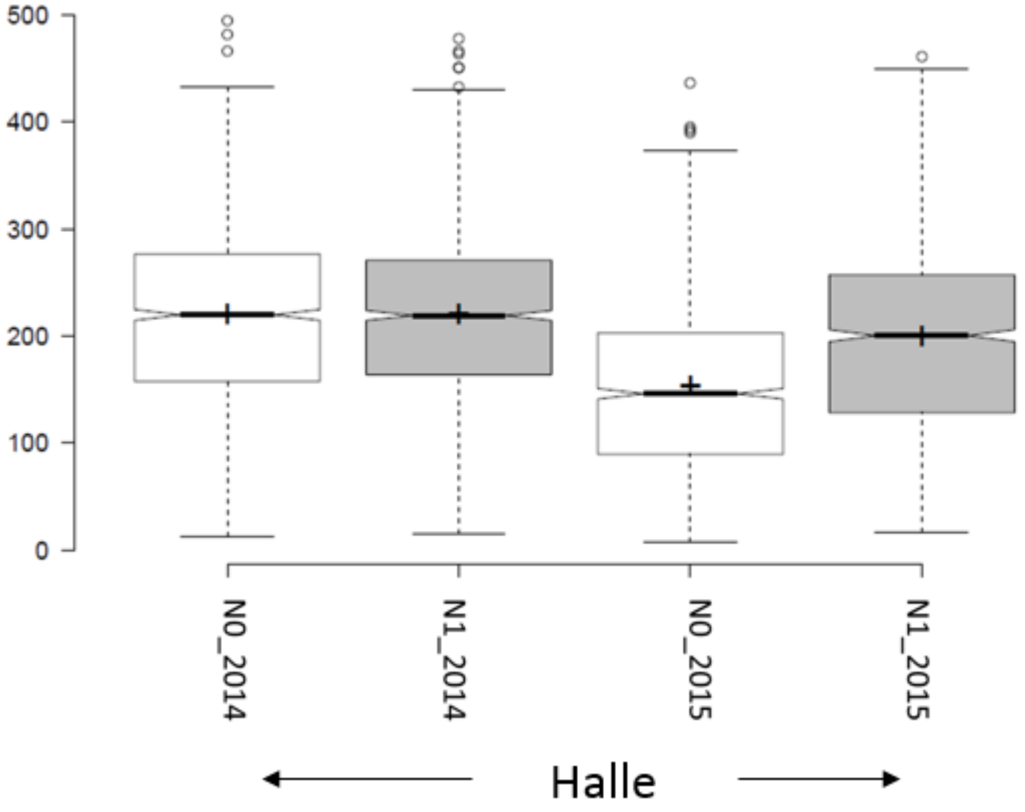


Figure S9: **Box plot of yield (YLD in grams, only from Halle).**

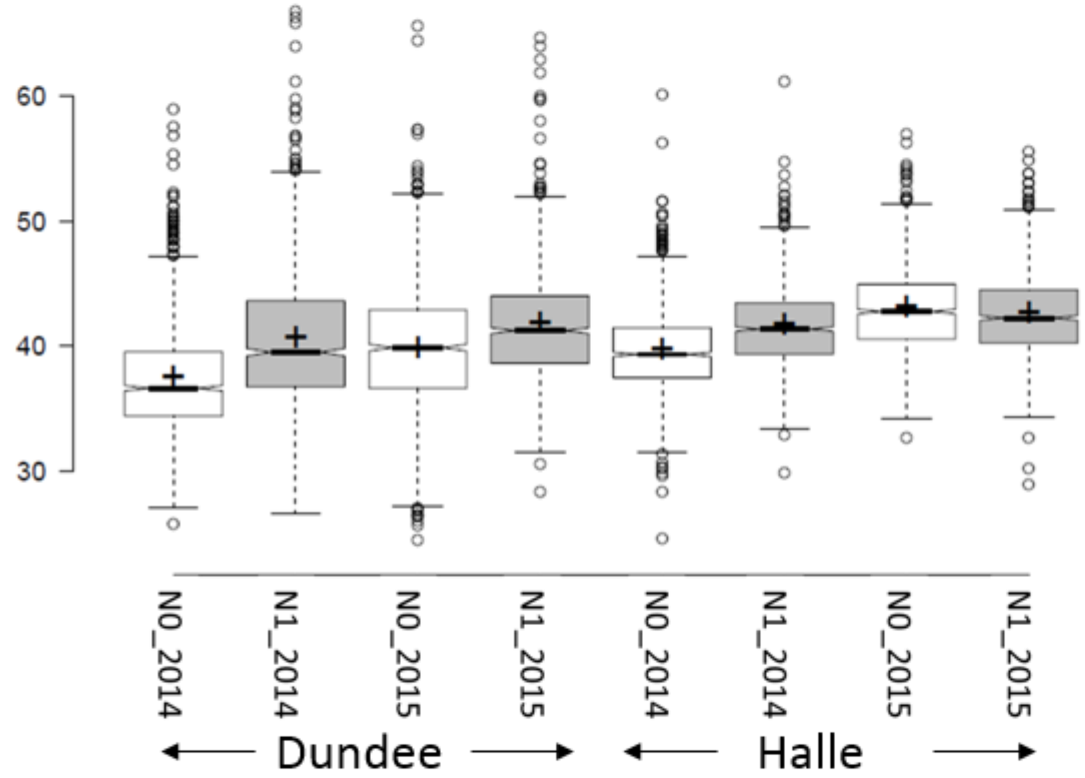


Figure S10: Box plot of standard error of grain width (SE_GW). To ease displaying, values are multiplied by 10.

