

Figure S1

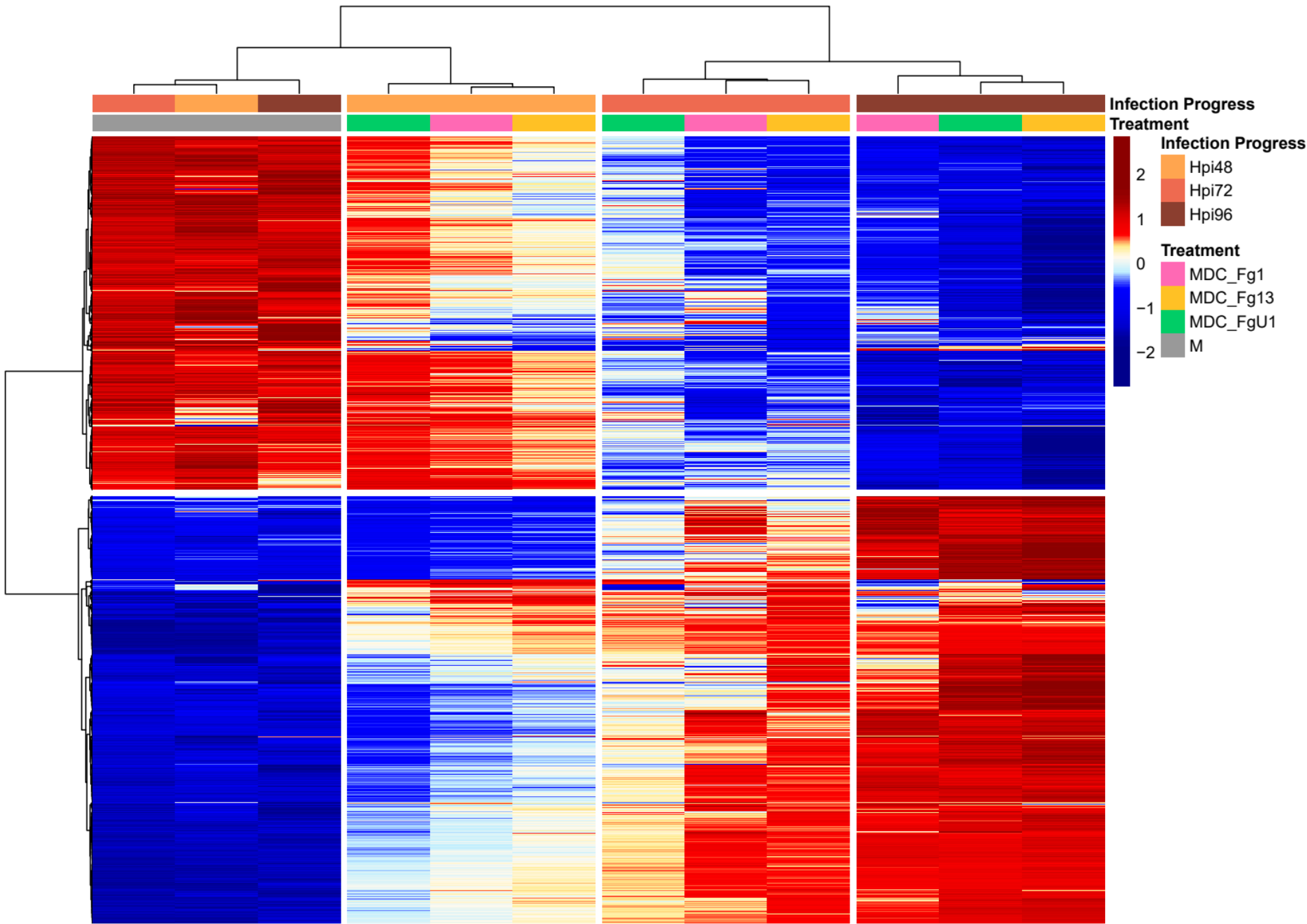


Figure S1. Expression regulation patterns of the All strain -responsive gene set in 'Recital' along the time course for control and infected samples. The structure of gene and sample data sets were determined by HAC based on Ward's minimum variance method using the z-score transformed gene expression values. Heatmap color scales represent the z-score transformed expression values of the genes from the All strain -responsive gene set (26,779 genes) for each sample. The clustering on top of the heatmap represents the experimental conditions which are labeled according to the factors Time Course (48hpi, 72hpi, 96hpi) and Treatment (MDC_Fg1, MDC_Fg13, MDC_FgU1, Mock). The clustering on the right side of the heatmap represents the clustering of genes.

