

Supplementary Figures

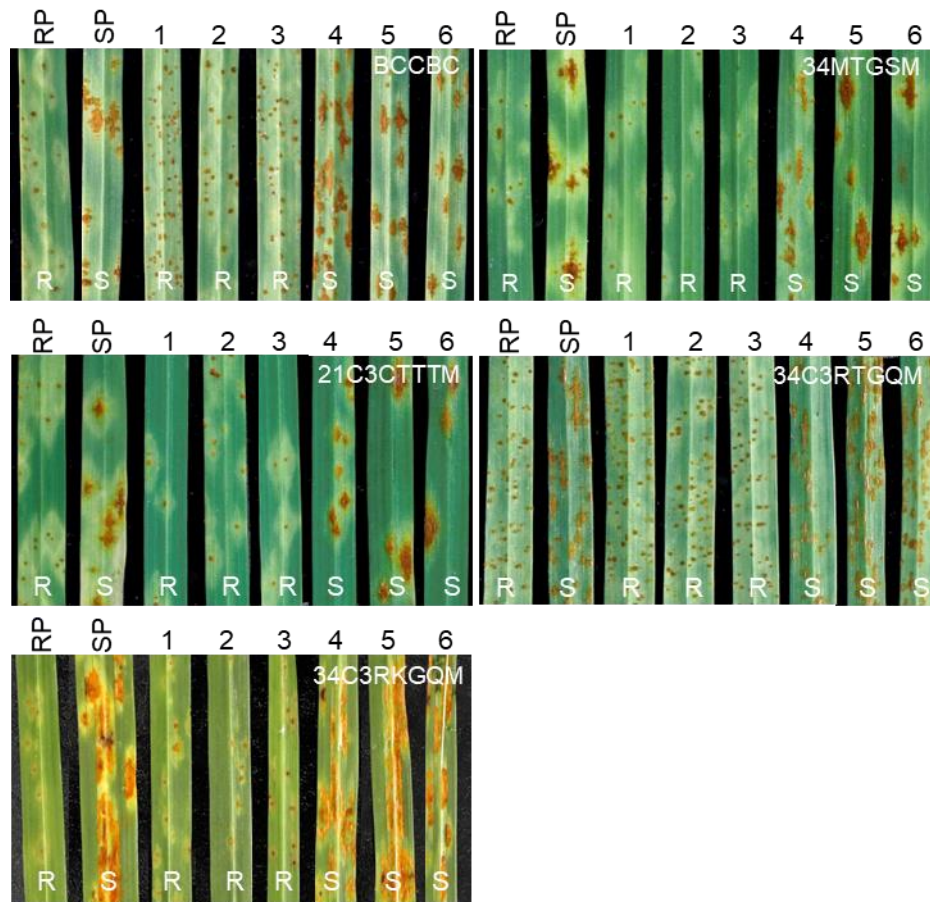


Figure S1 Infection types to *Pgt* races BCCBC, 34MTGSM, 21C3CTTTM, 34C3RTGQM, and 34C3RKGQM in F_{2:3} families selected from the PI 94701 × Rusty cross. Plants were grown in five independent growth chambers at 22-24 °C with 16 h light/8 h dark. RP, resistant parent; SP, susceptible parent; 1-3, resistant F₃ plants; 4-6, susceptible F₃ plants; R, resistant; S, susceptible.