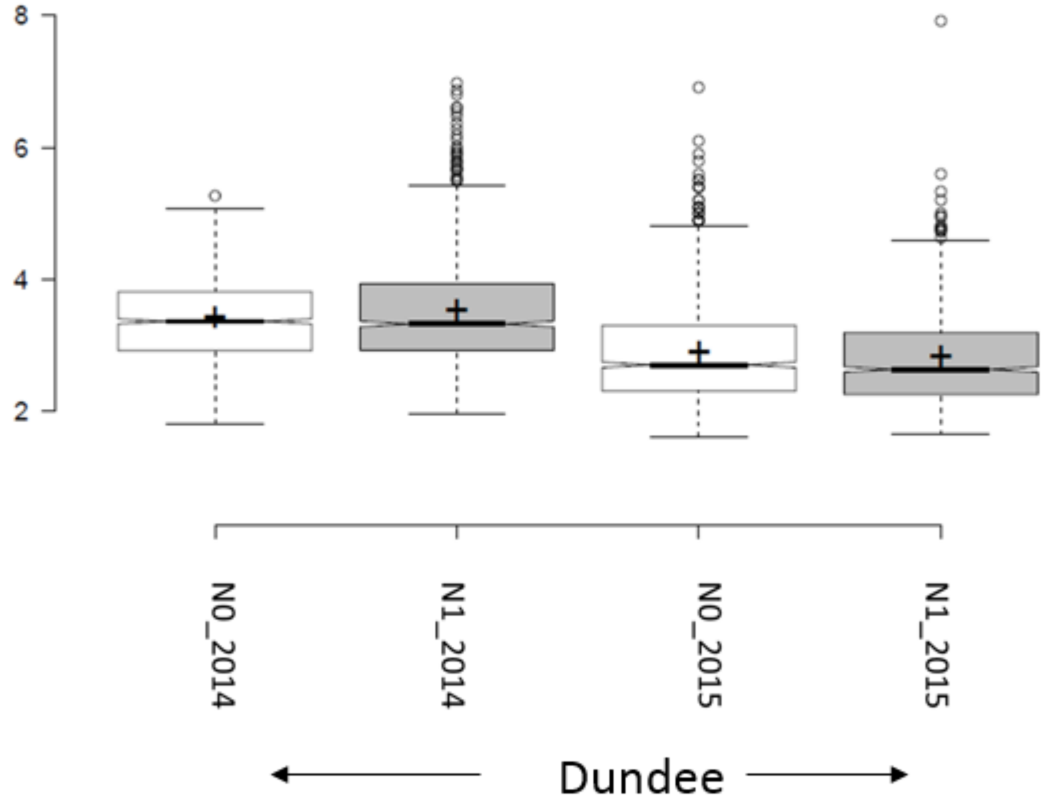
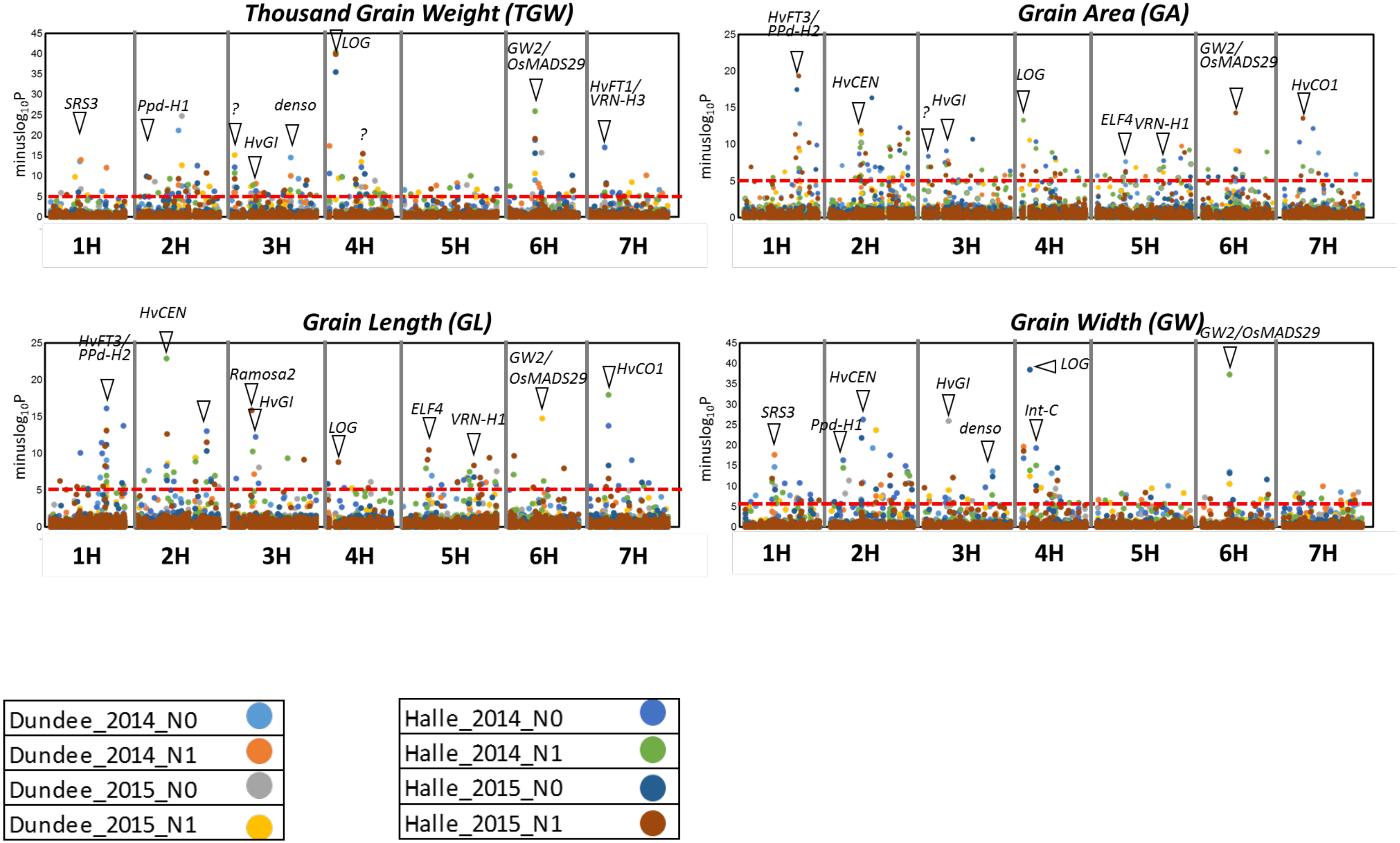
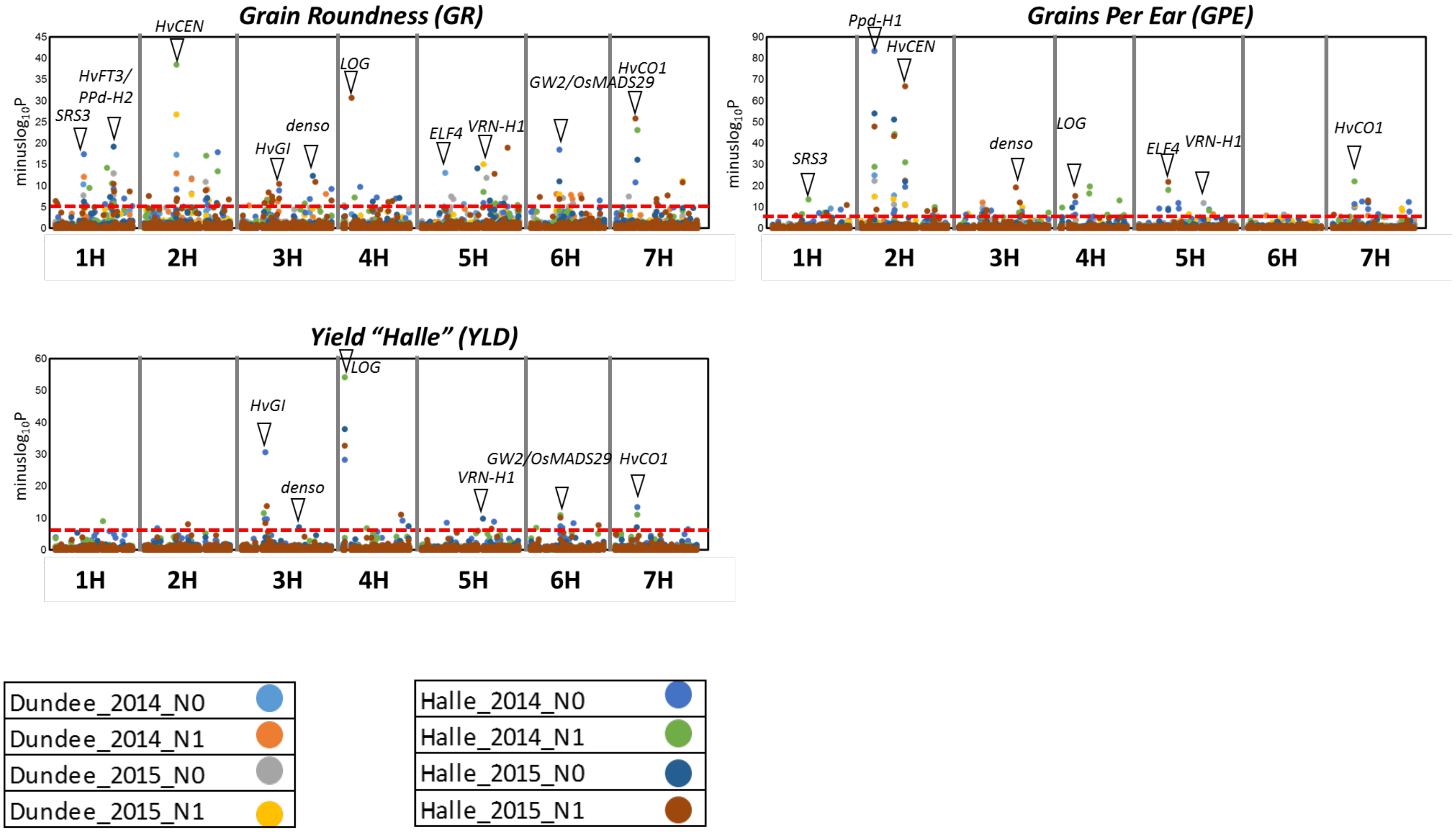


