

# **Genome-wide association mapping of partial resistance to *Phytophthora sojae* in soybean plant introductions from the Republic of Korea**

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**Supplemental Tables (S1-S2) and Supplemental Figures (S1-S3).**

**Supplemental Table S1.** Summary of mean lesion lengths from tray tests and virulence profiles from hypocotyl inoculations utilizing 22 different isolates of *P. sojae*.

Isolate	Average Lesion Length (mm)		Virulence profile
	Conrad	Sloan	
1S11	14.19	16.56	1a, 1b, 1d, 1k, 2, 3a, 3b, 3c, 4, 5, 6, 7, 8
9d	ND <sup>b</sup>	ND	1a, 1b, 1c, 1d, 1k, 3a, 3b, 4, 5, 6, 7, 8
Ash 1-1	12.44	12.08	1a, 1b, 1c, 1d, 1k, 3a, 3b, 7, 8
Butler MU S.1.	9.13	15.25	1a, 1b, 1c, 1d, 1k, 3a, 7
<b>C2S1<sup>a</sup></b>	<b>12.50</b>	<b>ND</b>	<b>1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 4, 5, 6, 7, 8</b>
DFL-1	5.94	20.19	1a, 1b, 1d, 1k, 7
DP5	16.44	18.63	1a, 1b, 1d, 1k, 3a, 7, 8
MMI12004_04_0.2	18.19	29.94	1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 4, 5, 6, 7
OH1200110.1	15.88	20.69	1a, 1b, 1c, 3a, 3b, 5, 6, 7, 8
OH120049.1	23.38	16.88	1a, 1c, 1d, 1k, 2, 3a, 3b, 3c, 5, 7, 8
OH120484.1	15.78	ND	1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 5, 7, 8
OH121033.4	15.38	21.94	1a, 1b, 1c, 1d, 1k, 2, 3a, 3c, 4, 7, 8
OH121047.1	ND	ND	1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 5, 6, 7, 8
OH121074.4	10.00	ND	1a, 1b, 1c, 1d, 1k, 3a, 3b, 3c, 4, 5, 7, 8
<b>OH121086.3</b>	<b>14.00</b>	<b>23.00</b>	<b>1a, 1b, 1c, 1d, 1k, 2, 3a, 3c, 4, 5, 6, 7, 8</b>
OH121087.1	19.88	22.06	1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 5, 6, 7
OH121108.2	16.69	22.43	1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 4, 5, 6, 7, 8
OH121187.2	12.00	20.63	1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 4, 5, 6, 7
OH121189.1	20.92	ND	1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 4, 5, 6, 7, 8
OH121215.1	25.56	21.81	1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 5, 6, 7, 8
OH121018.1	17.31	16.13	1a, 1b, 1c, 1d, 1k, 2, 3a, 3c, 5, 7, 8
OH121215.1	29.88	28.26	1a, 1b, 1c, 1d, 2, 3a, 3b, 3c, 4, 5, 6, 7, 8

<sup>a</sup> Isolates selected for disease assays in this study are indicated in bold.

<sup>b</sup> ND: Not determined

**Supplemental Table S2a.** Hypocotyl assay with isolate C2S1 and genotypic data of markers within QTL for 94 randomly selected accessions included in the GWA analysis.

