

Supplemental Table 1. Genotypes of QTL detected using 199 RILs and phenotype of RILs('Tokei 758'/'To-8E')

QTL detected using 199 RILs			Number of RILs ^c	Percent number of cysts ^d			t-test <i>P</i> ^d	Reported resistant gene /QTL in the location
Chromosome	Marker interval ^a	Allele ^b		Average	SD			
4	Satt607 - <u>AW277661</u>	<u>To-8E</u>	91	44.5	± 12.4	ns		
		Tokei 758	107	45.4	± 10.3			
18	<u>Sat_210</u> - Satt235	<u>To-8E</u>	58	36.7	± 13.0	2.91E-12	<i>rhg1</i>	
		Tokei 758	140	48.5	± 5.2			
18	Satt199 - <u>Satt288</u>	To-8E	93	45.7	± 12.4	ns		
		<u>Tokei 758</u>	106	44.3	± 10.3			

^a Nearest marker is underlined

^b Resistant allele is underlined.

^c RILs were grouped according to genotype of the nearest marker in each QTL region.

^d Percent number of cysts to that of susceptible control variety, 'Suzumaru'.

Supplemental Table 2. Segregation distortion in RILs('Tokei 758'/'To-8E')

Total number of RILs	Observed number of RILs			Expected rate of resistant RILs
	Resistant	Susceptible		
199	8	198	2 loci	$1/2 \times 1/2$
			3 loci	$1/2 \times 1/2 \times 1/2$
			4 loci	$1/2 \times 1/2 \times 1/2 \times 1/2$

Expected segregation rate	Expected value		P-value	
	Resistant	Susceptible		
1:3	49.8	149.3	9.43E-13	***
1:7	24.9	174.1	1.25E-04	***
1:15	12.4	186.6	0.131	ns