Figure S11: Box plot of standard error of grain length (SE_GL only from Dundee). To ease displaying, values are multiplied by 10.


Thousand Grain Weight (TGW)
minuslog10P
0
5
10
15
20
25
30
35
40
45
SRS3
Ppd-H1
?
HvGI
denso
LOG
?
GW2/ OsMADS29
HvFT1/ VRN-H3
1H
2H
3H
4H
5H
6H
7H
Grain Area (GA)
minuslog10P
0
5
10
15
20
25
HvFT3/ PPd-H2
HvCEN
?
HvGI
LOG
ELF4
VRN-H1
GW2/ OsMADS29
HvCO1
1H
2H
3H
4H
5H
6H
7H
Grain Length (GL)
minuslog10P
0
5
10
15
20
25
HvFT3/ PPd-H2
HvCEN
Ramosa2
HvGI
LOG
ELF4
VRN-H1
GW2/ OsMADS29
HvCO1
1H
2H
3H
4H
5H
6H
7H
Grain Width (GW)
minuslog10P
0
5
10
15
20
25
30
35
40
45
GW2/OsMADS29
SRS3
Ppd-H1
HvCEN
HvGI
denso
LOG
Int-C
1H
2H
3H
4H
5H
6H
7H
Dundee_2014_N0 ●
Dundee_2014_N1 ●
Dundee_2015_N0 ●
Dundee_2015_N1 ●
Halle_2014_N0 ●
Halle_2014_N1 ●
Halle_2015_N0 ●
Halle_2015_N1 ●


Grain Roundness (GR)
minuslog$_{10}$P
0
5
10
15
20
25
30
35
40
45
SRS3
HvFT3/
PPd-H2
HvCEN
HvGI
denso
LOG
ELF4
VRN-H1
GW2/OsMADS29
HvCO1
1H
2H
3H
4H
5H
6H
7H
Grains Per Ear (GPE)
minuslog$_{10}$P
0
10
20
30
40
50
60
70
80
90
SRS3
Ppd-H1
HvCEN
denso
LOG
ELF4
VRN-H1
HvCO1
1H
2H
3H
4H
5H
6H
7H
Yield "Halle" (YLD)
minuslog$_{10}$P
0
10
20
30
40
50
60
HvGI
denso
LOG
VRN-H1
GW2/OsMADS29
HvCO1
1H
2H
3H
4H
5H
6H
7H
Dundee_2014_N0 ●
Dundee_2014_N1 ●
Dundee_2015_N0 ●
Dundee_2015_N1 ●
Halle_2014_N0 ●
Halle_2014_N1 ●
Halle_2015_N0 ●
Halle_2015_N1 ●

