

Figure S1. (a) Manhattan plot on 21 wheat chromosomes for Type_2_2019&2020 trait. Red horizontal dash represents the GWAS threshold of $-\log(p) = 5.22$ for Bonferroni correction and dots above the red line indicate significant MTAs. (b) Q-Q plot for GWAS results for Type_2_2019&2020 trait. (c) Boxplots indicating the phenotype value of Type_2_2019&2020 trait corresponding to the two haplotypes (H1 and H2) in the same haploblock (Ch2D_B35) on chromosome 2D. (d) Haplotype block based on two SNP markers on chromosome 2D; both haplotypes are significantly associated with the Type_2_2019&2020 trait (MTA). Frequency shows occurrence (percentage) of haplotypes in the group of families.

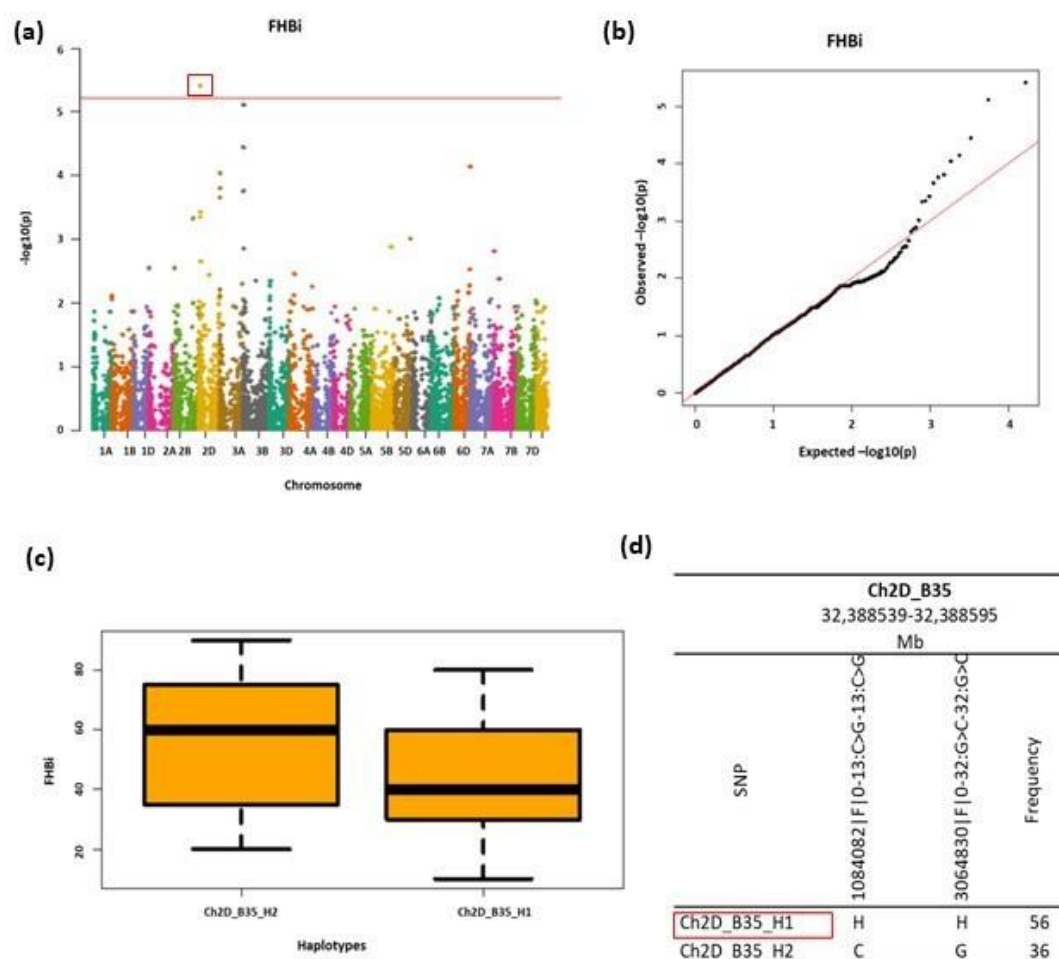


Figure S2. (a) Manhattan plot on 21 wheat chromosomes for FHBi trait. Red horizontal dash represents the GWAS threshold of $-\log(p) = 5.22$ for Bonferroni correction and dot above the red line indicate significant MTA. (b) Q-Q plot for GWAS results for FHBi trait. (c) Boxplots indicating the phenotype value of FHBi trait corresponding to haplotypes in the haploblock Ch2D_B35 on chromosome 2D. (d) Haplotype block based on two SNP markers on chromosome 2D; haplotype significantly associated with the FHBi trait (MTA) marked with red. Frequency shows occurrence (percentage) of haplotypes in the group of families.

