

Supplementary figure 1: Histograms of distributions of (a) complete panel, (b) European panel for AE, (c) complete panel, (d) European panel for DONcPHDH and (e) complete panel, (f) European panel for FHBcPHDH for all tested environments and across environment means.



Supplementary figure 2: Principal Component Analysis showing the correlations among the traits AE, DONCPHDH and FHBcPHDH in different tested environments and across environment means.



4A.1 4A.2 4B.1 5A.1 418.0 AX.94472479 430.0 435.0 AX.94795980 AX-158564968 AD_c21248_511 ACX3391 wsnp_EX_c6044_10590220 wsnp_CAP7_c32_19340 RAC875_c38663_2179 wsnp_Ku_c61953_63254478 JAX-158542171 TA004056-0809 wsnp_JD_c14769_14413046 AX.94478215 AX-158564968 Excalibur_c7180_862 AX-158550608 BobWhite_c4336_127 AX.94675521 BS00100107_51 RAC875_c35993_308 AX.94639537 AX.9466191 3.0 1.0 \ AX-158564576 3.0 --22.0 --- JD_c21248_511 - IACX3391 438.0 AX.94535452 AX.94651230 2.0 -102.0 103.0 482.0 102.0 wsnp Ex c6044 10590220 104.0 489.0 494.0 503.0 535.0 AX.94669191 Ra_c5508_706 105.0 164.0 Ra_c5508_706 AX_94536022 AX_94536022 AX_9472861 AX_95243984 AX_9408726 AX_94418483 AX_95684846 AX_95684846 AX_95684846 AX_94442743 RAC875_rep_c113313_607 AX_94482861 TA001299-0711 AX_95850811 tplb0048905_866 550.0 553.0 AX.94639509 AX.94623317 AX.94392530 AX.95652956 AX.94502357 AX.94624099 AX.95123219 AX.94664472 495.0 569.0 527.0 584.0 486.0 537.0 543.0 576.0 577.0 wsnp_JD_rep_c51623_35119179 AX.94514228 585.0 614.0 644.0 667.0 528.0 AX-108900808 AX-108820155 531.0 532.0 AX-108820155 AX.94432315 Kukri_c89772_150 AX.94687779 wsnp_BG604678A_Ta_1_2 AX.95248090 AX.95158169 Kukri_rep_c69389_1215 AX.95228002 AX.95228002 533.0 AX.94464472 AX-158550230 AX.94440542 wsnp_Ex_c41074_47987860 AX.94488428 AX.95096811 AX-158524646 AX.94510165 |AX-158533564 AX-94540165 |AX-168533564 AX-94667805 AX.94667805 AX.94667805 AX.94667805 AX-158550230 AX-95113297 BS00076033_51 wsnp_CAP12_c1101_569783 AX-158550265 IACX938 AX-158550265 IACX938 AX-158598892 BobWhite_c31044_482 BobWhite_c31044_482 BobWhite_c37751_206 AX-158598875 BobWhite_c27751_95 AX-158582427 581.0 690.0 609.0 tplb0048g05_866 AX.95018258 617.0 701.0 582.0 618.0 583.0 610.0 627.0 584.0 628.0 ~ 648.0 ~ 719.0 ~ 590.0 611.0 606.0 AX.95228002 AX.94440542 Wsnp_Ex_c41074_47987860 AX.94488428 617.0 721.0 619.0 618.0 728.0 734.0 738.0 740.0 744.0 620.0 AX.94750815 AX.94619716 627.0 AX.94980296

743.0



7A.2



Supplementary figure 3: Chromosome locations of quantitative trait loci (QTL) for FHB resistance that were detected in one or more environments. The positions of marker loci in Mega base pairs (Mbp) are shown along the left side of the linkage groups. Markers are shown on the right of the linkage groups. The most consistently detected markers for each QTL region are highlighted in both italics and blue colour (Note: Only the significant markers of the respective QTL regions from the GWAS results were shown in the maps).













Supplementary figure 4: Manhattan plots of traits AE (a and d), FHBcPHDH (b and e), and DONcPHDH (c and f) in complete panel and European panel respectively for 35K, red line represents significant threshold ($-\log 10p = 3.0$) and blue dotted line is FDR @ 0.05% based on across environment means. Suffix to the trait names indicate the names of experimental locations: "GV" for "GreenhouseVollebekk", "M" for "Morden", "S" for Staur, "T" for Tulln, and "V" for Vollebekk.













Supplementary figure 5: Manhattan plots of traits AE (a and d), FHBcPHDH (b and e), and DONcPHDH (c and f) in complete panel and European panel respectively for 25K, red line represents significant threshold ($-\log 10p = 3.0$) and blue dotted line is FDR @ 0.05% based on across environment means. Suffix to the trait names indicate the names of experimental locations: "GV" for "GreenhouseVollebekk", "M" for "Morden", "S" for Staur, "T" for Tulln, and "V" for Vollebekk.