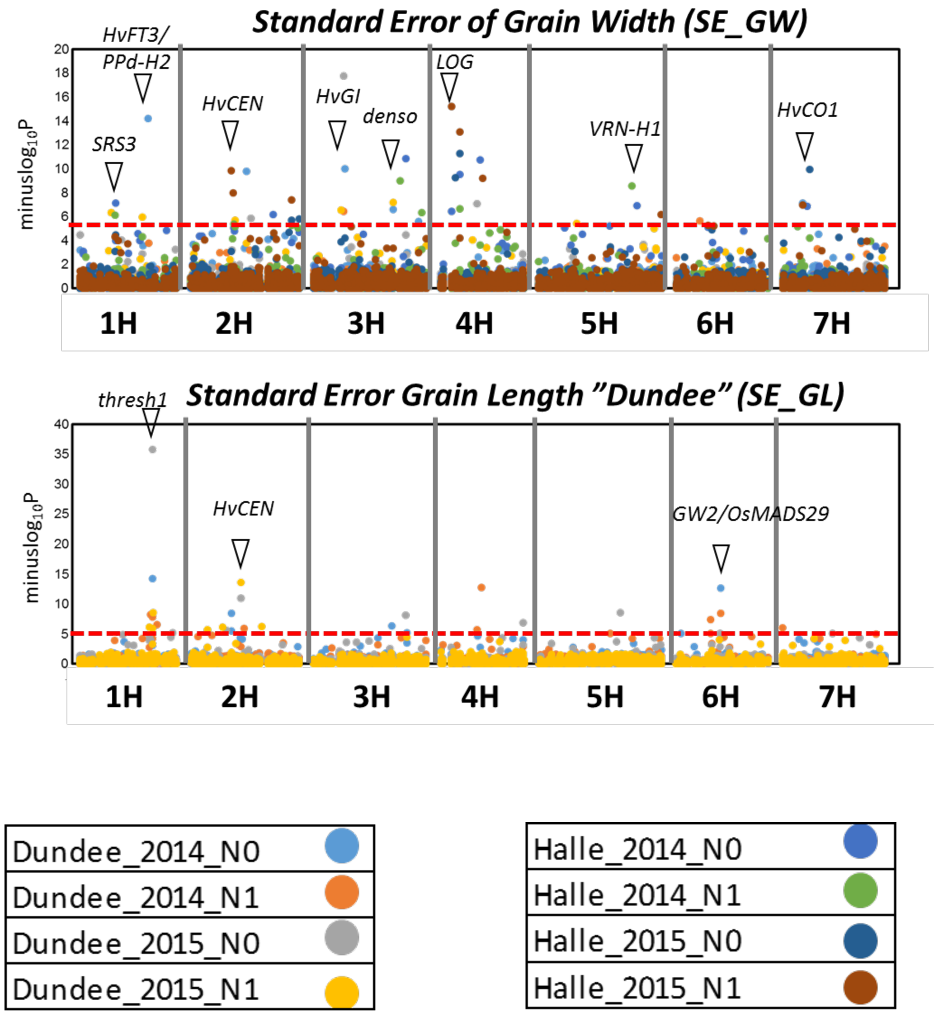
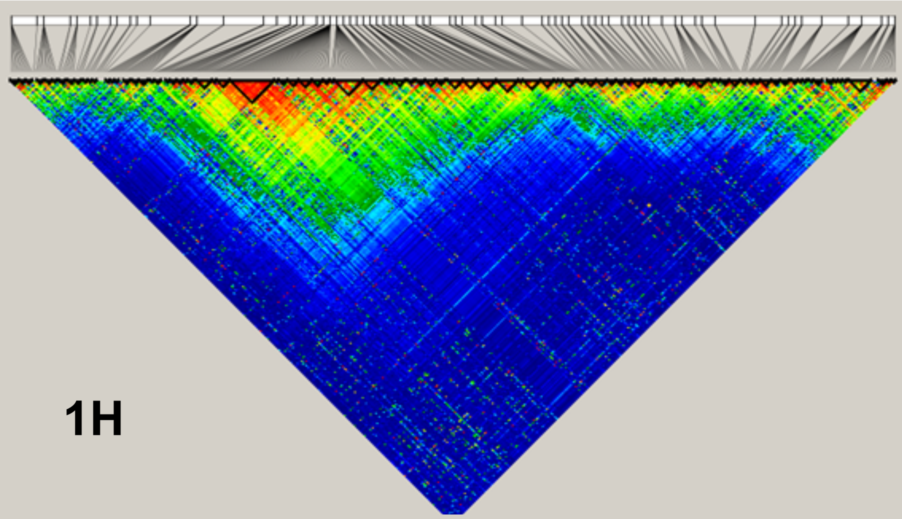
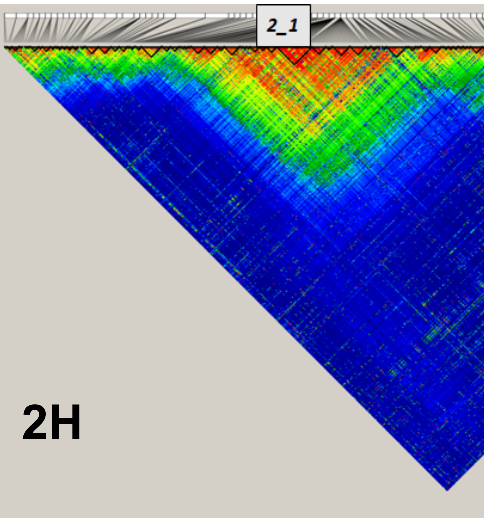
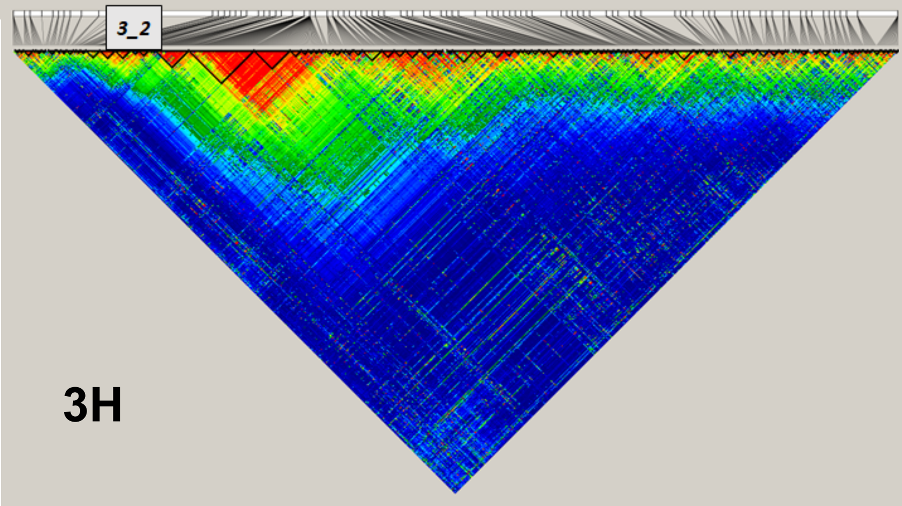


Figure S12: Genome-wide association scans of yield traits.

