

## 1. INTRODUCTION

Host resistance to Fusarium head blight (FHB) is a complex quantitative trait strongly affected by environmental conditions. Currently, only a few sources of FHB resistances have been used wheat breeding programs, including Sumai3 and its derivatives (Bai and Shaner 2004; Buerstmayr et al. 2009). Extensive utilization of one or a few sources of resistances over large crop production areas poses a concern to resistance breakdown accompanied by severe disease epidemics. Therefore, it is important to identify, characterize, and deploy new sources of FHB resistance.

Surpresa is a Brazilian spring wheat cultivar identified with moderate resistance to FHB and DON accumulation from screening over 1000 wheat accessions in the National Small Grains Collection (NSGC)(Zhang et al. 2008; Rajaram et al. 1988). Without known sources of FHB resistance in its pedigree, Surpresa may carry a new set of genes for FHB resistance. The objective of this study was to identify novel quantitative trait loci (QTL) for resistance to FHB and DON accumulation in Surpresa.

## 2. MATERIALS and METHOD

### 2.1 Plant Materials



Wheat

Surpresa

Surpresa was used as a parent to cross with a susceptible spring wheat cultivar Wheaton (PI469271) to generate a bi-parental mapping population containing 187 recombinant inbred lines (RILs)(F<sub>2:7</sub>) using the single-seed descent method.

### 2.2 Phenotypic evaluation

The RILs and parents were evaluated for type II and type III FHB resistances in three greenhouse and four field experiments between 2016 and 2018 using procedures described by Chu et al. (2011). Conidial suspension was prepared at 10<sup>5</sup> conidia/mL for inoculation.

Experimental design and disease assessments were done using the protocol described in Zhao et al. (2018). For DON evaluation, finely ground kernels from infected spikes of each RIL were sent to the USWBSI-supported laboratory.

### 2.3 Genotyping, linkage map, and QTL analysis

The RILs and parents were genotyped using the two-enzyme genotyping-by-sequencing (GBS) method (Liu et al. 2019). The SNP markers identified from GBS analysis were filtered for quality and resulting SNPs were used to construct a genetic linkage map in JoinMap® v. 5.0. Composite Interval Mapping (CIM) was used to detect QTL in QGene v. 4.4. LOD threshold for claiming significant QTL at *P* < 0.05 was determined by performing 1000 permutation.

## 3. RESULTS

### 3.1 Variation in disease severity and DON

Table 1. Phenotypic data and broad-sense heritability of FHB severity and DON content in parents and the Wheaton/Surpresa RIL population

Trait	Environments	Parents		RILs		H <sup>2</sup>
		Surpresa	Wheaton	Mean±SD	Range	
FHB severity	16GH	na	0.86	0.73 ± 0.19	0.13 – 1.00	
	17GH	0.401	0.89	0.60 ± 0.16	0.17 – 0.95	0.57
	18GH	0.36	0.91	0.61 ± 0.15	0.22 – 0.97	
	16FAR	0.28	0.86	0.50 ± 0.17	0.14 – 0.97	
	17FAR	0.59	0.85	0.37 ± 0.15	0.10 – 0.84	0.15
	18FAR_P	0.30	0.66	0.46 ± 0.10	0.19 – 0.71	
DON content	18FAR_C	0.35	0.76	0.55 ± 0.09	0.31 – 0.76	-
	18GH	7.35	47.10	37.45 ± 30.81	0.33 – 202.4	
	18FAR_P	3.40	5.90	11.42 ± 6.78	1.00 – 49.90	-
	18FAR_C	10.30	39.80	23.30 ± 12.48	6.80 – 72.10	

H<sup>2</sup>, broad-sense heritability; FHB severity, mean of the symptomatic proportions of infected spikes; FAR, field nursery at Fargo location; GH, greenhouse; P, point inoculation; C, corn-spawn inoculation