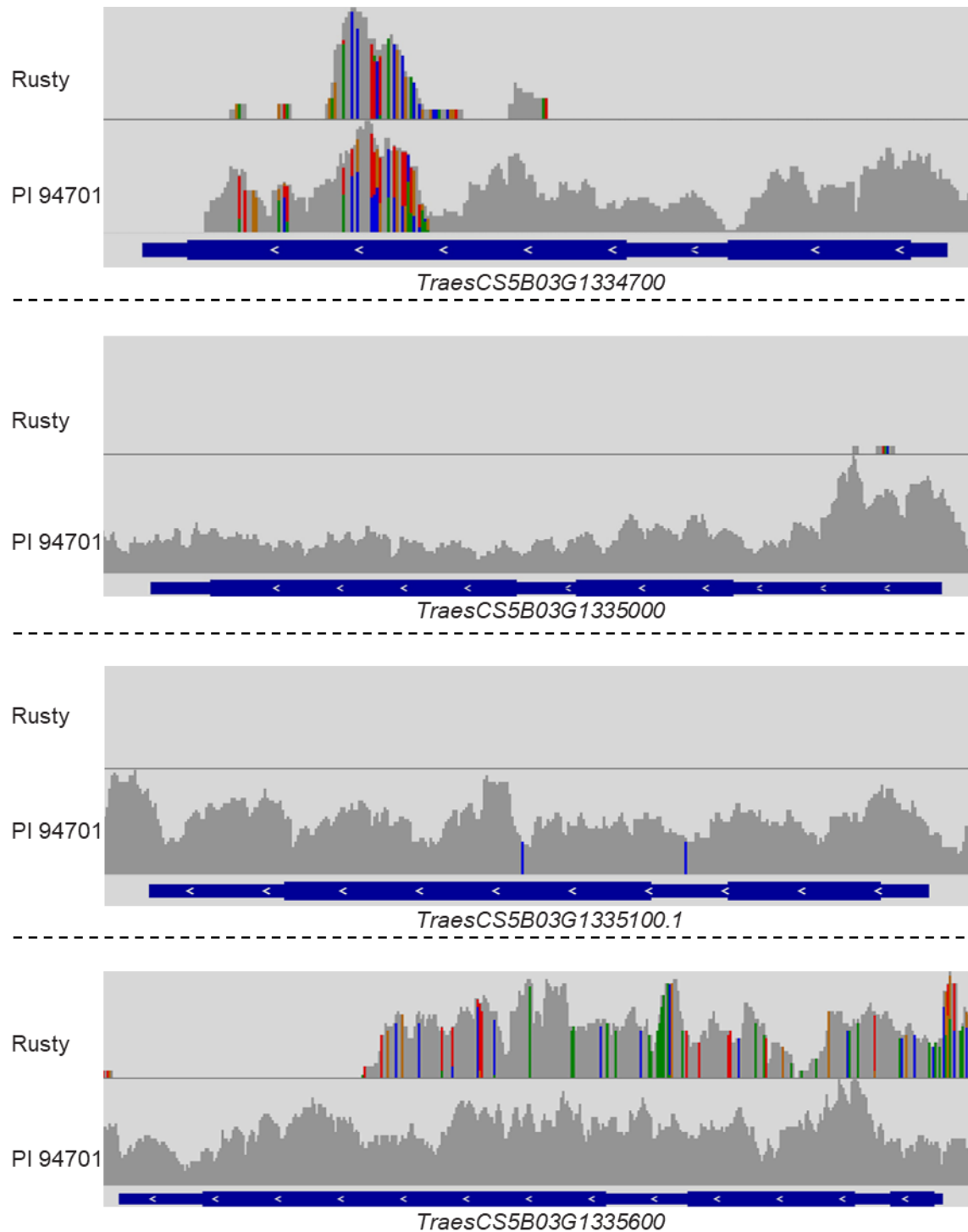


Figure S2 Comparison of the whole-genome resequencing reads from Rusty and PI 94701 for the candidate genes using the alignment algorithm BWA-MEM. For genes *TraesCS5B03G1335000* and *TraesCS5B03G1335100.1*, no reads from Rusty were detected in the whole-genome sequencing data. The image illustrates sequence read numbers (Y-axis) and position in the candidate gene contigs (X-axis). Colored rectangles (blue) represent the gene structure.