Figure S2

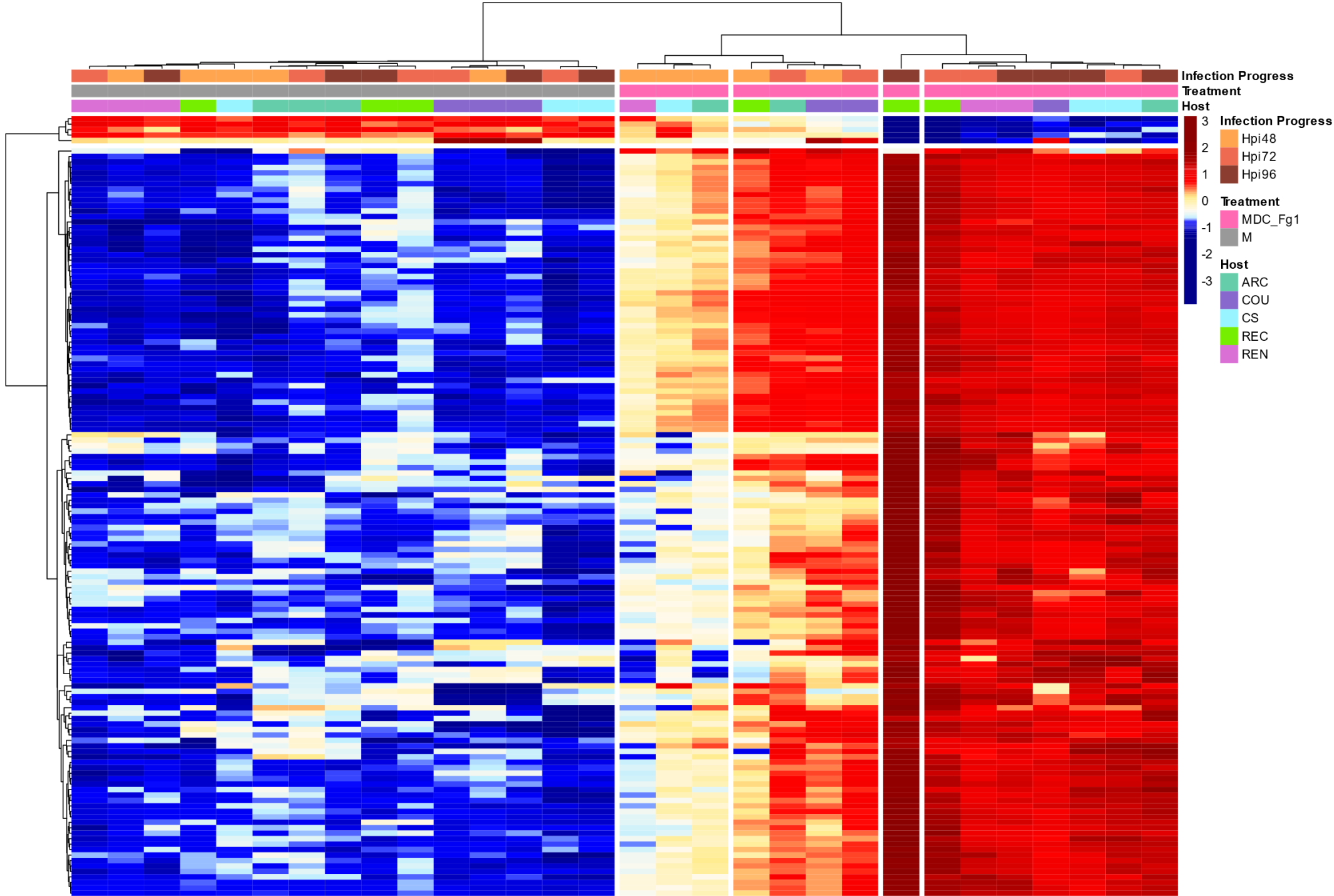


Figure S2. Expression regulation patterns of the 142 susceptibility genes targeted by *F. graminearum* nuclear effectors that are differentially expressed in response to FHB in the 5 wheat cultivars (HostV). The structure of gene and sample data sets were determined by HAC based on Ward's minimum variance method using the z-score transformed gene expression values. Heatmap color scales represent the z-score transformed expression values of the putative susceptibility genes for each sample. The clustering on top of the heatmap represents the experimental conditions which are labeled according to the factors Infection Progress, Treatment and Cultivar.