Accession	No. seedlings dead/Total no. seedlings <sup>a</sup>	Resistant (R) or susceptible (S) allele for significant markers at each QTL															
		ss715585712 (QTL 3-1)	ss715585728 (QTL 3-1)	ss715586320 (QTL 3-2)	ss715586321 (QTL 3-2)	ss715586376 (QTL 3-3)	ss715615031 (QTL 13-1)	ss715635897 (QTL 19-1)	ss715635934 (QTL 19-2)	ss715636056 (QTL 19-3)	ss715636059 (QTL 19-3)	ss715636064 (QTL 19-3)	ss715636073 (QTL 19-3)	ss715636076 (QTL 19-3)	ss715636077 (QTL 19-3)	ss715636083 (QTL 19-3)	ss715636084 (QTL 19-3)
PI 398588	6/6	R	S	R	S	S	S	S	S	S	S	S	R	R	R	R	R
PI 398600	8/8	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398601	8/8	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398604	5/5	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398620	5/5	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398624	4/4	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398627	4/4	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398637	8/8	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398638	8/8	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398639	7/7	S	R	S	R	S	R	S	S	S	S	S	R	R	R	R	R
PI 398641	4/4	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398642	5/5	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398644	6/6	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398654	4/4	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398655	6/6	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398657	5/5	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398686	6/6	R	S	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398696	6/6	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398698	4/4	R	S	R	S	S	R	S	S	S	S	S	R	R	R	R	R
PI 398706	7/7	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398708	7/7	R	S	R	S	S	S	S	S	S	S	S	R	R	R	R	R
PI 398710	9/9	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398712	6/6	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398727	5/5	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398735	5/5	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398744	4/4	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398750	10/10	R	S	R	S	S	S	S	S	S	S	S	R	R	R	R	R
PI 398751	6/6	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398752	8/8	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398753	4/4	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398754	6/6	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398776	8/8	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398788	7/7	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398802	5/5	R	S	R	S	S	S	S	S	S	S	S	R	R	R	R	R
PI 398803	6/6	R	R	R	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398806	8/8	S	R	S	R	S	R	S	S	S	S	S	R	R	R	R	R
PI 398807	4/4	S	R	S	R	R	R	R	S	S	S	S	R	R	R	R	R