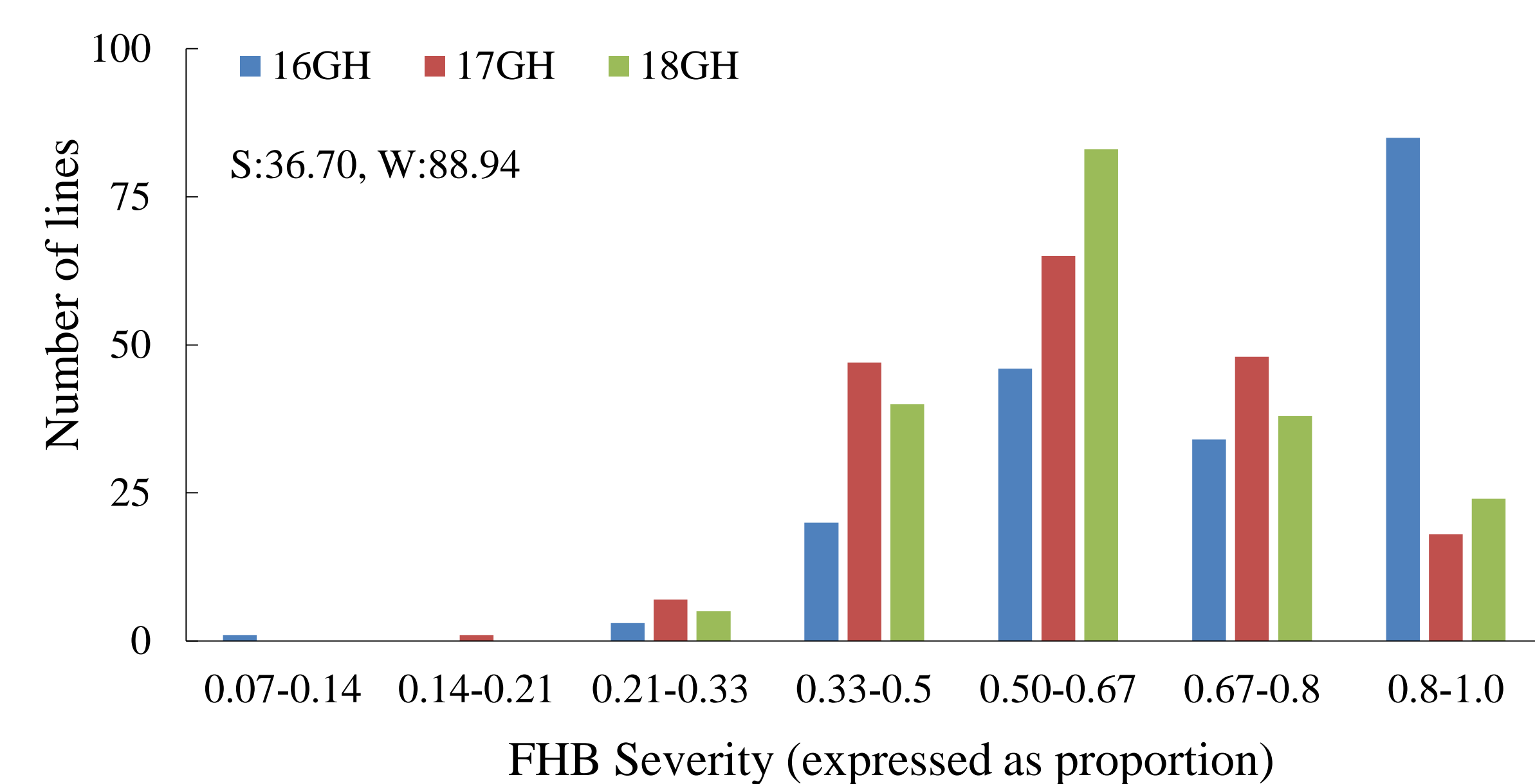


Figure 1. Frequency distribution of FHB severity in the Wheaton/Surpresa RIL population across greenhouse experiments. (GH, greenhouse; S, Surpresa, W, Wheaton)