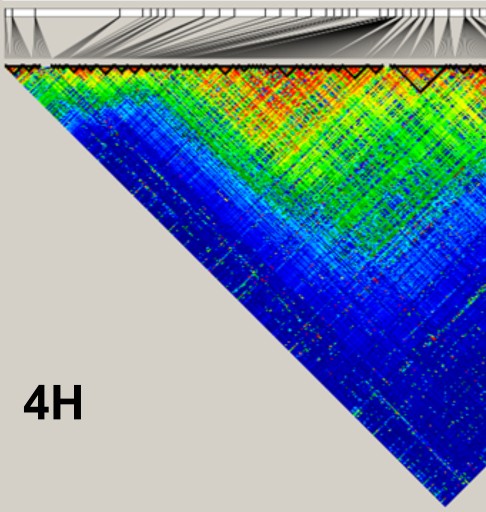

1H

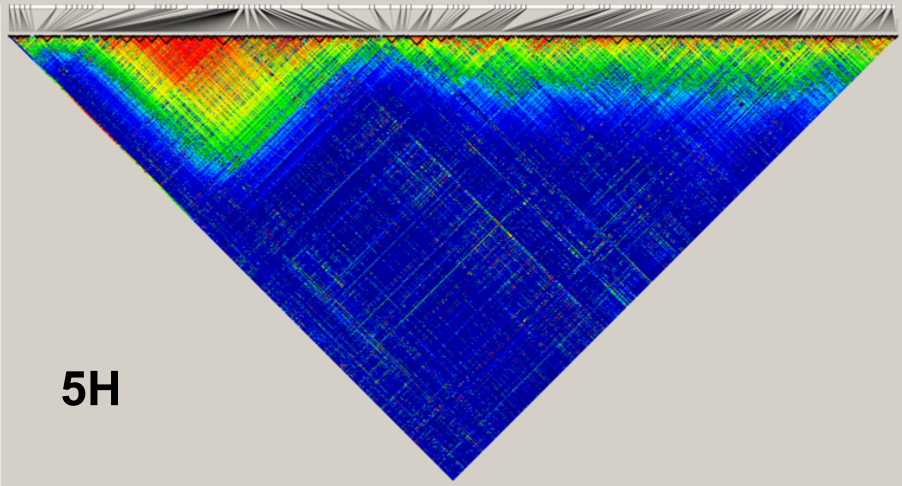


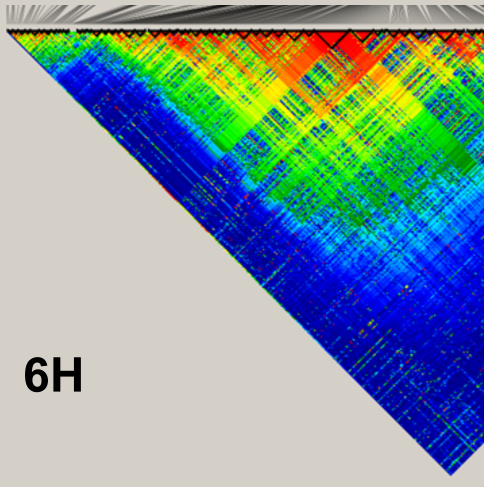
2H

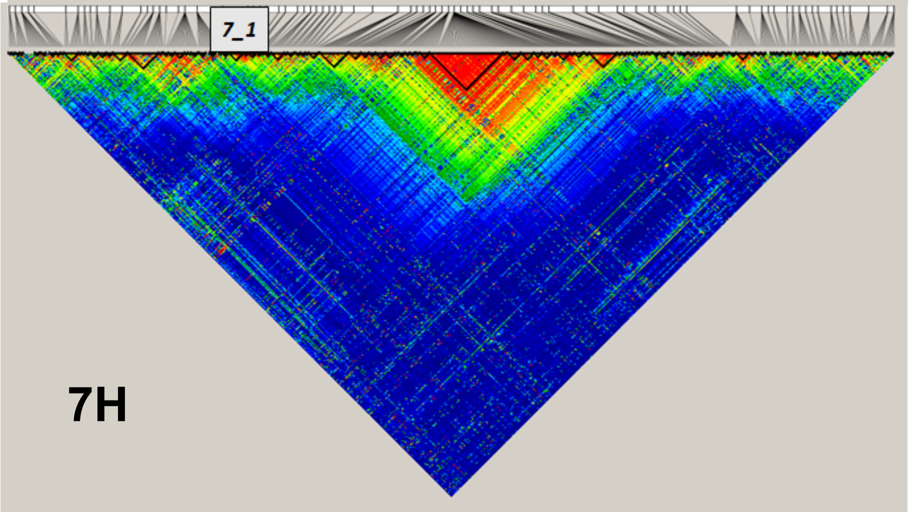


3H


4H


5H


6H



7H

Figure S13: LD of mapped SNP markers in HEB-25 population. The plot uses a GOLD heatmap color scheme implimented in Haploview 4.2. Blocks of LD based on the Solidspine alogarithm of Haploview4.2 are indicated as black outlines. The four QTL-hotspots discussed here are shown on chromsomes 2H, 3H and 7H.

Figure S14: Distribution of thousand grain weight (TGW) QTLs across barley chromosomes.

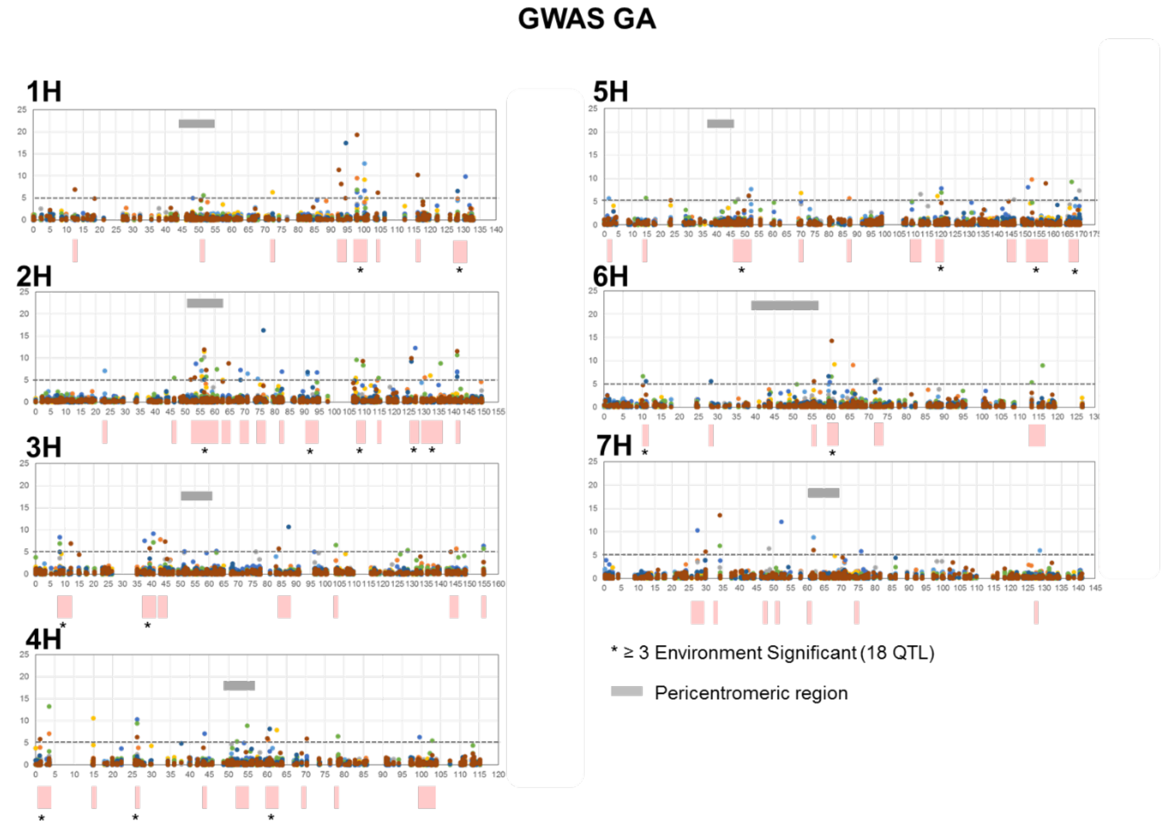


Figure S15: Distribution of grain area (GA) QTLs across barley chromosomes.

