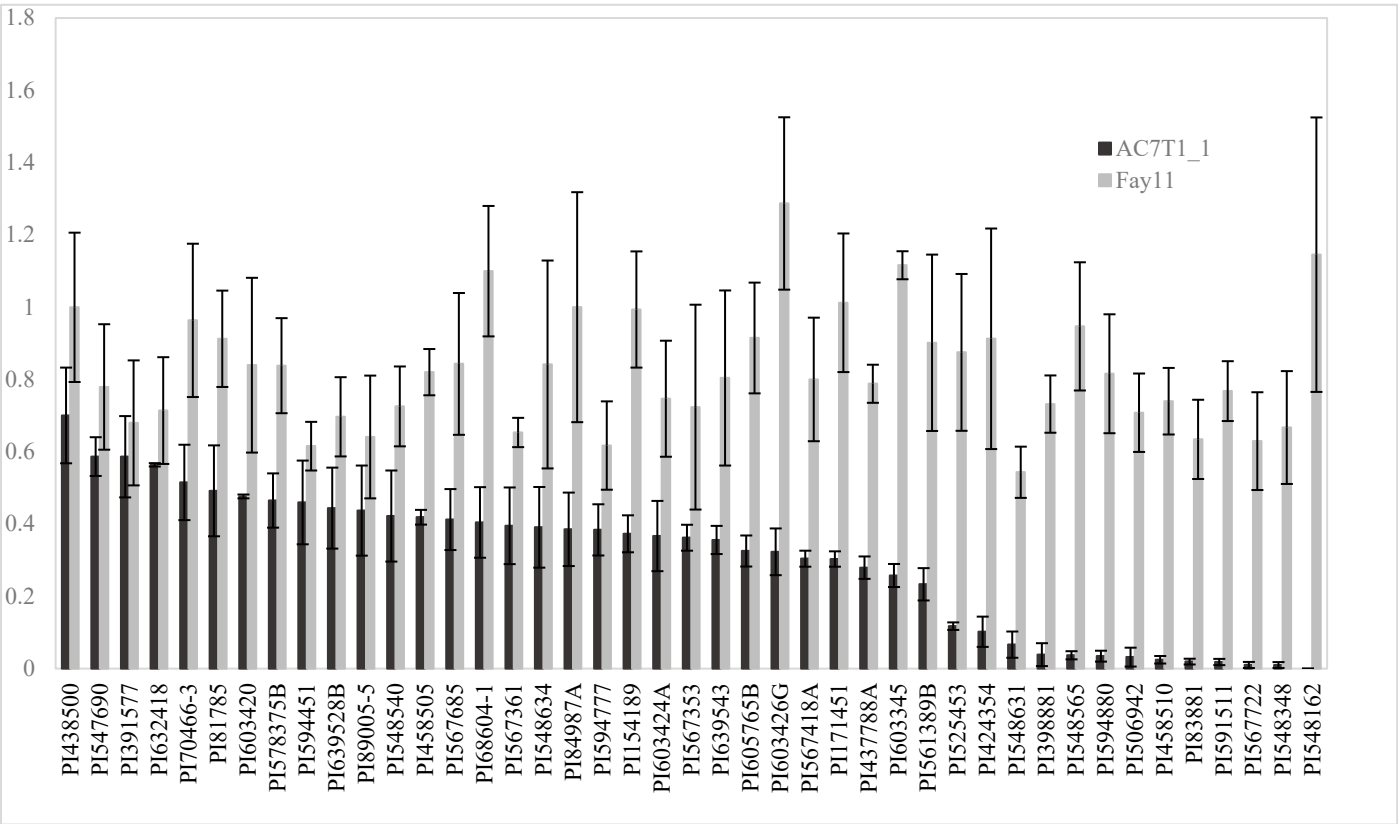

Supplemental Figure 1 Mean RRW scores with standard error bars after inoculation with *Fay11* of the 30 highest and 10 lowest RRW scoring accessions identified after inoculation with *AC7T1_1*.

Supplemental Table 1. SNP markers associated with susceptible and resistant phenotypes to *Fusarium graminearum* before FDR-adjustment.

