

Table S1. Infection type (IT) scores and reaction types of 45 germplasm with a known leaf rust resistance gene. These accessions were inoculated with *Pt2013* in 2015, and *Pt52-2* and *Pt54-1* in 2016.

Accession	<i>Lr</i> gene	<i>Pt2013</i>		<i>Pt52-2</i>		<i>Pt54-1</i>	
		IT score	Reaction type*	IT score	Reaction type*	IT score	Reaction type*
GSTR402	<i>Lr1</i>	9	HS	9	HS	7	MS
GSTR403	<i>Lr2a</i>	9	HS	1	HR	6	MS
GSTR 404	<i>Lr2b</i>	9	HS	1	HR	6	MS
GSTR 405	<i>Lr2c</i>	9	HS	2	HR	6	MS
GSTR 406	<i>Lr3</i>	9	HS	9	HS	7	MS
GSTR 407	<i>Lr3bg</i>	9	HS	9	HS	7	MS
GSTR 408	<i>Lr3ka</i>	9	HS	8	HS	7	MS
GSTR 409	<i>Lr9</i>	8	HS	7	MS	6	MS
GSTR 410	<i>Lr10</i>	9	HS	8	HS	8	HS
GSTR 411	<i>Lr11</i>	7	MS	5	MR	5	MR
GSTR 412	<i>Lr12</i>	9	HS	8	HS	7	MS
GSTR 413	<i>Lr13</i>	7	MS	8	HS	7	MS
GSTR 414	<i>Lr14a</i>	8	HS	8	HS	6	MS
GSTR 415	<i>Lr14b</i>	9	HS	9	HS	6	MS
GSTR 416	<i>Lr15</i>	8	HS	9	HS	6	MS
GSTR 417	<i>Lr16</i>	8	HS	4	MR	6	MS
GSTR 418	<i>Lr17</i>	8	HS	8	HS	5	MR
GSTR 419	<i>Lr18</i>	5	MR	2	HR	2	HR
GSTR 420	<i>Lr19</i>	0;	HR	0	HR	1	HR
GSTR 421	<i>Lr20</i>	9	HS	8	HS	4	MR
GSTR 422	<i>Lr21</i>	6	MS	3	HR	2	HR
GSTR 423	<i>Lr22a</i>	9	HS	8	HS	5	MR
GSTR 424	<i>Lr23</i>	7	MS	8	HS	6	MS
GSTR 425	<i>Lr24</i>	8	HS	2	HR	6	MS
GSTR 426	<i>Lr25</i>	1	HR	1	HR	2	HR
GSTR 427	<i>Lr26</i>	6	MS	6	MS	5	MR
GSTR 428	<i>Lr28</i>	8	HS	1	HR	4	MR
GSTR 429	<i>Lr29</i>	3	HR	1	HR	2	HR
GSTR 430	<i>Lr30</i>	7	MS	7	MS	5	MR
GSTR 431	<i>Lr32</i>	8	HS	7	MS	4	MR
GSTR 432	<i>Lr33</i>	9	HS	4	MR	5	MR
GSTR 434	<i>Lr35</i>	8	HS	9	HS	5	MR
GSTR 435	<i>Lr36</i>	6	MS	2	HR	2	HR
GSTR 436	<i>Lr37</i>	9	HS	8	HS	7	MS
GSTR 437	<i>Lr38</i>	5	MR	1	HR	2	HR

GSTR 438	<i>Lr44</i>	9	HS	6	MS	6	MS
GSTR 439	<i>Lr45</i>	3	HR	1	HR	2	HR
GSTR 440	<i>Lr47</i>	1	HR	1	HR	1	HR
GSTR 441	<i>Lr51</i>	1	HR	2	HR	2	HR
GSTR 442	<i>Lr52</i>	5	MR	3	HR	4	MR
GSTR 443	<i>Lr60</i>	7	MS	2	HR	2	HR
GSTR 444	<i>Lr63</i>	4	MR	0	HR	2	HR
GSTR 445	<i>Lr64</i>	6	MS	2	HR	2	HR
GSTR 446	<i>LrB</i>	9	HS	6	MS	7	MS