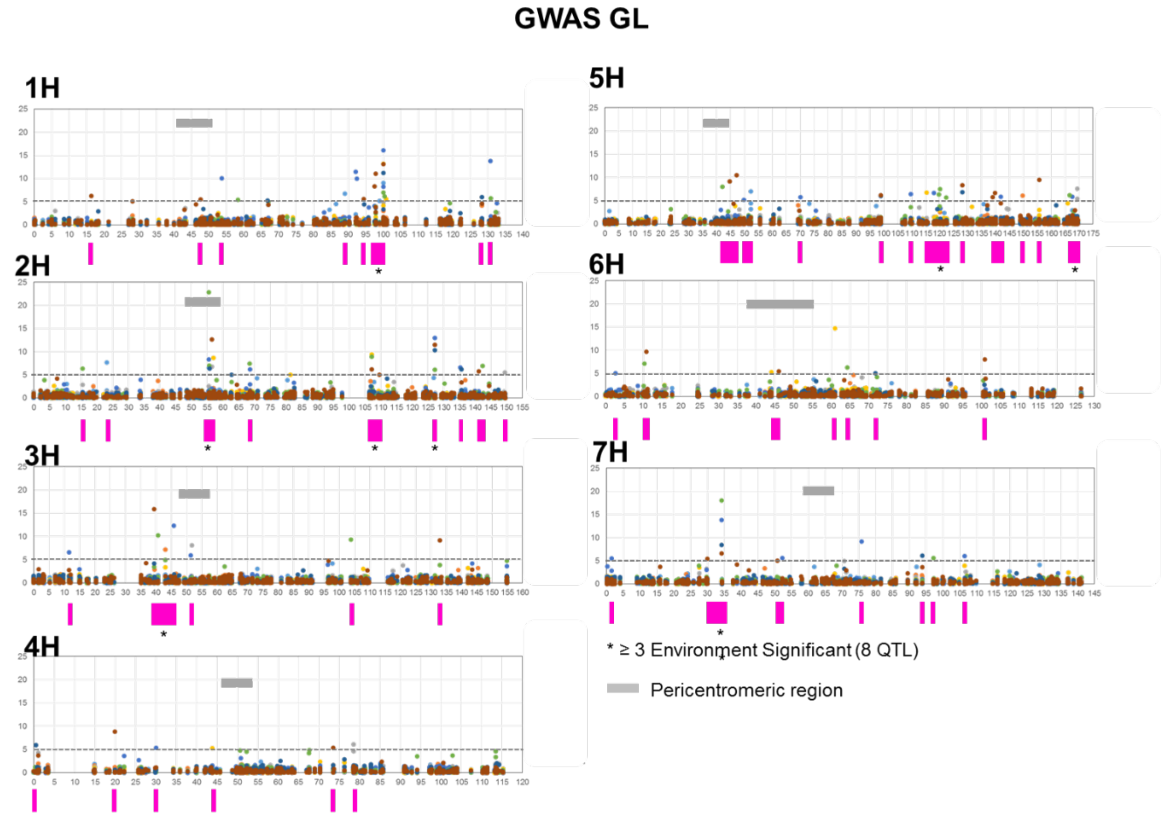


Figure S16: Distribution of grain length (GL) QTLs across barley chromosomes.

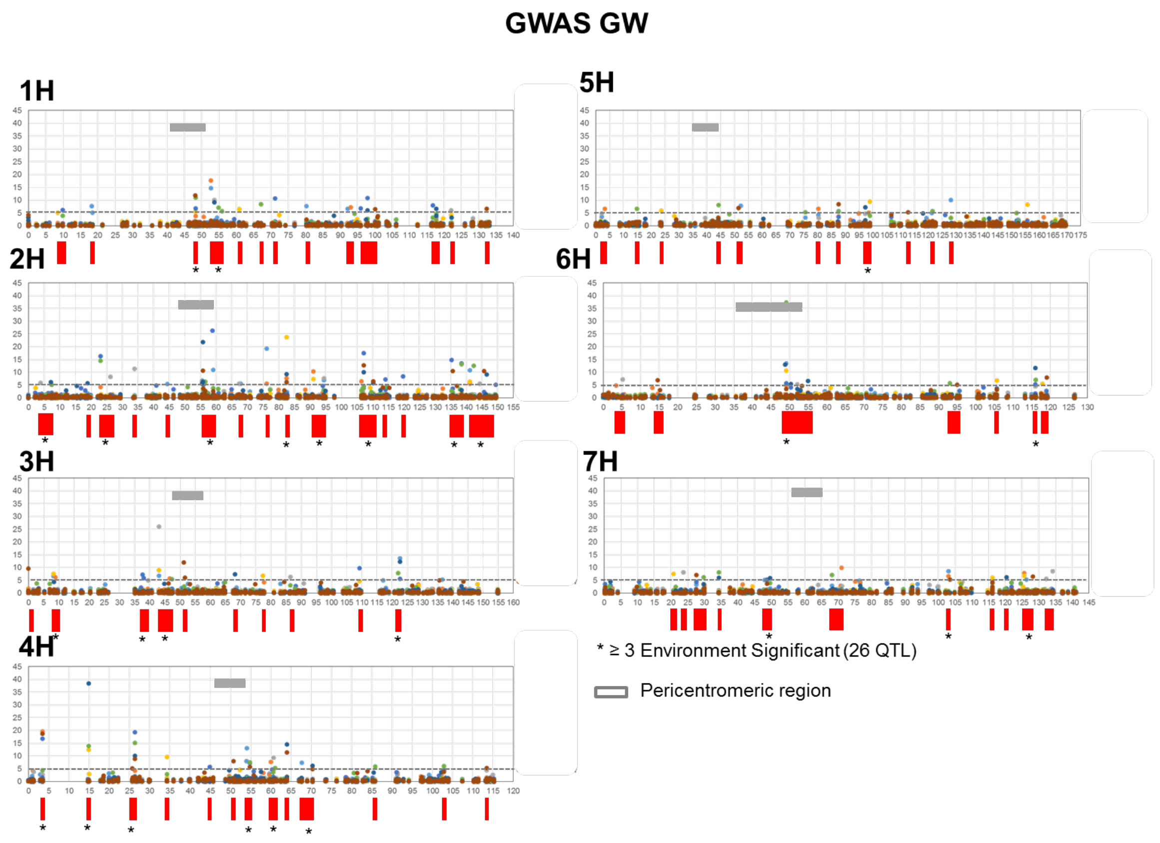


Figure S17: Distribution of grain width (GW) QTLs across barley chromosomes.