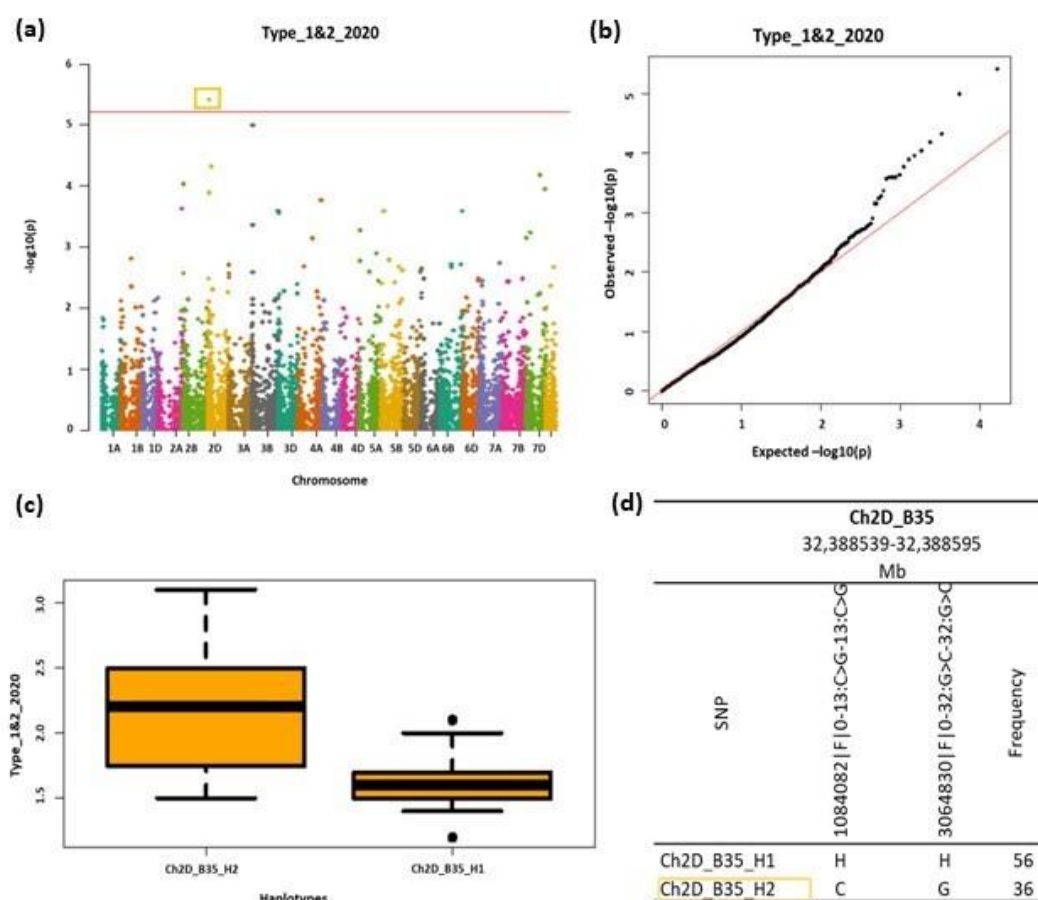


Figure S3. (a) Manhattan plot on 21 wheat chromosomes for Type_1&2_2020 trait. Red horizontal dash represents the GWAS threshold of $-\log(p) = 5.22$ for Bonferroni correction and a dot above the red line indicate significant MTA. (b) Q-Q plot for GWAS results for Type_1&2_2020 trait. (c) Boxplots indicating the phenotype value of Type_1&2_2020 trait corresponding to haplotypes in the haploblock Ch2D_B35 on chromosome 2D. (d) Haplotype block based on two SNP markers on chromosome 2D; haplotype significantly associated with the Type_1&2_2020 trait (MTA) marked with yellow. Frequency shows occurrence (percentage) of haplotypes in the group of families.