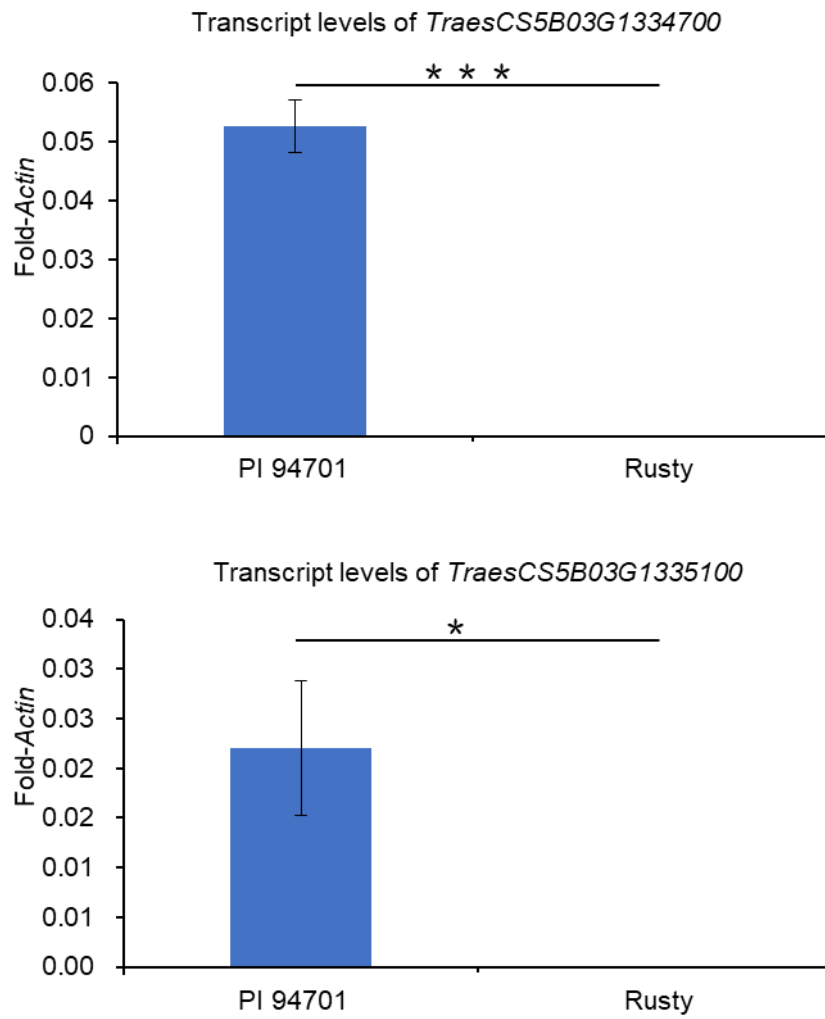


Figure S3 Transcript levels of the candidate genes *TraesCS5B03G1334700* and *TraesCS5B03G1335100* in F₄ sister lines S73 and R32. Seedlings of S73 and R32 were inoculated with *Pgt* race 34MKGQM and leaf samples from multiple plants were collected at 6 dpi. Transcript levels were expressed as fold-*Actin* (n = 4), and error bars represent standard errors of the mean.

Supplementary Tables

Table S1. Avirulence / virulence formulae of the *Puccinia graminis* f. sp. *tritici* races used in this study.