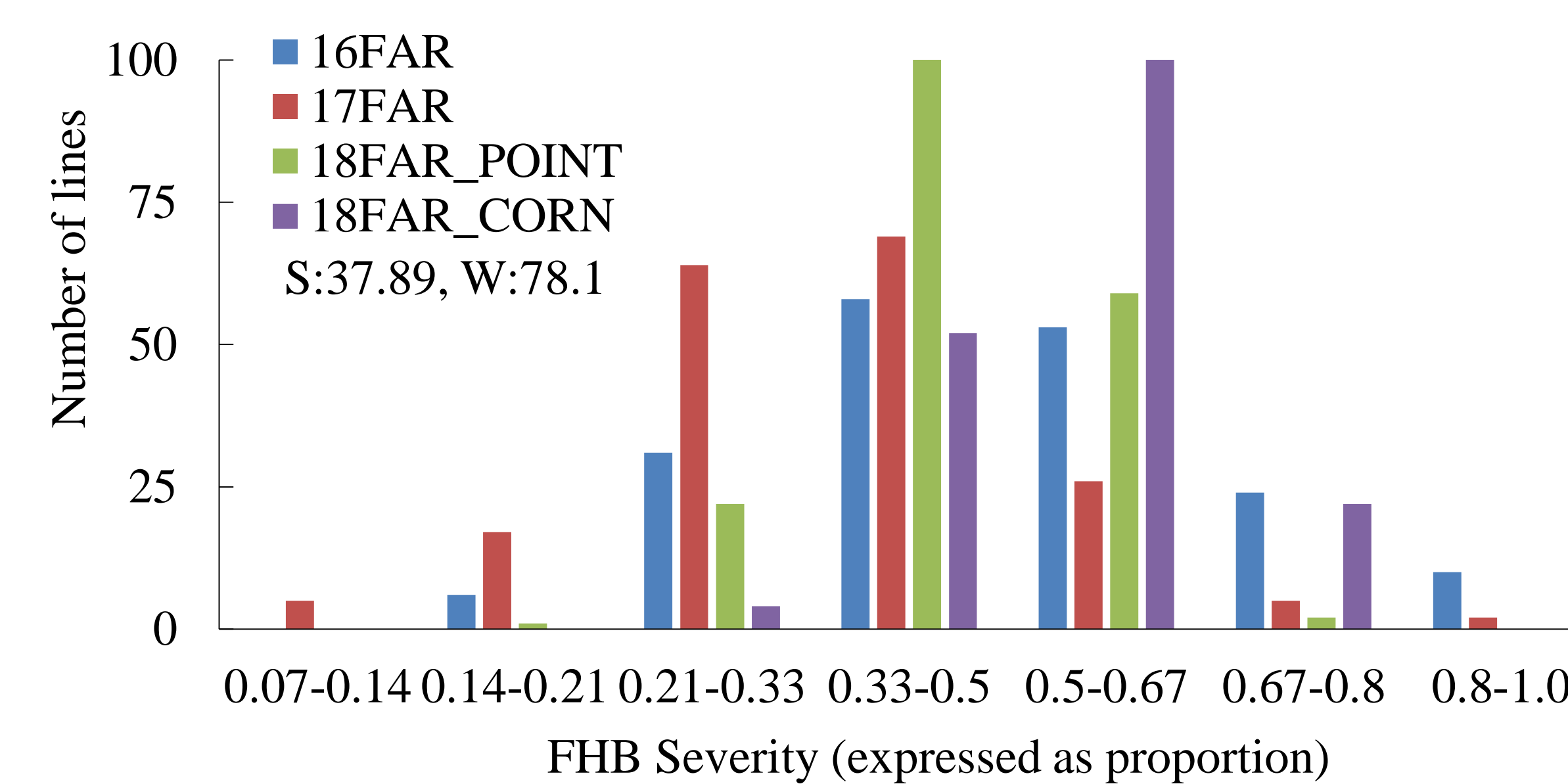


Figure 2. Frequency distribution of FHB severity in the Wheaton/Surpresa RIL population across field experiments. (FAR, field nursery at Fargo location; Point, point inoculation; Corn, corn-spawn inoculation. S, Surpresa; W, Wheaton)