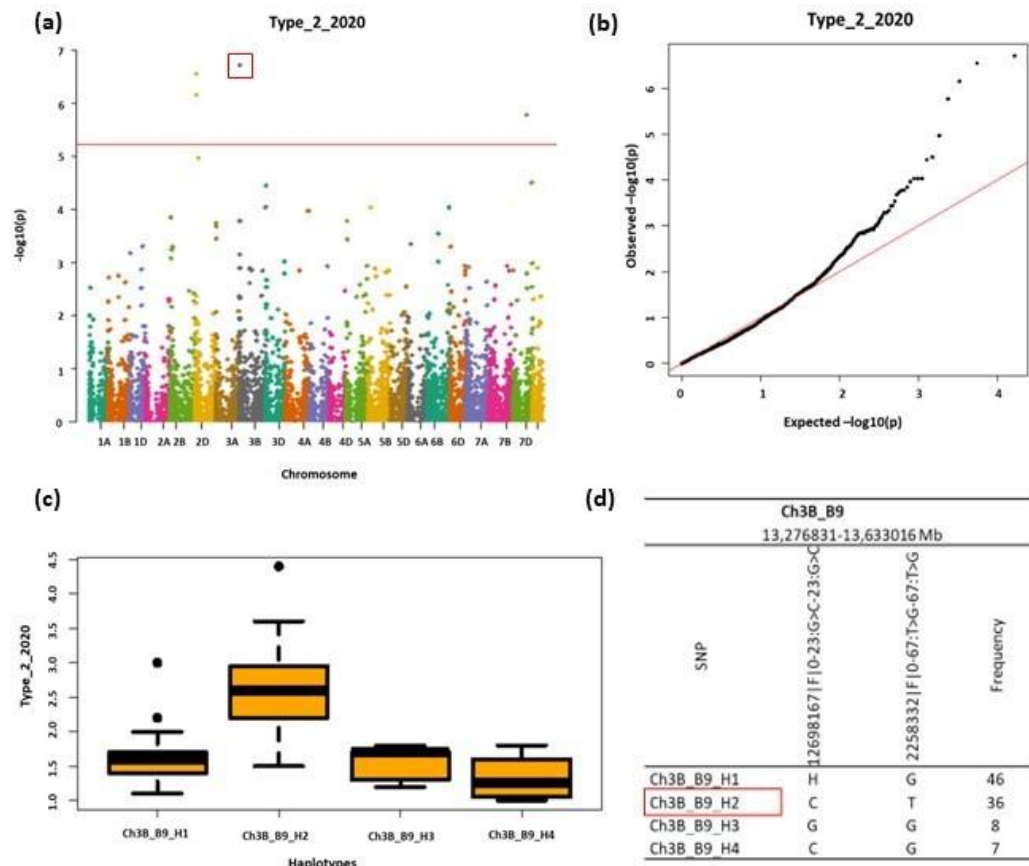


Figure S4. (a) Manhattan plot on 21 wheat chromosomes for Type_2_2020 trait. Red horizontal dash represents the GWAS threshold of $-\log(p) = 5.22$ for Bonferroni correction and dots above the red line indicate significant MTAs. (b) Q-Q plot for GWAS results for Type_2_2020 trait. (c) Boxplots indicating the phenotype value of Type_2_2020 trait corresponding to haplotypes in the haploblock Ch3B_B9 on chromosome 3B. (d) Haplotype block based on two SNP markers on chromosome 3B; haplotype significantly associated with the Type_2_2020 trait (MTA) marked with red. Frequency shows occurrence (percentage) of haplotypes in the group of families.