Race (isolate)	Origin	Avirulence	Virulence
BCCBC (09CA115-2)	USA	<i>SrPI94701</i> 5 6 7b 8a 9a 9d 9e 9b 10 11 21 24 30 31 36 38 <i>Tmp</i>	<i>Sr9g</i> 17 <i>McN</i>
34MTGSM (20GSA1)	China	<i>SrPI94701</i> 8155b 9e 12 13 14 17 21 22 23 26 30 31 33 35 36 37 38 47 <i>Tmp</i>	<i>Sr5</i> 6 7b 8a 9a 9b 9d 9f 9g 10 11 15 16 18 19 20 24 25 27 28 29 32 34 39 <i>McN</i>
34C3RTGQM (20IAL32)	China	<i>SrPI94701</i> 8155b 9e 10 12 13 15 17 19 20 23 27 30 31 33 35 36 37 38 <i>Tmp</i>	<i>Sr5</i> 6 7b 8a 9a 9b 9d 9g 11 14 18 21 24 25 28 29 32 34 <i>McN</i>
21C3CTTTM (20GH13)	China	<i>SrPI94701</i> 8155b 5 9e 14 19 21 22 23 26 27 31 33 35 37 38 39 47	<i>Sr6</i> 7b 8a 9a 9b 9d 9f 9g 10 11 12 13 15 16 17 18 20 24 25 28 29 30 32 34 36 <i>Tmp</i> <i>McN</i>
34MKGQM (20IAL06)	China	<i>SrPI94701</i> 8155b 9e 10 11 13 14 17 18 19 21 22 23 25 26 30 31 33 34 35 36 37 38 47 <i>Tmp</i>	<i>Sr5</i> 6 7b 8a 9a 9b 9d 9f 9g 12 15 16 20 24 27 28 29 32 39 <i>McN</i>
34C3RKGQM (21PK9)	China	<i>SrPI94701</i> 8155b 10 11 13 14 15 17 18 20 22 25 30 31 33 34 35 36 37 <i>Tmp</i>	<i>Sr5</i> 8a 12 19 21 23 24 27 28 29 32 <i>McN</i>

Table S2. SNPs linked with *SrPI94701* and their locations in the Svevo Rel.1.0.

Chromosome	Location (bp)	Allele	Rusty (SP)	PI 94701 (RP)	S-Bulk	R-Bulk
5B	673537026	A/C	A	C	A	C
5B	673538615	C/T	C	T	C	T
5B	673538642	A/G	A	G	A	G
5B	690132538	A/G	A	G	A	G
5B	690132553	T/C	T	C	T	C
5B	690132681	C/T	C	T	C	T
5B	690132702	T/C	T	C	T	C
5B	690132780	T/C	T	C	T	C
5B	690132918	A/G	A	G	A	G
5B	690133547	A/G	A	G	A	G
5B	690134308	T/C	T	C	T	C
5B	690134560	T/G	T	G	T	G
5B	690134566	A/C	A	C	A	C
5B	690134809	C/A	C	A	C	A
5B	690134913	G/A	G	A	G	A
5B	690450276	G/T	G	T	G	T
5B	690450564	T/C	T	C	T	C
5B	690450594	T/C	T	C	T	C
5B	690450645	C/G	C	G	C	G
5B	690451829	T/C	T	C	T	C
5B	690452397	G/A	G	A	G	A
5B	690452463	G/A	G	A	G	A
5B	690452487	C/T	C	T	C	T
5B	690452862	G/A	G	A	G	A
5B	690452906	T/C	T	C	T	C
5B	690452930	T/C	T	C	T	C
5B	690452960	C/T	C	T	C	T
5B	690548168	G/A	G	A	G	A
5B	690548198	C/G	C	G	C	G
5B	690548266	C/G	C	G	C	G
5B	690548320	G/C	G	C	G	C
5B	690548365	G/A	G	A	G	A
5B	690549265	A/G	A	G	A	G
5B	690549283	T/C	T	C	T	C
5B	690550559	C/T	C	T	C	T
5B	690696603	T/C	T	C	T	C
5B	690696608	G/A	G	A	G	A
5B	690696623	G/C	G	C	G	C
5B	690696749	C/T	C	T	C	T
5B	690696846	T/C	T	C	T	C
5B	690699742	C/G	C	G	C	G