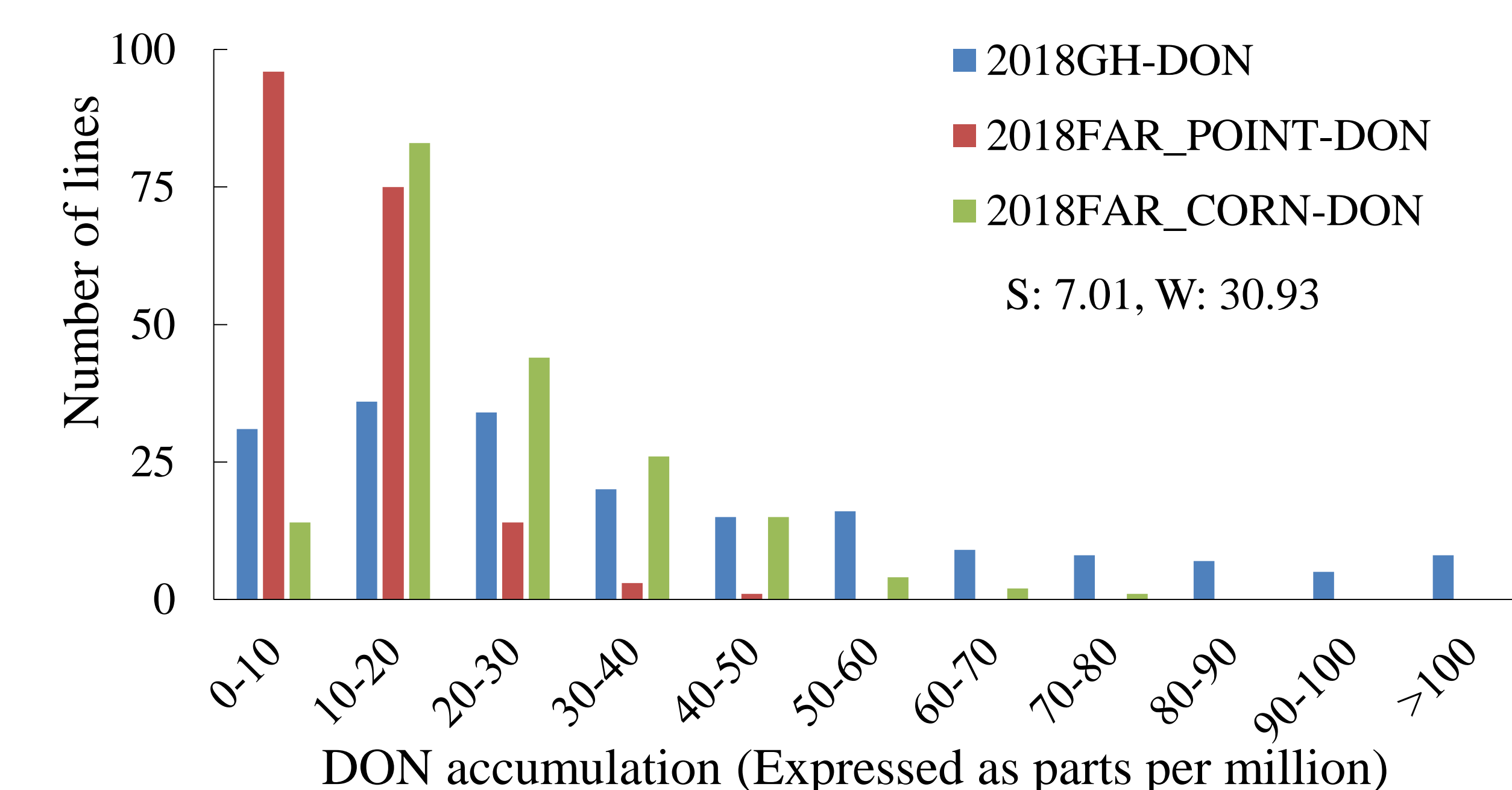