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\*: HR: highly resistant; MR: moderately resistant; MS: moderately susceptible; HS: highly susceptible

Table S2. Designated name, representative SNP (TagSNP), chromosome arm, location on the Illumina SNP9K consensus map,  $p$ -value, and  $R^2$  value of each QTL that was significant at a false discovery rate of 0.05 when the association panel was evaluated using *Pt* pathotypes *Pt2013*, *Pt52-2* and *Pt54-1*.

	QTL	tagSNP	SNPs	Chromosome arm	Map location (cM)	$P$ -value	$R^2$ (%)
<i>Pt2013</i>	Qlr.stars-1AC1	<i>IWA7115</i>	2	1AC	48.55-51.13	1.79E-04	1.11
	Qlr.stars-1AL1	<i>IWA8198</i>	5	1AL	69.30-69.98	3.10E-04	1.03
	<i>Qlr.stars-1BS3</i>	<i>IWA5702</i>	1	1BS	30.23	1.09E-04	1.18
	<i>Qlr.stars-2BL2</i>	<i>IWA837</i>	1	2BL	179.53	4.74E-04	0.97
	Qlr.stars-4AL1	<i>IWA5699</i>	2	4AL	73.40-83.38	2.25E-04	1.08
	<i>Qlr.stars-4BL1</i>	<i>IWA2823</i>	2	4BL	72.30-82.131	2.29E-04	1.08
	<i>Qlr.stars-7AL2</i>	<i>IWA808</i>	1	7AL	104.37	1.60E-04	1.13
<i>Pt52-2</i>	Qlr.stars-2DL2	<i>IWA7332</i>	1	2DL	141.20	2.92E-04	1.08
	Qlr.stars-1AL2	<i>IWA2314</i>	1	1AL	99.76	2.21E-04	1.13
	<i>Qlr.stars-1BL1</i>	<i>IWA3892</i>	1	1BL	153.09	6.68E-05	1.28
	<i>Qlr.stars-1BL4</i>	<i>IWA5445</i>	1	1BL	132.02	2.26E-04	1.11
	<i>Qlr.stars-1BL5</i>	<i>IWA2928</i>	1	1BL	170.89	5.39E-04	1.00
	<i>Qlr.stars-1DC1</i>	<i>IWA362</i>	1	1DC	48.81	1.08E-04	1.29
	<i>Qlr.stars-2AL1</i>	<i>IWA2230</i>	3	2AL	179.25	5.96E-04	0.98
	<i>Qlr.stars-2BL1</i>	<i>IWA1488</i>	1	2BL	193.90	6.04E-05	1.29
	<i>Qlr.stars-2BC1</i>	<i>IWA3657</i>	2	2BC	142.87	3.06E-04	1.08
	<i>Qlr.stars-3AS1</i>	<i>IWA5067</i>	1	3AS	53.98	2.25E-04	1.11
	<i>Qlr.stars-3AC1</i>	<i>IWA2095</i>	1	3AC	75.97	1.70E-04	1.15
	<i>Qlr.stars-3AL1</i>	<i>IWA4810</i>	4	3AL	133.79-143.93	1.31E-04	1.19
	<i>Qlr.stars-3BS1</i>	<i>IWA4796</i>	1	3BS	13.45	4.59E-04	1.04
	<i>Qlr.stars-4AL3</i>	<i>IWA4859</i>	1	4AL	206.49	4.50E-04	1.69
	<i>Qlr.stars-4BS1</i>	<i>IWA3290</i>	1	4BS	29.89	4.69E-04	1.02
	<i>Qlr.stars-4DC1</i>	<i>IWA5381</i>	1	4DC	80.68	4.64E-04	1.02

