

**Table S2 Chromosome locations, and other summary statistics for SNPs significantly associated with stalk rot resistance in the overall combined, Manhattan combined and Ottawa performed using the unified mixed model.**

Chromosome	SNP Physical Position, bp	P-Value	MAF <sup>a</sup>	Disease traits <sup>b</sup>
Combined analysis				
9	57816733	2.87E-06	0.28	MLL ( <i>FT</i> )
9	57272115	4.18E-06	0.25	MLL ( <i>FT</i> )
6	60030948	5.65E-06	0.10	MLL ( <i>FT</i> )
9	57222599	1.48E-07	0.28	MLL ( <i>MP</i> )
9	57476134	2.28E-07	0.30	MLL ( <i>MP</i> )
9	57272296	5.58E-07	0.27	MLL ( <i>MP</i> )
9	56152890	6.56E-07	0.34	MLL ( <i>MP</i> )
9	57169768	7.50E-07	0.23	MLL ( <i>MP</i> )
9	57272115	7.72E-07	0.25	MLL ( <i>MP</i> )
3	60176979	4.97E-05	0.23	RMLL ( <i>FT</i> )
2	64623580	9.16E-05	0.44	RMLL ( <i>FT</i> )
7	58280357	1.43E-05	0.35	RMLL ( <i>MP</i> )
7	56256841	1.95E-05	0.39	RMLL ( <i>MP</i> )
3	60176979	7.62E-05	0.23	RTLL ( <i>FT</i> )
7	56152038	1.35E-05	0.47	RTLL ( <i>MP</i> )
9	56152890	1.87E-05	0.34	RTLL ( <i>MP</i> )
9	57272115	1.72E-06	0.25	TLL ( <i>FT</i> )
9	57222599	2.07E-06	0.28	TLL ( <i>FT</i> )
9	57816733	2.66E-06	0.28	TLL ( <i>FT</i> )
9	57222599	8.93E-08	0.28	TLL ( <i>MP</i> )
9	56152890	1.17E-07	0.34	TLL ( <i>MP</i> )
9	57476134	2.25E-07	0.30	TLL ( <i>MP</i> )
9	56508161	4.94E-07	0.41	TLL ( <i>MP</i> )
9	57236778	5.82E-07	0.29	TLL ( <i>MP</i> )
9	57272296	6.91E-07	0.27	TLL ( <i>MP</i> )
9	57272115	7.47E-07	0.25	TLL ( <i>MP</i> )
9	56562984	9.71E-07	0.34	TLL ( <i>MP</i> )
Manhattan combined analysis				
9	57272115	2.93E-06	0.25	MLL ( <i>FT</i> )
9	57816733	3.36E-06	0.28	MLL ( <i>FT</i> )
9	57383556	6.39E-06	0.30	MLL ( <i>FT</i> )
9	57236791	6.70E-06	0.30	MLL ( <i>FT</i> )
9	57272115	4.04E-07	0.25	MLL ( <i>MP</i> )
9	57272296	6.16E-07	0.27	MLL ( <i>MP</i> )
9	57476134	6.53E-07	0.30	MLL ( <i>MP</i> )
9	57169768	6.69E-07	0.23	MLL ( <i>MP</i> )
9	57383556	9.89E-07	0.30	MLL ( <i>MP</i> )

Chromosome	SNP Physical Position, bp	P-Value	MAF <sup>a</sup>	Disease traits <sup>b</sup>
2	60129082	9.67E-06	0.40	RMLL ( <i>MP</i> )
6	59739236	1.89E-05	0.46	RTLL ( <i>FT</i> )
2	64623580	1.61E-05	0.44	RMLL ( <i>FT</i> )
7	59890439	1.07E-05	0.32	RTLL ( <i>MP</i> )
9	57272115	2.48E-06	0.25	TLL ( <i>FT</i> )
9	57816733	5.56E-06	0.28	TLL ( <i>FT</i> )
9	57236791	6.72E-06	0.30	TLL ( <i>FT</i> )
9	56152890	2.82E-07	0.34	TLL ( <i>MP</i> )
9	57272115	4.34E-07	0.25	TLL ( <i>MP</i> )
9	57383556	4.99E-07	0.30	TLL ( <i>MP</i> )
9	57222599	5.93E-07	0.28	TLL ( <i>MP</i> )
9	57476134	9.28E-07	0.30	TLL ( <i>MP</i> )
Ottawa analysis				
1	11814753	1.70E-05	0.12	MLL ( <i>FT</i> )
4	55646941	1.78E-05	0.31	MLL ( <i>FT</i> )
2	69967056	3.73E-05	0.17	MLL ( <i>MP</i> )
1	42155829	5.19E-05	0.10	MLL ( <i>MP</i> )
3	60195553	4.48E-05	0.31	RMLL ( <i>FT</i> )
4	55646941	6.59E-05	0.31	RMLL ( <i>FT</i> )
1	66836006	1.20E-05	0.08	RMLL ( <i>MP</i> )
8	51279094	2.55E-05	0.40	RMLL ( <i>MP</i> )
6	54221186	6.27E-05	0.17	RTLL ( <i>FT</i> )
10	3137796	8.26E-05	0.17	RTLL ( <i>FT</i> )
1	61119284	2.68E-05	0.32	RTLL ( <i>MP</i> )
8	51279094	3.48E-05	0.40	RTLL ( <i>MP</i> )
10	3137796	2.38E-05	0.17	RTLL ( <i>FT</i> )
9	56802949	2.61E-05	0.18	RTLL ( <i>FT</i> )
1	27040589	6.39E-05	0.32	TTL ( <i>MP</i> )
1	61119285	6.57E-05	0.32	TTL ( <i>MP</i> )

<sup>a</sup>MAF, minor allele frequency.

<sup>b</sup>Disease traits: TLL and MLL – total lesion length and major lesion length, respectively; RTLL and RMLL – relative total lesion length and relative major lesion length, respectively; *MP* and *FT* – *Macrophomina phaseolina* and *Fusarium thapsinum*, respectively.