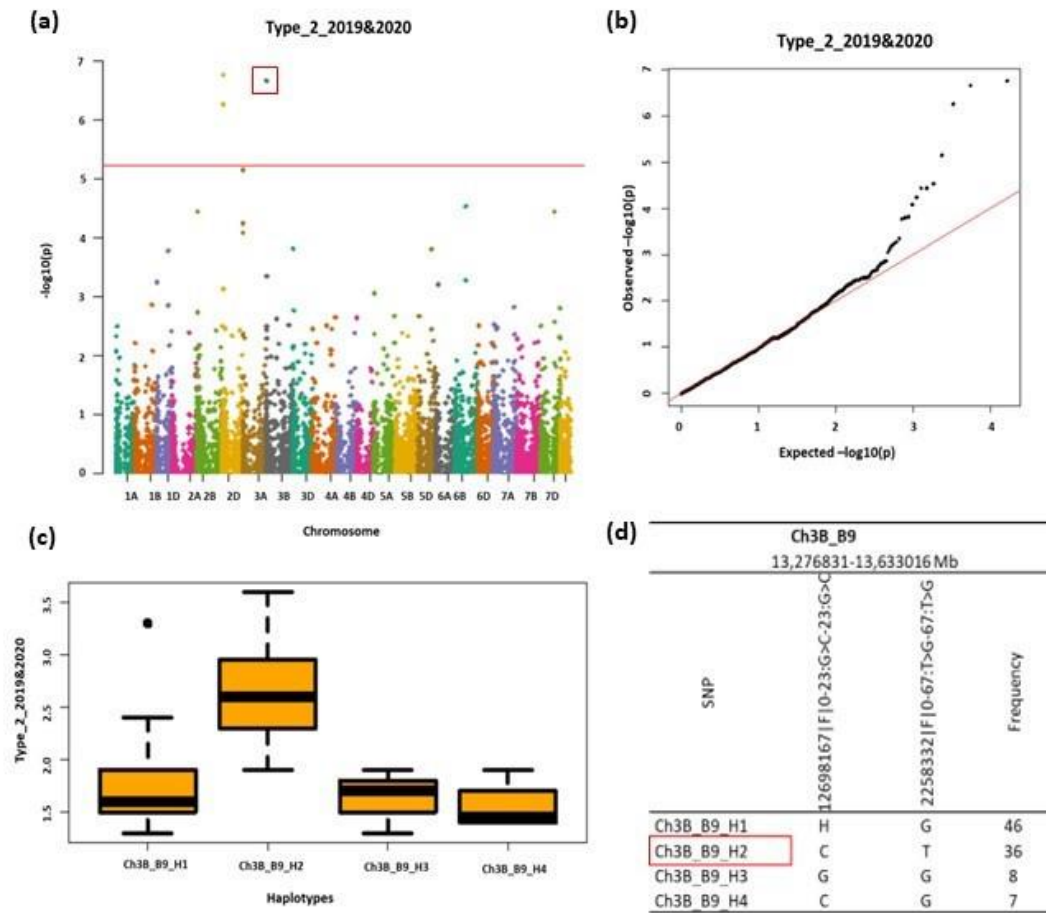


Figure S5. (a) Manhattan plot on 21 wheat chromosomes for Type_2_2019&2020 trait. Red horizontal dash represents the GWAS threshold of $-\log(p) = 5.22$ for Bonferroni correction and dots above the red line indicate significant MTAs. (b) Q-Q plot for GWAS results for Type_2_2019&2020 trait. (c) Boxplots indicating the phenotype value of Type_2_2019&2020 trait corresponding to haplotypes in the haploblock Ch3B_B9 on chromosome 3B. (d) Haplotype block based on two SNP markers on chromosome 3B; haplotype significantly associated with the Type_2_2019&2020 trait (MTA) marked with red. Frequency shows occurrence (percentage) of haplotypes in the group of families.