(b)



(a)





(d)







Supplementary figure 6: QQ-plots of traits AE (a and d), FHBcPHDH (b and e), and DONcPHDH (c and f) in complete panel and European panel respectively for 35K, red line represents significant threshold (-log10p = 3.0) and blue dotted line is FDR @ 0.05% based on across environment means. Suffix to the trait names indicate the names of experimental locations: "GV" for "GreenhouseVollebekk", "M" for "Morden", "S" for Staur, "T" for Tulln, and "V" for Vollebekk.













(d)



(e)





Supplementary figure 7: QQ-plots of traits AE (a and d), FHBcPHDH (b and e), and DONcPHDH (c and f) in complete panel and European panel respectively for 35K, red line represents significant threshold $(-\log_{10} = 3.0)$ and blue dotted line is FDR @ 0.05% based on across environment means. Suffix to the trait names indicate the names of experimental locations: "GV" for "GreenhouseVollebekk", "M" for "Morden", "S" for Staur, "T" for Tulln, and "V" for Vollebekk.



Supplementary figure 8: Boxplot showing the haplotype effect of QTL *Qfhb.nmbu.1A.1* on chromosome 1A based on the a) mean AE, b) mean corrected DON content, c) mean corrected FHB disease severity of complete panel, and d) mean AE, e) mean corrected DON content, f) mean corrected FHB disease severity of European panel. Wilcoxon method is used for pair-wise comparisons (***P < 0.0001, **P < 0.001, *P < 0.05, ns > 0.05). Comparisons with ns are not shown in this figure.



Supplementary figure 9: Boxplot showing the haplotype effect of QTL *Qfhb.nmbu.3A.1* on chromosome 3A based on the a) mean AE, b) mean corrected DON content, c) mean corrected FHB disease severity of complete panel, and d) mean AE, e) mean corrected DON content, f) mean corrected FHB disease severity of European panel. Wilcoxon method is used for pair-wise comparisons (***P < 0.0001, **P < 0.001, *P < 0.05, ns > 0.05). Comparisons with ns are not shown in this figure.



Supplementary figure 10: Boxplot showing the haplotype effect of QTL *Qfhb.nmbu.4B.1* on chromosome 4B based on the a) mean AE, b) mean corrected DON content, c) mean corrected FHB disease severity of complete panel, and d) mean AE, e) mean corrected DON content, f) mean corrected FHB disease severity of European panel. Wilcoxon method is used for pair-wise comparisons (***P < 0.0001, **P < 0.001, *P < 0.05, ns > 0.05). Comparisons with ns are not shown in this figure.



Supplementary figure 11: Boxplot showing the haplotype effect of QTL *Qfhb.nmbu.5A.1* on chromosome 5A based on the a) mean AE, b) mean corrected DON content, c) mean corrected FHB disease severity of complete panel, and d) mean AE, e) mean corrected DON content, f) mean corrected FHB disease severity of European panel. Wilcoxon method is used for pair-wise comparisons (***P < 0.0001, **P < 0.001, *P < 0.05, ns > 0.05). Comparisons with ns are not shown in this figure.



Supplementary figure 12: Boxplot showing the haplotype effect of QTL *Qfhb.nmbu.6A.1* on chromosome 6A based on the a) mean AE, b) mean corrected DON content, c) mean corrected FHB disease severity of complete panel, and d) mean AE, e) mean corrected DON content, f) mean corrected FHB disease severity of European panel. Wilcoxon method is used for pair-wise comparisons (***P < 0.0001, **P < 0.001, *P < 0.05, ns > 0.05). Comparisons with ns are not shown in this figure.



Supplementary figure 13: Boxplot showing the haplotype effect of QTL *Qfhb.nmbu.7A.2* on chromosome 7A with KASP markers based on the a) mean AE, b) mean corrected DON content, c) mean corrected FHB disease severity of complete panel, and d) mean AE, e) mean corrected DON content, f) mean corrected FHB disease severity of European panel. Wilcoxon method is used for pair-wise comparisons (***P < 0.0001, **P < 0.001, *P < 0.05, ns > 0.05). Comparisons with ns are not shown in this figure.



Supplementary figure 14: Cluster plots for the three KASP markers used for genotyping the NMBU spring wheat panel: a) BS00098483_51, b) AX-95248570, and c) Kukri_c57593_79. Genotype calls for allele one (FAM) and two (HEX) are indicated in *blue* and *red*, respectively. Heterozygous scores are shown in *pink* and negative controls in *black*. The source of the resistant allele of *Qfhb.nmbu.7A.2*, Ning8343, for is shown in *green*.