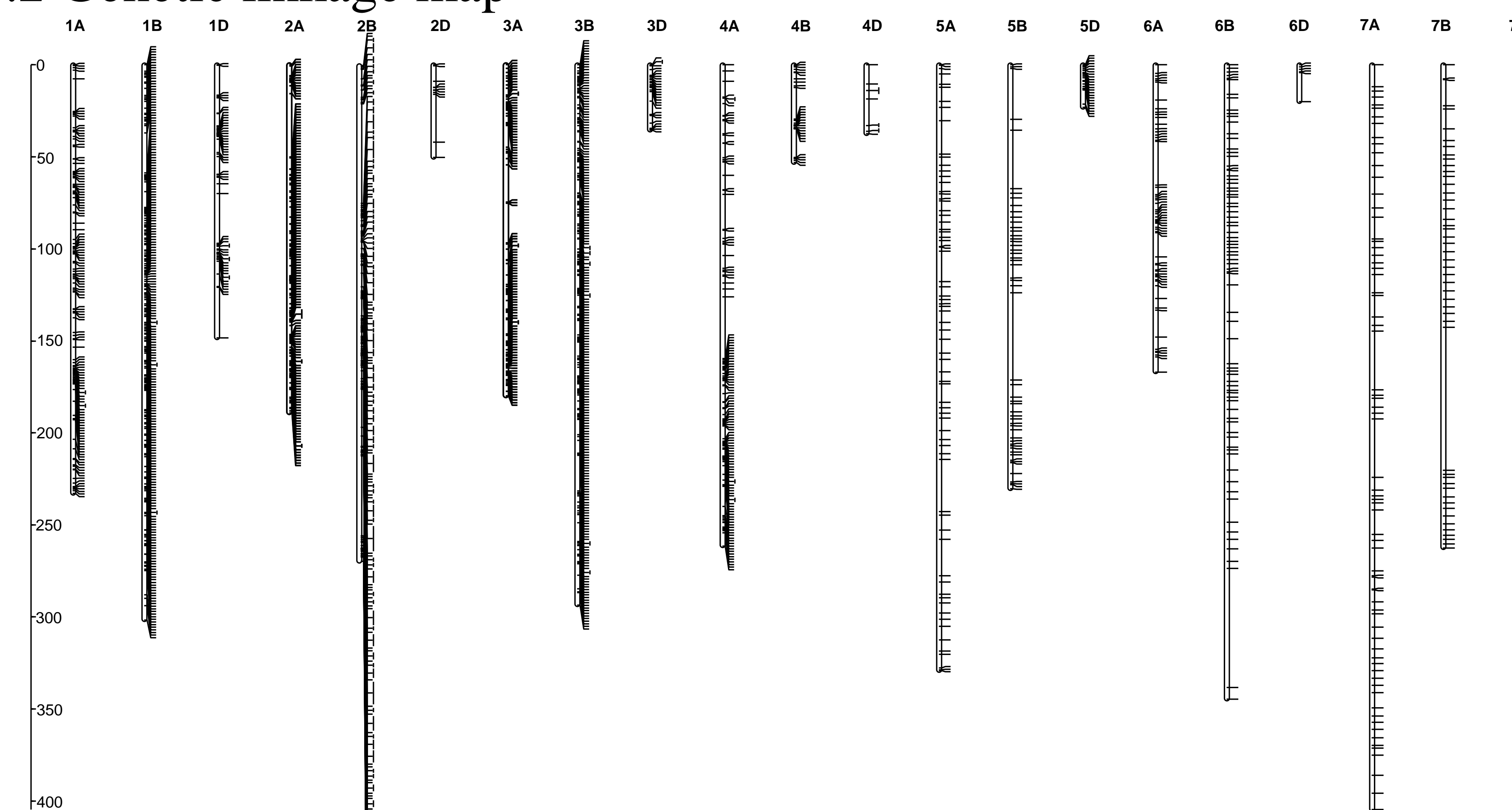