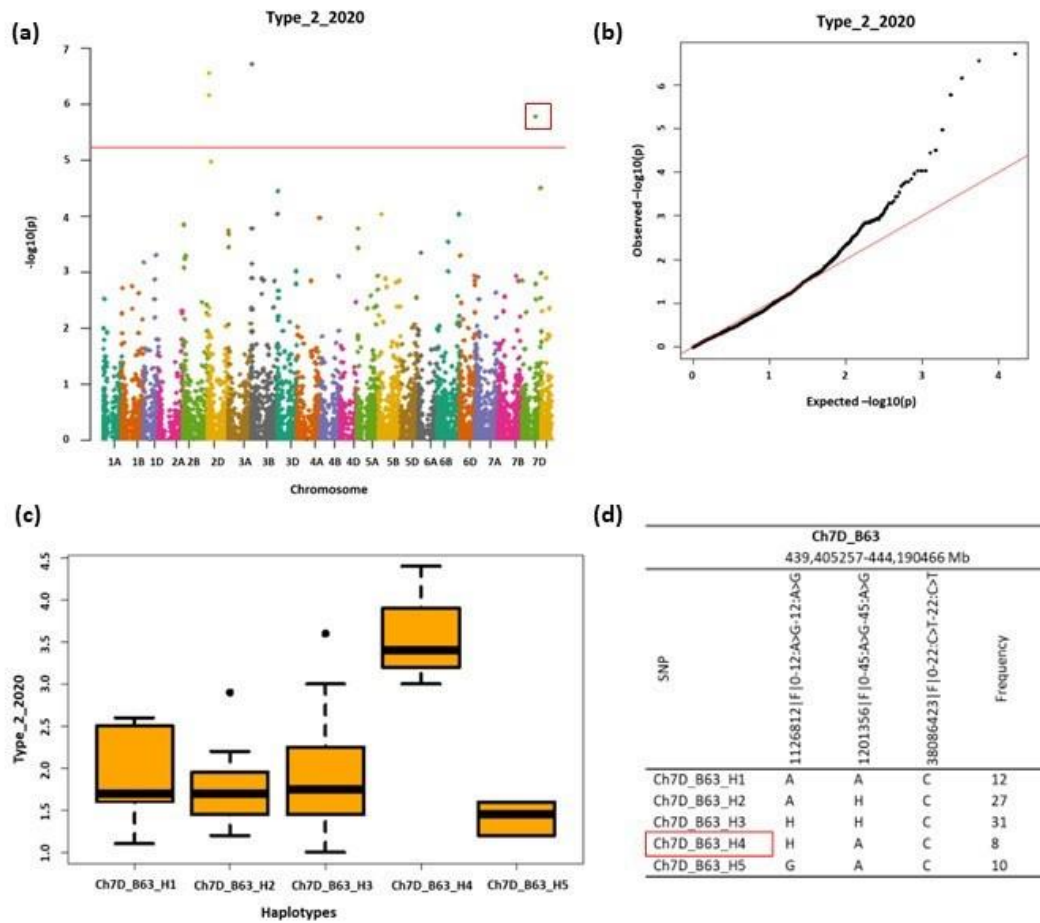


Figure S6. (a) Manhattan plot on 21 wheat chromosomes for Type_2_2020 trait. Red horizontal dash represents the GWAS threshold of $-\log(p) = 5.22$ for Bonferroni correction and dots above the red line indicate significant MTAs. (b) Q-Q plot for GWAS results for Type_2_2020 trait. (c) Boxplots indicating the phenotype value of Type_2_2020 trait corresponding to haplotypes in the haploblock Ch7D_B63 on chromosome 7D. (d) Haplotype block based on three SNP markers on chromosome 7D; haplotype significantly associated with the Type_2_2020 trait (MTA) marked with red. Frequency shows occurrence (percentage) of haplotypes in the group of families.