PI 398808	5/5	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398813	7/7	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398814	5/5	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398816	4/4	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398820	4/4	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398821	9/9	S	R	S	R	R	R	R	S	S	S	S	R	R	R	R	R
PI 398822	8/8	S	R	S	R	R	R	R	S	S	S	S	R	R	R	R	R
PI 398831	8/8	S	R	S	R	R	R	R	S	S	S	S	R	R	R	R	R
PI 398832	5/5	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R

PI 398843	9/9	R	S	S	R	S	S	S	S	S	S	S	R	R	R	R	R
PI 398858	5/5	R	S	R	S	S	R	S	S	S	S	S	R	R	R	R	R
PI 398868	5/5	S	R	S	R	S	R	S	S	S	S	S	R	R	R	R	R
PI 398871	4/4	R	S	R	S	R	S	S	S	S	S	S	R	R	R	R	R
PI 398878	8/8	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398881	9/9	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398883	5/5	S	R	S	R	R	S	S	S	S	S	S	R	R	R	R	R
PI 398885	6/6	S	R	S	R	R	S	S	S	S	S	S	R	R	R	R	R
PI 398886	5/5	R	S	R	S	S	S	S	S	S	S	S	R	R	R	R	R
PI 398887	7/7	R	S	R	S	S	S	S	S	S	S	S	R	R	R	R	R
PI 398888	6/6	S	R	S	R	R	S	S	S	S	S	S	R	R	R	R	R
PI 398889	6/6, 7/7	S	R	S	R	R	S	S	S	S	S	S	R	R	R	R	R
PI 398891	6/6	S	R	S	R	R	S	S	S	S	S	S	R	R	R	R	R
PI 398898	8/8	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398899	8/8	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398901	4/4	S	R	S	R	R	S	S	S	S	S	S	R	R	R	R	R
PI 398908	7/7	S	R	S	R	R	S	S	S	S	S	S	R	R	R	R	R
PI 398921	8/8	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398923	7/7	R	S	S	R	S	R	S	S	S	S	S	R	R	R	R	R
PI 398924	10/10	S	R	S	R	R	S	S	S	S	S	S	R	R	R	R	R
PI 398927	4/4	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398929	5/5	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398930	8/8	S	R	S	R	R	S	S	S	S	S	S	R	R	R	R	R
PI 398931	6/6	S	R	S	R	R	S	S	S	S	S	S	R	R	R	R	R
PI 398934	10/10	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398936	5/5	R	S	S	R	S	R	S	S	S	S	S	R	R	R	R	R
PI 398941	7/7	S	R	S	R	R	S	S	S	S	S	S	R	R	R	R	R
PI 398942	5/5	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398953	10/10	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398957	5/5	S	R	S	R	S	S	S	S	S	S	S	R	R	R	R	R
PI 398960	6/6	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398980	6/6	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 398982	6/6	S	R	R	S	S	S	S	S	S	S	S	R	R	R	R	R
PI 398987	4/4	S	R	S	R	R	S	S	S	S	S	S	R	R	R	R	R
PI 398990	5/5	R	S	R	S	S	R	S	S	S	S	S	R	R	R	R	R
PI 398995	8/8	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 399010	6/6	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 399011	7/7	S	R	S	R	R	S	S	S	S	S	S	R	R	R	R	R
PI 399018	6/6	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 399028	5/5	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 399031	4/4	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 399034	6/6	S	R	S	R	R	S	S	S	S	S	S	R	R	R	R	R
PI 399035	8/8	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 399039	7/7	S	R	S	R	R	S	S	S	S	S	S	R	R	R	R	R
PI 399043	5/5	S	R	S	R	R	R	S	S	S	S	S	R	R	R	R	R
PI 399046	7/7	S	R	S	R	R	S	S	S	S	S	S	R	R	R	R	R
PI 399051	7/7	S	R	S	R	R	S	S	S	S	S	S	R	R	R	R	R
PI 399063	4/4	S	R	S	R	R	S	S	S	S	S	S	R	R	R	R	R