5B	690700002	A/G	A	G	A	G
5B	690700038	A/G	A	G	A	G
5B	690700079	T/A	T	A	T	A
5B	690700693	G/A	G	A	G	A
5B	691140854	T/C	T	C	T	C
5B	691140864	G/A	G	A	G	A
5B	691140907	T/C	T	C	T	C
5B	691140978	A/G	A	G	A	G
5B	691142510	A/G	A	G	A	G
5B	691142522	G/A	G	A	G	A
5B	691142606	C/G	C	G	C	G
5B	691142630	G/C	G	C	G	C
5B	691142744	C/G	C	G	C	G
5B	691142884	G/C	G	C	G	C
5B	691142990	C/T	C	T	C	T
5B	691153376	G/A	G	A	G	A
5B	691155372	C/T	C	T	C	T
5B	691158423	A/G	A	G	A	G
5B	691162721	C/T	C	T	C	T
5B	691163268	T/C	T	C	T	C
5B	691453615	T/C	T	C	T	C
5B	691454084	C/T	C	T	C	T
5B	691455997	A/G	A	G	A	G
5B	691456015	C/T	C	T	C	T
5B	691456471	A/G	A	G	A	G
5B	691456611	A/G	A	G	A	G
5B	691456672	T/C	T	C	T	C
5B	691456696	G/T	G	T	G	T
5B	691456859	T/C	T	C	T	C
5B	691460240	G/A	G	A	G	A
5B	691460596	G/A	G	A	G	A
5B	691460602	A/T	A	T	A	T
5B	691460806	A/G	A	G	A	G
5B	691460858	C/A	C	A	C	A
5B	691676385	A/G	A	G	A	G
5B	691676406	A/G	A	G	A	G
5B	691676445	G/A	G	A	G	A
5B	691676493	C/G	C	G	C	G
5B	691676500	T/C	T	C	T	C
5B	691679615	G/C	G	C	G	C
5B	691679621	G/C	G	C	G	C
5B	691685590	G/A	G	A	G	A
5B	691685656	G/A	G	A	G	A
5B	691870564	C/T	C	T	C	T

5B	691870707	G/A	G	A	G	A
5B	691874455	G/A	G	A	G	A
5B	691874927	T/C	T	C	T	C
5B	691875084	A/C	A	C	A	C
5B	691875126	T/C	T	C	T	C
5B	691875285	C/T	C	T	C	T
5B	695900839	G/A	G	A	G	A
5B	695900896	C/T	C	T	C	T
5B	695901007	T/C	T	C	T	C
5B	695905265	C/T	C	T	C	T
5B	695905408	C/G	C	G	C	G
5B	695905497	C/A	C	A	C	A
5B	695905514	A/C	A	C	A	C
5B	695905562	C/T	C	T	C	T
5B	695905802	G/C	G	C	G	C
5B	695905892	A/G	A	G	A	G
5B	695905974	A/G	A	G	A	G
5B	696004071	A/G	A	G	A	G
5B	696004590	C/G	C	G	C	G
5B	696004614	G/A	G	A	G	A
5B	696006223	C/T	C	T	C	T
5B	696012374	G/C	G	C	G	C
5B	696012468	G/A	G	A	G	A
5B	696012965	C/A	C	A	C	A
5B	696013709	T/G	T	G	T	G
5B	696024115	A/G	A	G	A	G
5B	696027510	C/G	C	G	C	G
5B	696029048	T/C	T	C	T	C
5B	696375467	G/A	G	A	G	A
5B	696558983	T/C	T	C	T	C
5B	697067391	G/A	G	A	G	A
5B	697067436	A/C	A	C	A	C
5B	697093006	G/C	G	C	G	C
5B	697098140	G/A	G	A	G	A
5B	697412714	C/T	C	T	C	T
5B	697413013	C/T	C	T	C	T
5B	697413096	G/C	G	C	G	C
5B	697413597	T/A	T	A	T	A
5B	697413616	G/A	G	A	G	A
5B	697415781	G/T	G	T	G	T
5B	697415795	C/G	C	G	C	G
5B	697415801	T/C	T	C	T	C
5B	697416098	G/A	G	A	G	A
5B	697416206	G/A	G	A	G	A