Figure 3. Frequency distribution of DON accumulation in the Wheaton/Surpresa RIL population. (GH, greenhouse; FAR, field nursery at Fargo location; Point, point inoculation; Corn, corn-spawn inoculation; S, Surpresa; W, Wheaton)

### 3.2 Genetic linkage map



### 3.3 QTL Analysis

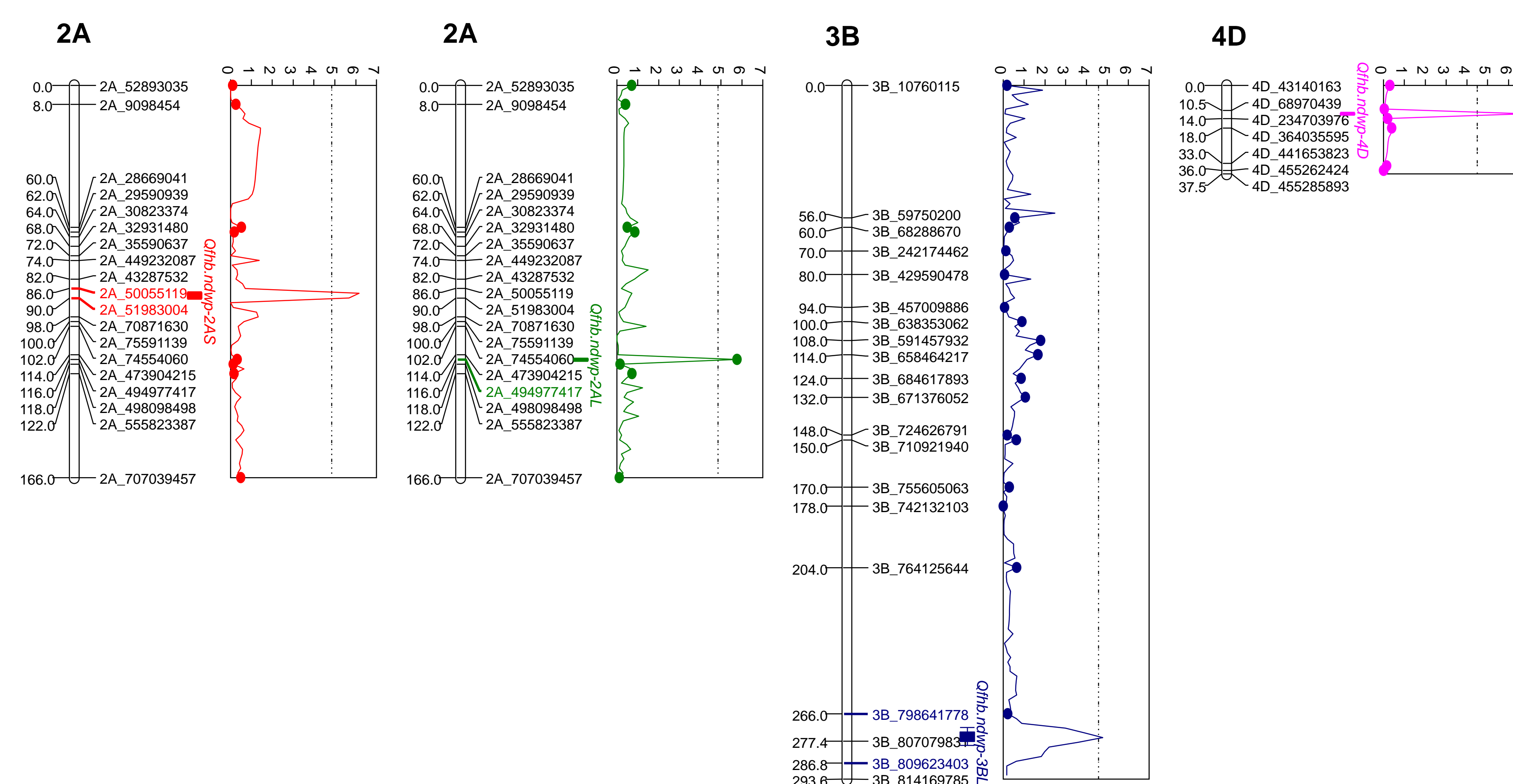


Figure 5. Putative QTL detected on chromosomes 2A, 3B, and 4D by composite interval mapping

## 4. SUMMARY

- 5370 SNP markers were mapped to 21 linkage groups covering all 21 chromosomes;
- Four QTL (*Qfhb.ndwp-2AS*, *Qfhb.ndwp-2AL*, *Qfhb.ndwp-3BL*, and *Qfhb.ndwp-4D*) for type II FHB resistance were detected in Surpresa;
- The QTL on chromosome 2A and 3B are likely novel based on physical locations of linked markers;
- The QTL for FHB resistance in Surpresa appears to be strongly affected by environment;
- Surpresa has some level of resistance to DON accumulation, however, no significant QTL were detected for resistance to DON accumulation in the greenhouse and field experiments.

## 5. ACKNOWLEDGEMENT

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