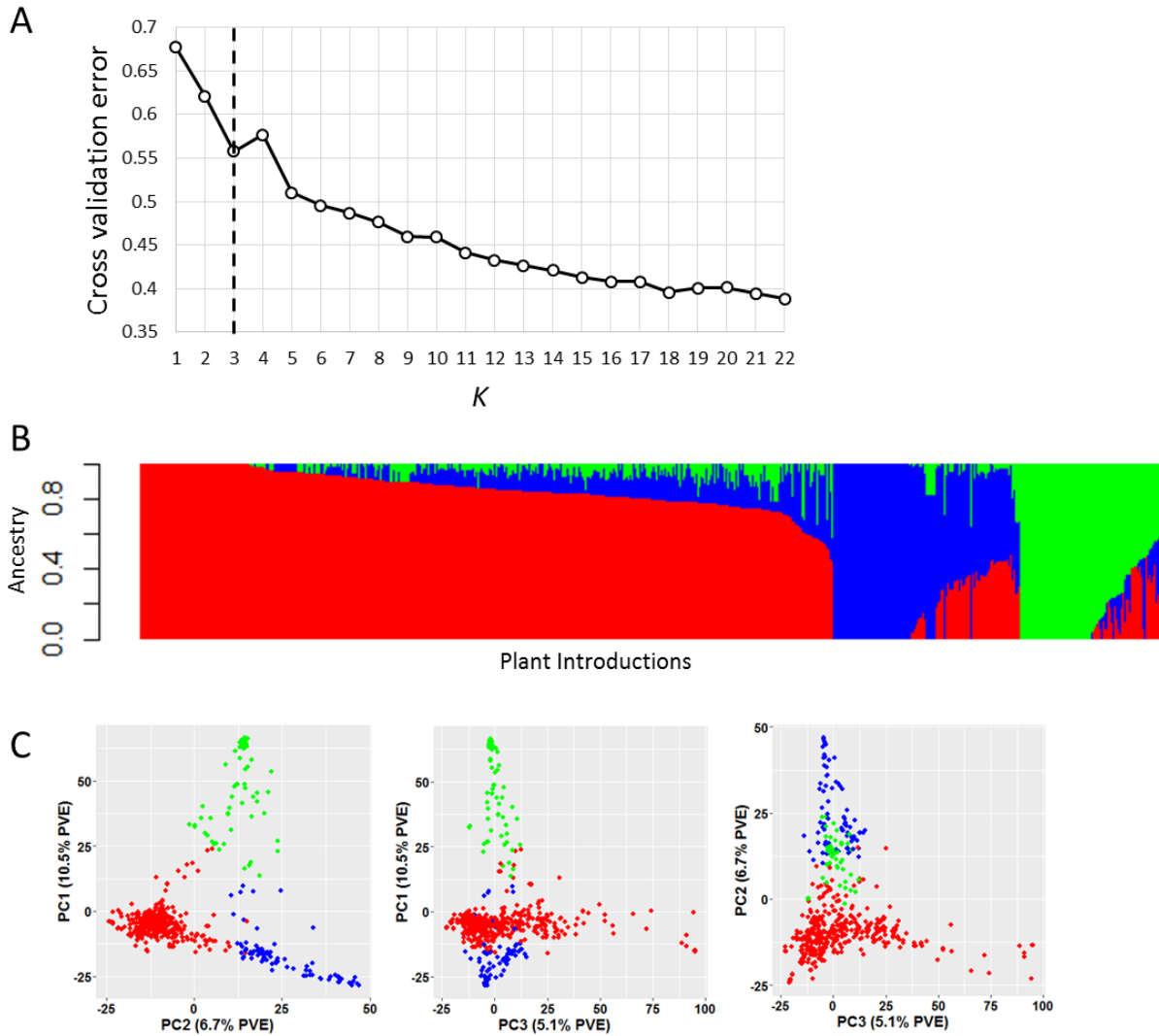
<sup>a</sup> Greater than 75% survival is considered an incompatible reaction, indicating avirulence of the isolate.