	<i>Qlr.stars-5BS1</i>	<i>IWA868</i>	1	5BS	4.18	1.15E-04	1.20
	<i>Qlr.stars-5BS2</i>	<i>IWA7400</i>	1	5BS	18.55	6.32E-05	1.28
	<i>Qlr.stars-5BS3</i>	<i>IWA1176</i>	1	5BS	54.10	1.38E-04	1.18
	<i>Qlr.stars-6AL1</i>	<i>IWA6116</i>	2	6AL	186.76-197.39	9.28E-05	1.23
	<i>Qlr.stars-6BL2</i>	<i>IWA596</i>	1	6BL	78.37	5.76E-04	0.99
	<i>Qlr.stars-7AS2</i>	<i>IWA2042</i>	1	7AS	63.61	3.50E-04	1.06
	<i>Qlr.stars-7AL2</i>	<i>IWA4062</i>	2	7AL	102.48	1.67E-04	1.16
	<i>Qlr.stars-7BC1</i>	<i>IWA2353</i>	1	7BC	48.48	6.88E-05	1.27
	<i>Qlr.stars-7BL1</i>	<i>IWA3387</i>	1	7BL	132.06	1.86E-04	1.54
<i>Pt54-1</i>	<i>Qlr.stars-5AC1</i>	<i>IWA5884</i>	1	5AC	71.41	7.05E-05	1.26
	<i>Qlr.stars-6BC1</i>	<i>IWA6293</i>	1	6BC	62.22	2.22E-04	1.10
	<i>Qlr.stars-1DC1</i>	<i>IWA362</i>	1	1DC	48.81	4.73E-04	1.04
	<i>Qlr.stars-1BS3</i>	<i>IWA5702</i>	1	1BS	30.23	4.32E-05	1.10

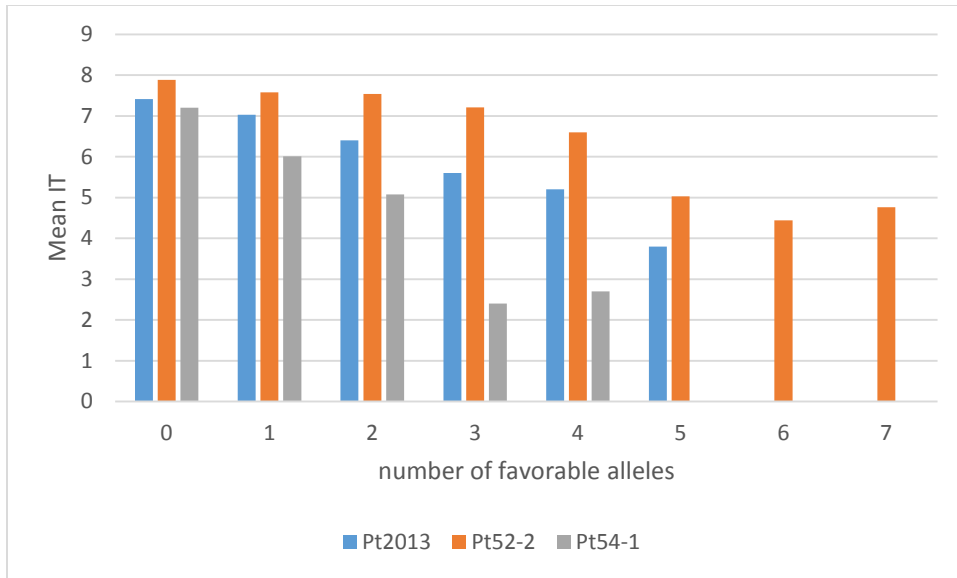


Figure S1. Mean IT scores of germplasm with different favorable alleles at seven loci in the *Pt2013*, eight loci in the *Pt52-2*, and five loci in the *Pt54-1* experiments.