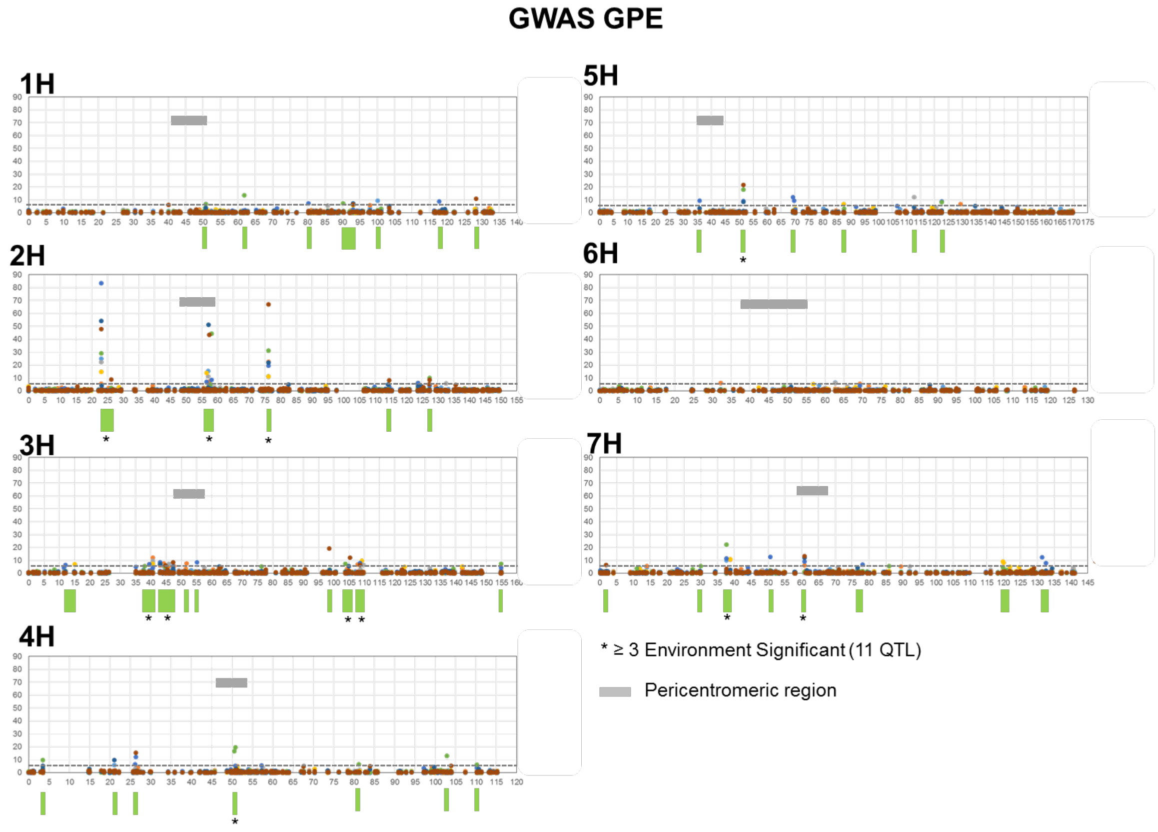


Figure S18: Distribution of grains per ear (GPE) QTLs across barley chromosomes.

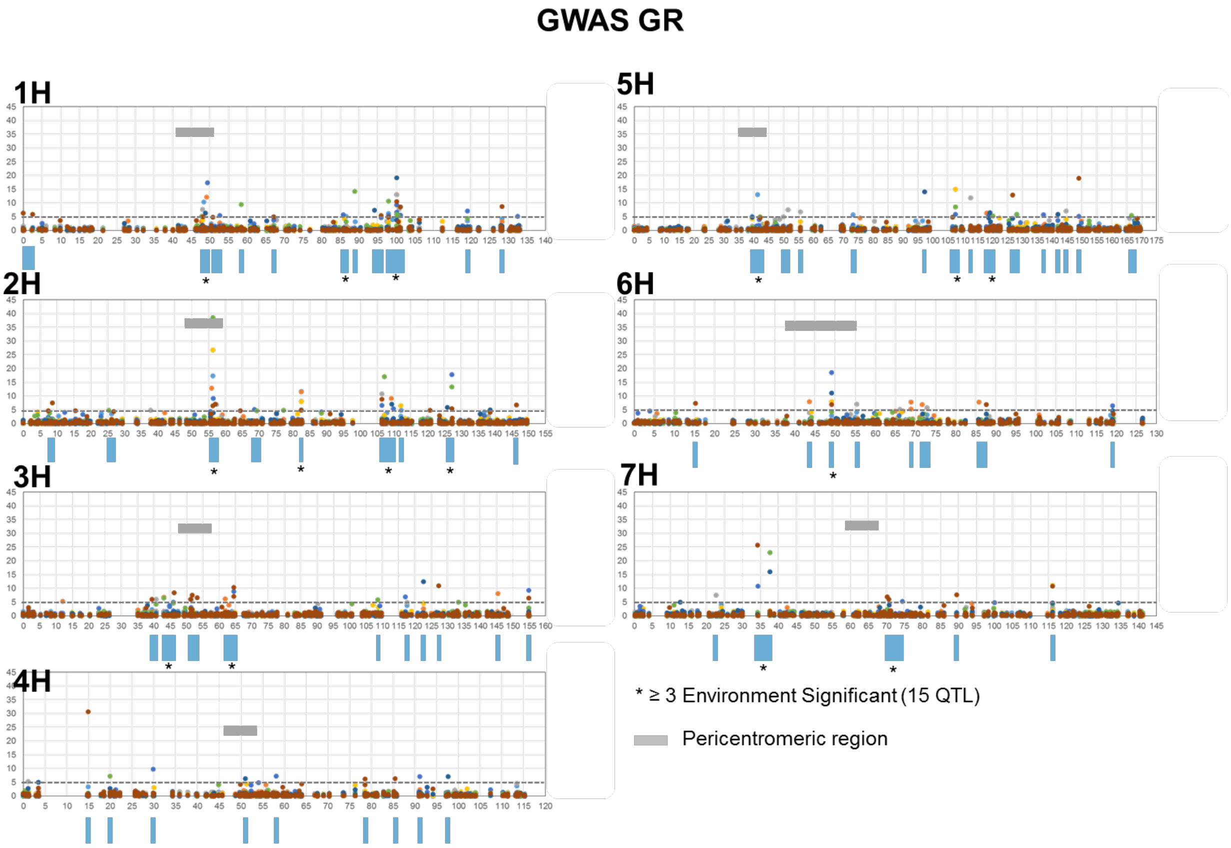


Figure S19: Distribution of grain roundness (GR) QTLs across barley chromosomes.

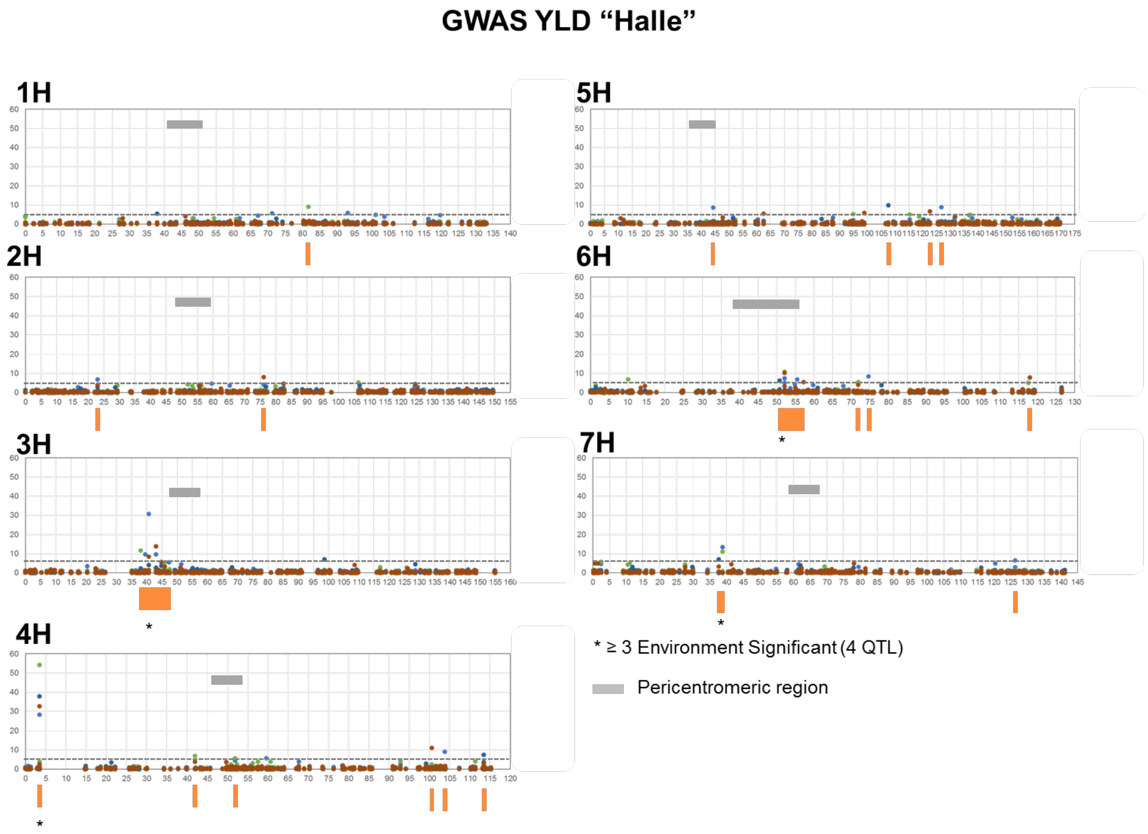


Figure S20: Distribution of grain yield (YLD) QTLs from Halle across barley chromosomes.