**Supplemental Table S2b.** Hypocotyl assay of differentials for isolate C2S1.

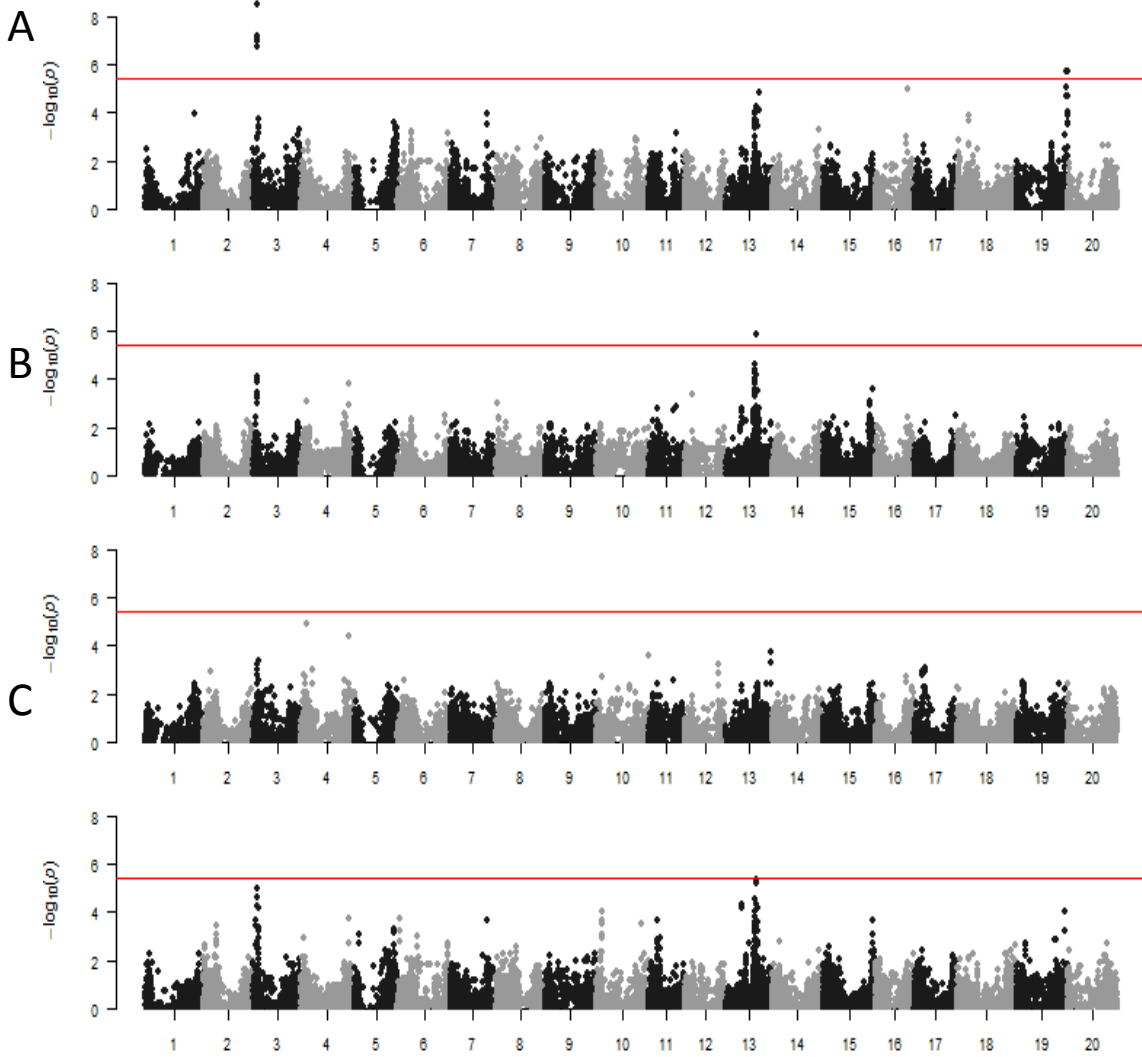
Differential line <sup>b</sup>	No. seedlings dead/ Total no. seedlings <sup>a</sup>			
	Rep 1	Rep 2	Rep 3	Rep 4
Williams	12/12	8/8	7/7	9/9
Harlon	10/10	10/10	8/8	8/8
Harosoy 13XX	10/10	11/11	9/9	7/7
Williams 79	9/9	7/7	8/8	7/7
PI 103091	10/10	7/7	6/7	9/9
Williams 82	8/8	10/10	8/8	6/6
L76-1988	9/9	12/12	10/10	8/8
L83-570	10/10	9/9	11/11	11/11
PRX 146-36	7/7	8/8	2/10	9/9
PRX 145-48	11/11	8/8	12/12	9/9
L85-2352	7/7	7/7	10/11	5/5
L85-3059	11/11	10/10	10/10	8/8
Harosoy 62XX	7/7	11/11	10/10	9/9
Harosoy	12/12	9/9	11/11	8/8
PI 399073	5/5	6/6	4/5	5/5

<sup>a</sup> Greater than 75% survival is considered an incompatible reaction, indicating avirulence of the isolate.