5B	697416227	T/C	T	C	T	C
5B	697416254	A/T	A	T	A	T
5B	697416305	A/G	A	G	A	G
5B	697416402	G/A	G	A	G	A
5B	697416416	G/A	G	A	G	A
5B	698037709	A/G	A	G	A	G
5B	698039600	A/G	A	G	A	G
5B	698194607	A/G	A	G	A	G
5B	698194686	T/C	T	C	T	C
5B	698195129	T/C	T	C	T	C
5B	698195167	G/A	G	A	G	A
5B	698195375	T/G	T	G	T	G
5B	698809491	C/G	C	G	C	G
5B	698809555	A/G	A	G	A	G
5B	698827028	T/C	T	C	T	C
5B	698828178	G/A	G	A	G	A
5B	698832399	C/T	C	T	C	T
5B	698834478	G/C	G	C	G	C
5B	698834524	G/A	G	A	G	A
5B	698834615	T/C	T	C	T	C
5B	698834843	G/C	G	C	G	C
5B	699873281	T/C	T	C	T	C
5B	699873308	C/T	C	T	C	T
5B	699873320	G/A	G	A	G	A
5B	699873359	G/A	G	A	G	A
5B	699873389	G/T	G	T	G	T
5B	699874865	C/G	C	G	C	G
5B	699874977	C/T	C	T	C	T
5B	699936236	C/A	C	A	C	A
5B	699936256	A/C	A	C	A	C
5B	699936373	C/G	C	G	C	G

Table S3. Predicted genes within the *SrPI94701* candidate region based on the genomic sequence of Svevo Rel.1.0. NBS-LRR (NLR) genes are highlighted in blue and protein kinases are highlighted in green.

Gene ID in Svevo Rel.1.0	Location(bp)	Gene annotation
<i>TRITD5Bv1G248710</i>	691246432:691253036	NBS-LRR Disease resistance protein
<i>TRITD5Bv1G248720</i>	691256419:691257925	Protein FAR1-RELATED SEQUENCE 5
<i>TRITD5Bv1G248730</i>	691257962:691258753	Protein FAR1-RELATED SEQUENCE 5
<i>TRITD5Bv1G248740</i>	691282213:691282788	Pol polyprotein
<i>TRITD5Bv1G248750</i>	691306412:691306741	Gag-pol polyprotein
<i>TRITD5Bv1G248760</i>	691338839:691341573	Acyl-[acyl-carrier-protein] desaturase
<i>TRITD5Bv1G248770</i>	691339761:691340111	—
<i>TRITD5Bv1G248780</i>	691370776:691371072	Retrotransposon protein
<i>TRITD5Bv1G248790</i>	691436922:691437227	Transposon protein
<i>TRITD5Bv1G248800</i>	691454049:691460239	Transducin/WD-like repeat-protein
<i>TRITD5Bv1G248810</i>	691501161:691501856	Retrovirus-related Pol polyprotein from transposon TNT 1-94 TE
<i>TRITD5Bv1G248820</i>	691503752:691504072	Potassium voltage-gated channel subfamily V member 1 G
<i>TRITD5Bv1G248830</i>	691514447:691514833	Transposon protein
<i>PTRITDBv1G248840</i>	691538292:691538983	Acyl-[acyl-carrier-protein] desaturase
<i>TRITD5Bv1G248850</i>	691539040:691539351	Acyl-[acyl-carrier-protein] desaturase
<i>TRITD5Bv1G248860</i>	691548302:691548911	Hydroxyproline-rich glycoprotein family protein G
<i>TRITD5Bv1G248870</i>	691559538:691560569	Ethylene-responsive transcription factor
<i>TRITD5Bv1G248880</i>	691566157:691566906	E3 ubiquitin-protein ligase pub1 G
<i>TRITD5Bv1G248890</i>	691595319:691595885	Ethylene-responsive transcription factor
<i>TRITD5Bv1G248900</i>	691599040:691599384	Retrovirus-related Pol polyprotein from transposon TNT 1-94 TE
<i>TRITD5Bv1G248910</i>	691599928:691600257	Reverse transcriptase
<i>TRITD5Bv1G248920</i>	691600525:691600935	Retrovirus-related Pol polyprotein from transposon TNT 1-94 TE
<i>TRITD5Bv1G248930</i>	691601784:691602509	Retrovirus-related Pol polyprotein from transposon TNT 1-94
<i>TRITD5Bv1G248940</i>	691657895:691658254	RNA-dependent RNA polymerase 6 G
<i>TRITD5Bv1G248950</i>	691659748:691660071	NAD(P)-binding Rossmann-fold superfamily protein G
<i>TRITD5Bv1G248960</i>	691666704:691668634	Hydroxyproline-rich glycoprotein family protein G
<i>TRITD5Bv1G248970</i>	691670573:691671654	Pentatricopeptide repeat-containing protein
<i>TRITD5Bv1G248980</i>	691672790:691673122	Polynucleotidyl transferase
<i>TRITD5Bv1G248990</i>	691676349:691680291	Derlin; Ahrd_quality_code
<i>TRITD5Bv1G249000</i>	691685567:691689823	DNA polymerase epsilon subunit
<i>TRITD5Bv1G249010</i>	691690959:691691510	Myb domain protein
<i>TRITD5Bv1G249020</i>	691732804:691733645	Retrotransposon protein
<i>TRITD5Bv1G249030</i>	691735599:691736756	Retrovirus-related Pol polyprotein from transposon TNT 1-94
<i>TRITD5Bv1G249040</i>	691815441:691815758	Retrotransposon protein
<i>TRITD5Bv1G249050</i>	691839589:691840263	Hydroxyproline-rich glycoprotein G
<i>TRITD5Bv1G249060</i>	691863162:691866572	Receptor-like protein kinase
<i>TRITD5Bv1G249070</i>	691868660:691868971	Gamma-glutamyltranspeptidase 3 G
<i>TRITD5Bv1G249080</i>	691870608:691872047	Alanine--tRNA ligase G
<i>TRITD5Bv1G249090</i>	691872523:691874891	Ycf20-like protein