SNP Marker	Chromosome	Position (bp)[a]	Variants	Favorable allele	MAF[b]	*p* value	B&H *p* value[c]	Effect[d]
ss715579282	1	40,820,115	C/T	C	0.47	7.51×10^{-4}	9.00×10^{-1}	0.0306
ss715579283	1	40,846,544	C/T	C	0.47	3.02×10^{-4}	8.49×10^{-1}	0.0326
ss715579290	1	40,986,460	A/G	A	0.47	7.51×10^{-4}	9.00×10^{-1}	0.0306
ss715579292	1	41,008,191	C/T	C	0.47	7.51×10^{-4}	9.00×10^{-1}	0.0306
ss715579293	1	41,041,227	G/A	A	0.46	4.36×10^{-4}	9.00×10^{-1}	0.0322
ss715579297	1	41,143,830	G/A	A	0.47	7.51×10^{-4}	9.00×10^{-1}	0.0306
ss715579298	1	41,174,361	G/A	A	0.47	7.51×10^{-4}	9.00×10^{-1}	0.0306
ss715583097	2	46,134,722	A/G	G	0.39	7.81×10^{-5}	2.37×10^{-1}	0.0376
ss715583130	2	46,379,738	A/G	G	0.48	1.66×10^{-6}	1.41×10^{-2}	0.0301
ss715584827	3	2,309,023	A/G	A	0.39	2.46×10^{-9}	1.05×10^{-4}	0.0484
ss715584672	3	19,452,288	T/C	C	0.17	7.80×10^{-5}	2.37×10^{-1}	0.0410
ss715584677	3	19,308,375	A/G	A	0.17	7.80×10^{-5}	2.37×10^{-1}	0.0410
ss715584680	3	19,202,826	T/C	C	0.17	7.80×10^{-5}	2.37×10^{-1}	0.0410
ss715584683	3	19,077,938	A/G	A	0.17	7.61×10^{-5}	2.37×10^{-1}	0.0413
ss715584686	3	19,032,505	C/T	C	0.17	7.80×10^{-5}	2.37×10^{-1}	0.0410
ss715584692	3	18,928,367	T/G	G	0.17	7.80×10^{-5}	2.37×10^{-1}	0.0410
ss715592177	5	38,944,353	T/C	C	0.20	3.32×10^{-4}	8.49×10^{-1}	0.0382
ss715592178	5	38,940,358	C/T	C	0.21	4.56×10^{-4}	9.00×10^{-1}	0.0363
ss715594767	6	47,356,804	C/A	C	0.24	1.11×10^{-6}	1.18×10^{-2}	0.0418
ss715597247	7	34,593,871	C/T	C	0.37	2.89×10^{-8}	6.15×10^{-4}	0.0431
ss715599471	8	13,661,519	A/G	A	0.35	6.23×10^{-4}	9.00×10^{-1}	0.0319
ss715610550	11	39,073,365	T/G	G	0.30	6.58×10^{-4}	9.00×10^{-1}	0.0299
ss715610570	11	38,912,266	G/A	A	0.41	7.30×10^{-5}	2.37×10^{-1}	0.0345
ss715617247	13	12,663,715	C/A	C	0.34	4.66×10^{-7}	6.60×10^{-3}	0.0381
ss715621799	15	3,923,154	A/C	C	0.20	6.24×10^{-4}	9.00×10^{-1}	0.0335
ss715621801	15	3,924,296	G/A	G	0.20	6.24×10^{-4}	9.00×10^{-1}	0.0335
ss715623260	15	9,616,878	G/A	A	0.30	4.69×10^{-4}	9.00×10^{-1}	0.0318
ss715627484	17	3,614,648	C/T	C	0.31	7.96×10^{-6}	5.64×10^{-2}	0.0361
ss715635930	19	49,928,254	C/T	T	0.22	3.95×10^{-4}	8.83×10^{-1}	0.0362

[a] Williams 82 version 4 reference genome (www.soybase.org).

[b] MAF, minor allele frequency.

[c] B&H *p*-value, FDR adjusted p-value by Benjamini and Hochberg method.

[d] Estimated effect size of the minor allele variant.