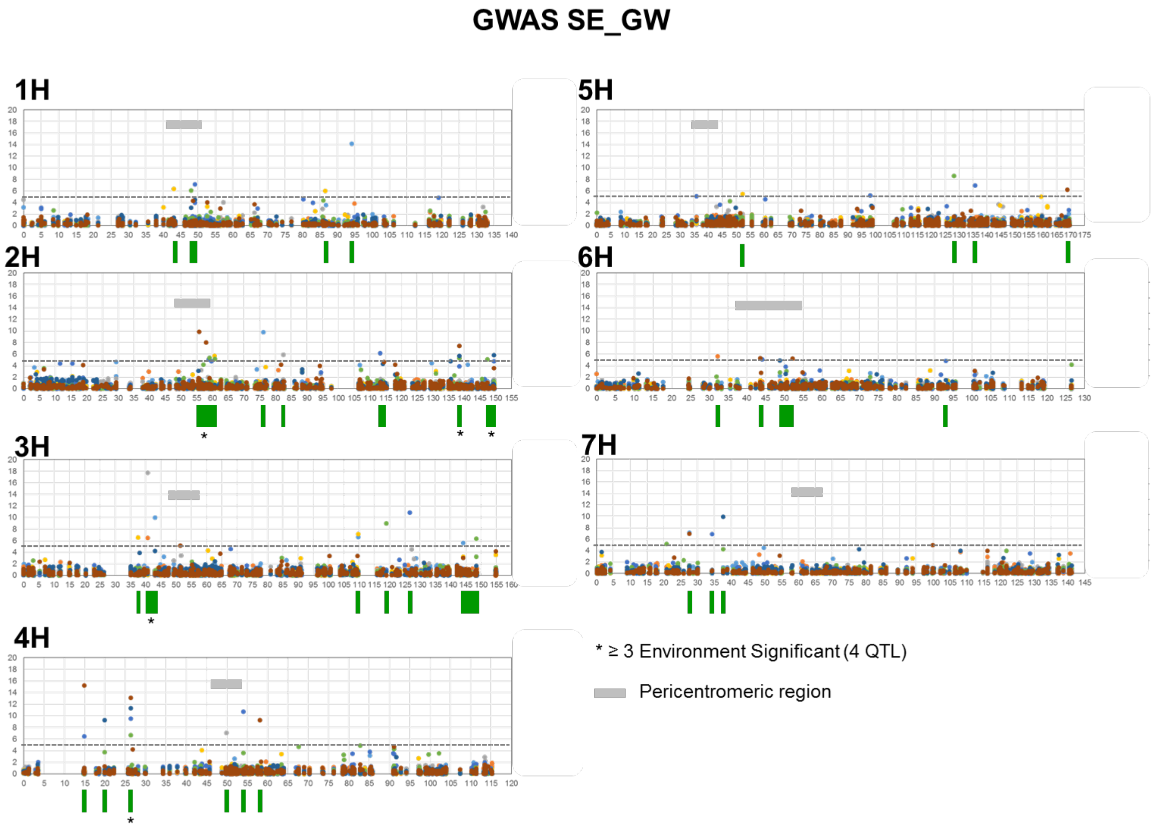


Figure S21: Distribution of standard error of grain width (SE_GW) QTLs across barley chromosomes.

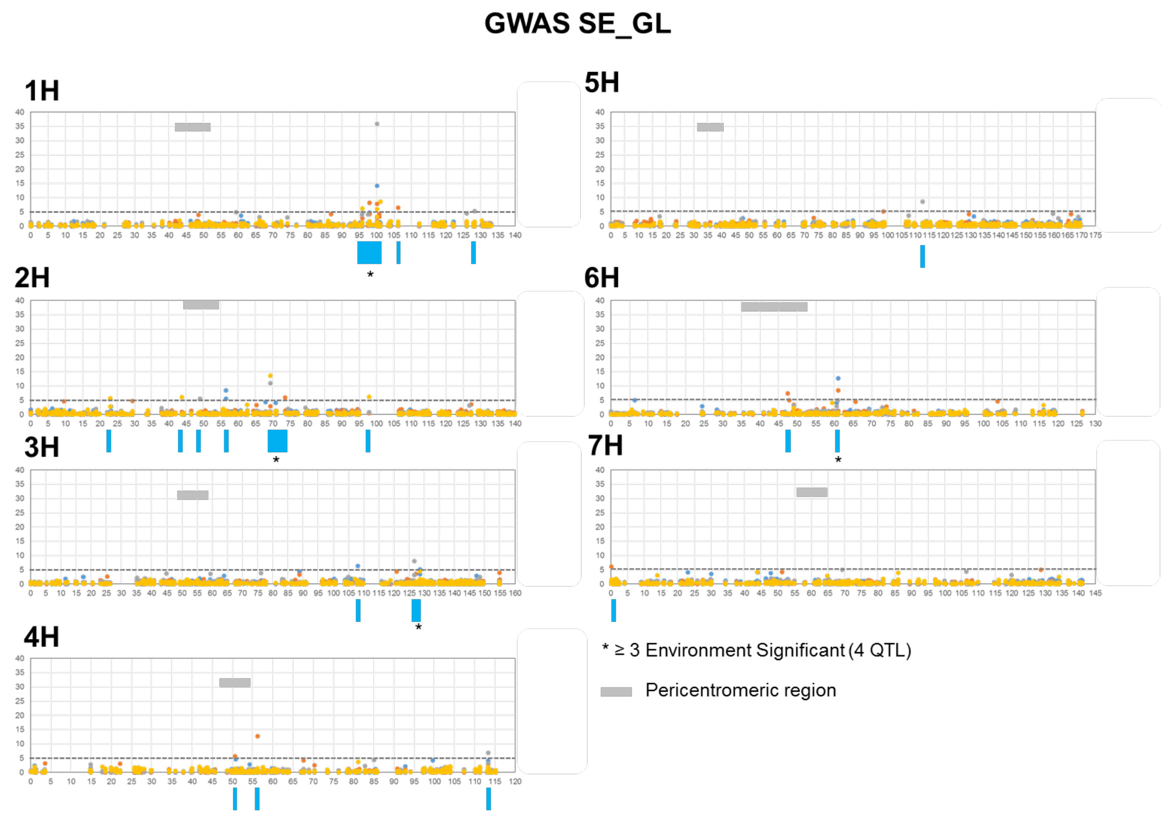


Figure S22: Distribution of standard error of grain length (SE_GL) QTLs across barley chromosomes.