Figure S3A

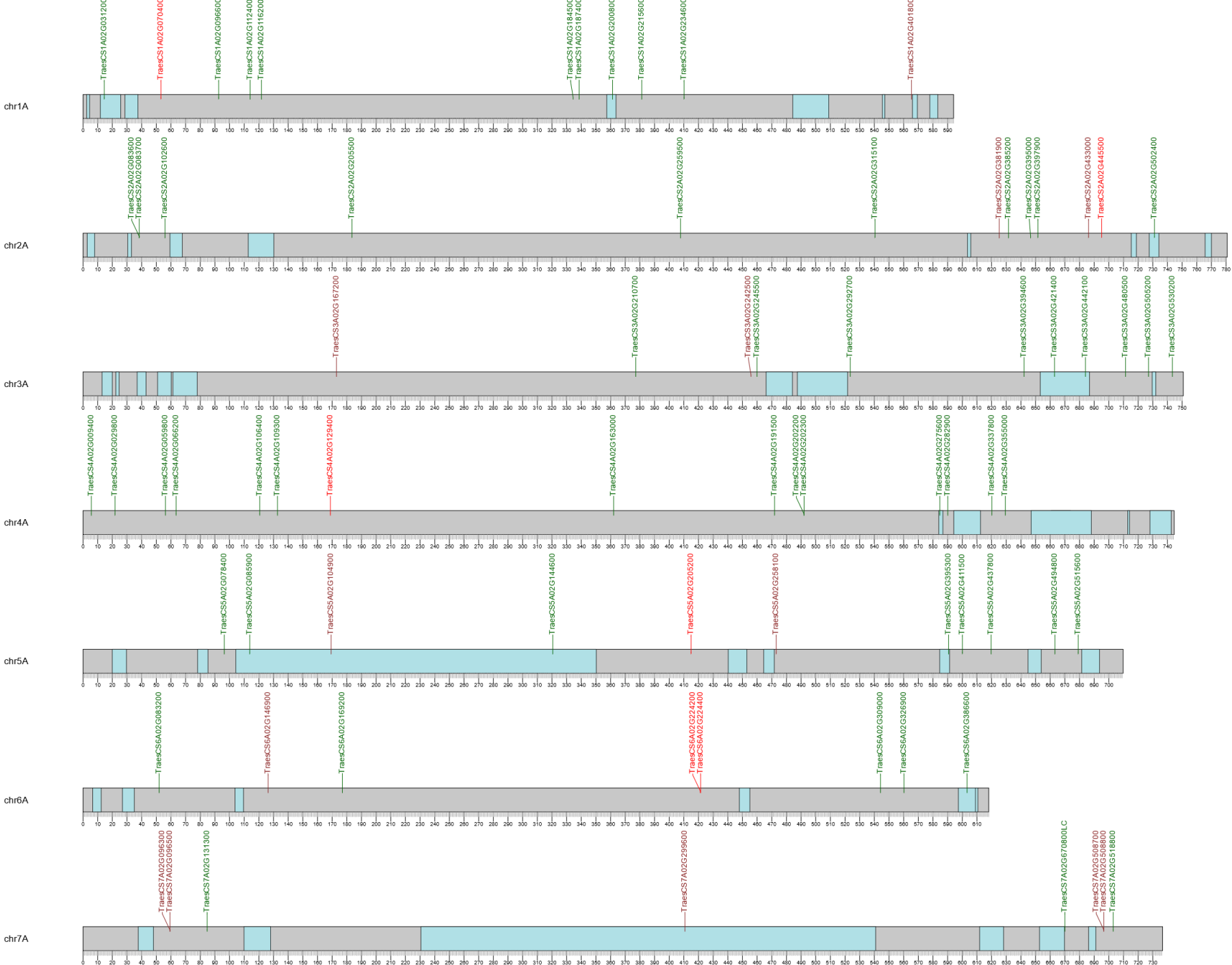


Figure S3B

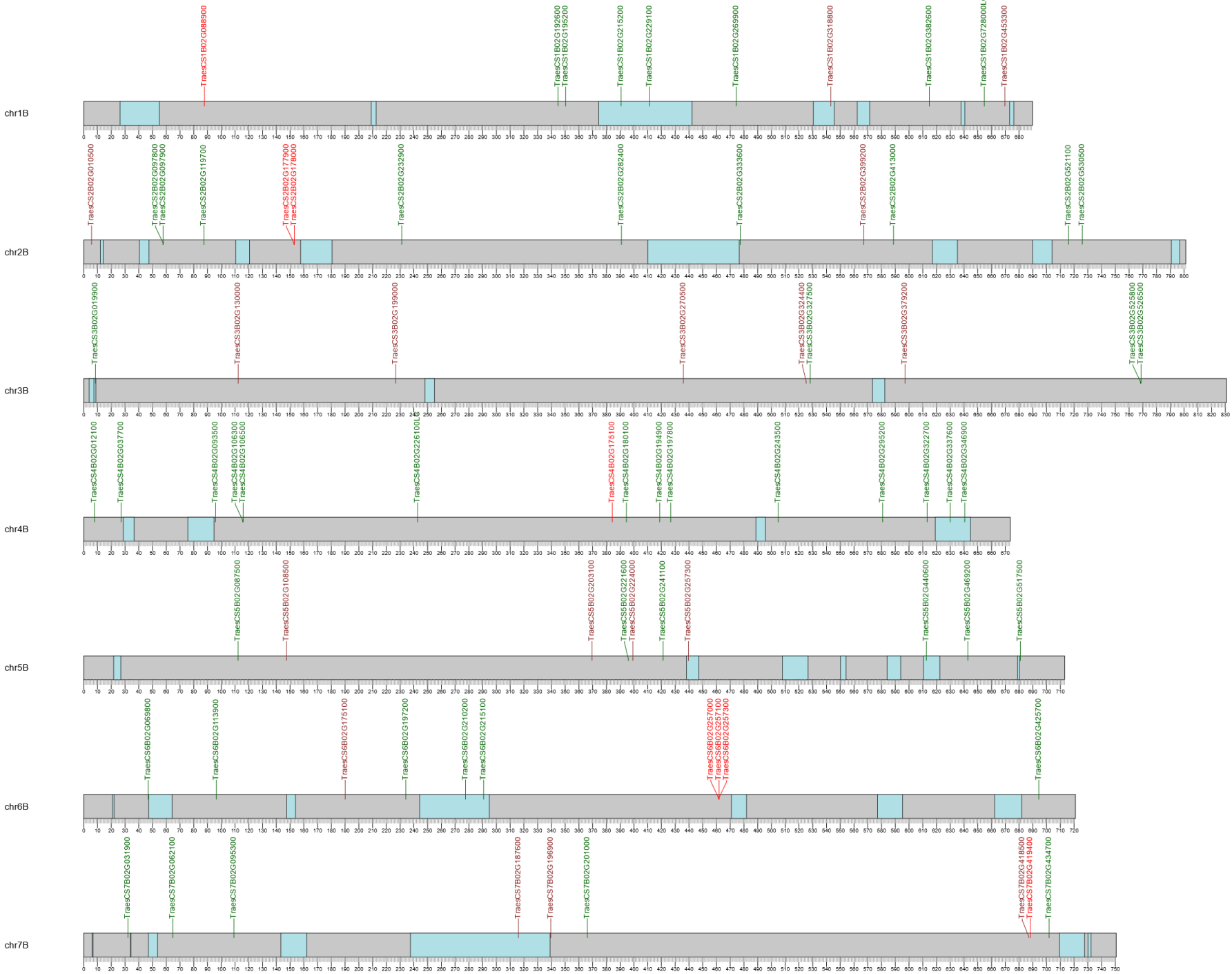


Figure S3C

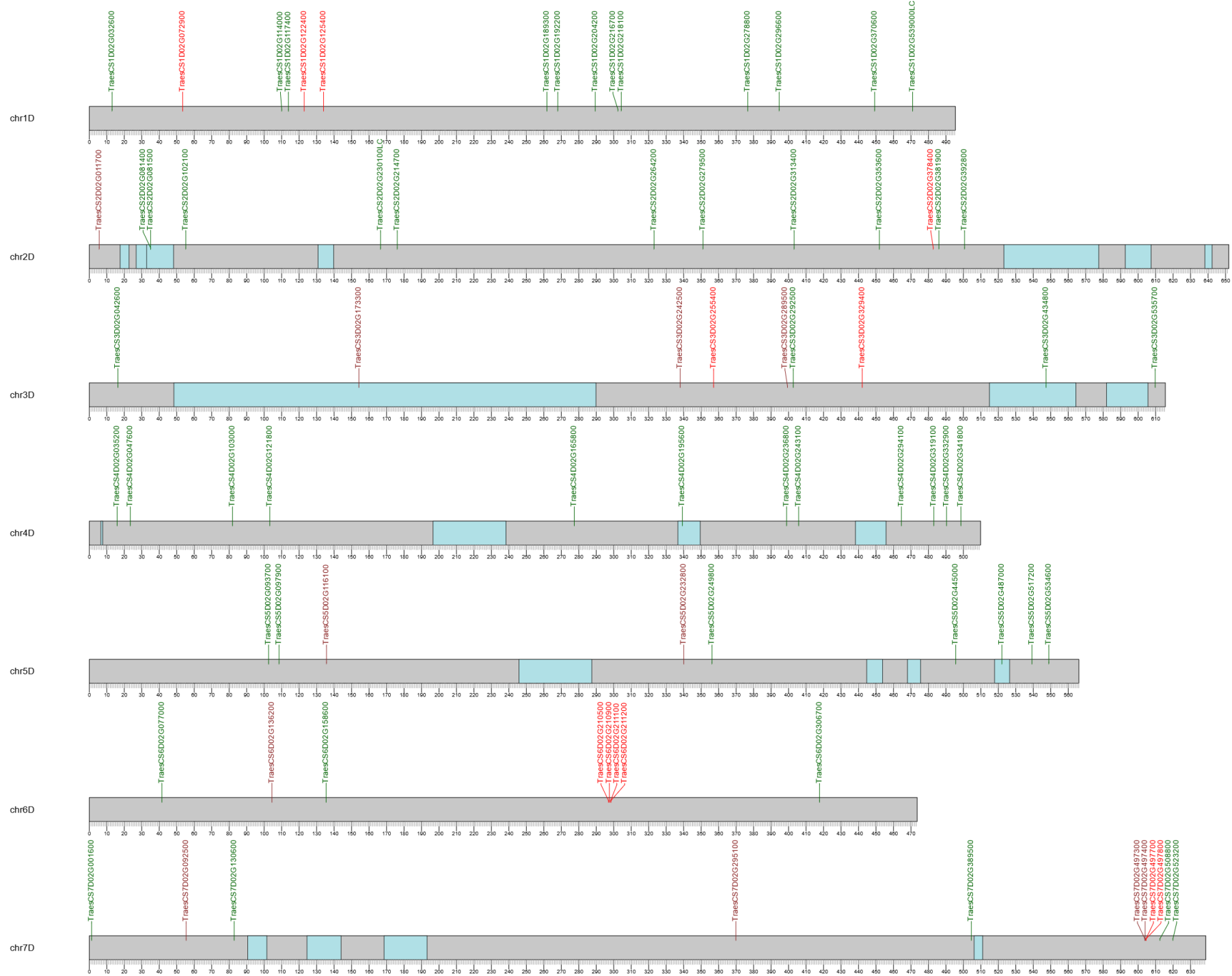


Figure S3. Genomic distribution of the 233 putative S genes on wheat subgenomes A (S3A), B (S3B) and D (S3C). S genes were colored according to their categories : Master TF gene (brick red), TF gene (orange), not TF gene (green). The FHB meta-QTLs built by Zheng et al., 2021 were represented by sky blue boxes directly on the chromosomes.