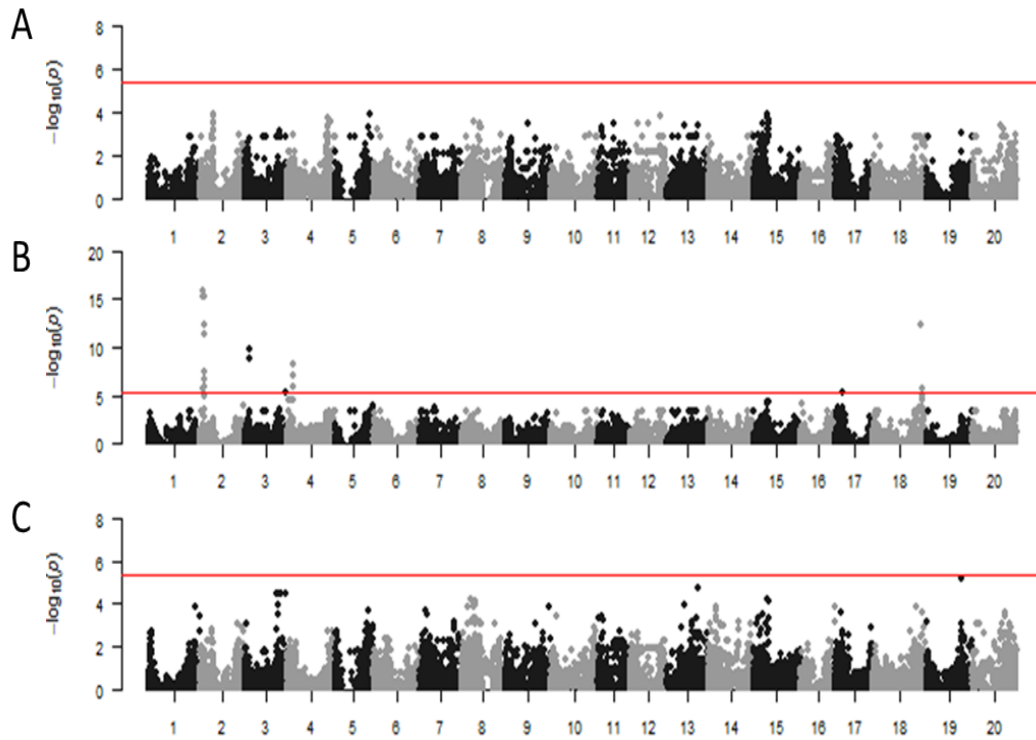
<sup>b</sup> The Rps genotype of the soybean differentials used to verify the pathotype of C2S1 were as follows: Williams (*rps/rps*), Harlon (*Rps1a/Rps1a*), Harosoy 13XX (*Rps1b/Rps1b*), Williams 79 (*Rps1c/Rps1c*), PI 103091 (*Rps1d/Rps1d*), Williams 82 (*Rps1k/Rps1k*), L76-1988 (*Rps2/Rps2*), L83-570 (*Rps3a/Rps3a*), PRX 146-36 (*Rps3b/Rps3b*), PRX 145-48 (*Rps3c/Rps3c*), L85-2352 (*Rps4/Rps4*), L85-3059 (*Rps5/Rps5*), Harosoy 62XX (*Rps6/Rps6*), Harosoy (*Rps7/Rps7*), and PI 399073 (*Rps8/Rps8*).



**Supplemental Figure S1.** Examination of population structure of 800 Plant Introductions. Cross validation cross validation error from analysis with ADMIXTURE [1] at  $K = 1$  to  $K = 22$ , where the vertical dashed line corresponds with the selected value of  $K$  (A). Ancestry of plant introductions based on at  $K=3$  (B). Dispersion of predicted populations at  $K=3$  based on the first three principle components (PCs) with percent variance explained (PVE) for each PC indicated in parentheses (C).



**Supplemental Figure S2.** Manhattan plot of the soybean genome depicting the extent of associations of 19,138 SNPs with inoculated root rot score (A), inoculated root weight (B), inoculated shoot weight (C), and inoculated plant height (D). The  $-\log_{10}(p)$ -value on the y-axis is a measure of the degree to which a SNP is associated with the trait. Chromosomes are displayed on the x-axis. The red horizontal line indicates the genome-wide threshold for significance.



**Supplemental Figure S3.** Manhattan plot of the soybean genome depicting the extent of associations of 19,138 SNPs with non-inoculated root weight (A), non-inoculated shoot weight (B), and non-inoculated plant height (C). The  $-\log_{10}(p\text{-value})$  on the y-axis is a measure of the degree to which a SNP is associated with the trait. Chromosomes are displayed on the x-axis. The red horizontal line indicates the genome-wide threshold for significance.

## References

1. Alexander DH, Novembre J, Lange K. Fast model-based estimation of ancestry in unrelated individuals. *Genome Res.* 2009, 19:1655–1664.