<i>TRITD5Bv1G249100</i>	691883573:691883971	Cytoplasmic FMR1-interacting protein 1 G
<i>TRITD5Bv1G249110</i>	691890931:691891428	GRF zinc finger family protein TE?
<i>TRITD5Bv1G249120</i>	691894360:691894905	Transposon protein
<i>TRITD5Bv1G249130</i>	691902419:691902742	Retrovirus-related Pol polyprotein from transposon TNT 1-94
<i>TRITD5Bv1G249140</i>	691930058:691930432	Retrovirus-related Pol polyprotein from transposon TNT 1-94
<i>TRITD5Bv1G249150</i>	691943897:691944693	Homeodomain-like superfamily protein G
<i>TRITD5Bv1G249160</i>	691945345:691945959	Ulp1 protease family
<i>TRITD5Bv1G249170</i>	691946772:691950677	tRNA-dihydrouridine(20/20a) synthase G
<i>TRITD5Bv1G249180</i>	691950741:691951342	Lipoxygenase G
<i>TRITD5Bv1G249190</i>	691958543:691958899	Werner Syndrome-like exonuclease
<i>TRITD5Bv1G249200</i>	691973655:691974086	Retrotransposon protein
<i>TRITD5Bv1G249210</i>	692004485:692019358	Flavin-containing monooxygenase
<i>TRITD5Bv1G249230</i>	692056751:692057218	—
<i>TRITD5Bv1G249240</i>	692080884:692081324	Transcription elongation factor SPT5 G
<i>TRITD5Bv1G249250</i>	692095406:692096778	Retrovirus-related Pol polyprotein from transposon TNT 1-94
<i>TRITD5Bv1G249260</i>	692105390:692107005	Ankyrin repeat family protein
<i>TRITD5Bv1G249270</i>	692107641:692108152	Ankyrin repeat family protein
<i>TRITD5Bv1G249280</i>	692110261:692117686	Ankyrin repeat family protein
<i>TRITD5Bv1G249290</i>	692164235:692164801	Retrotransposon protein
<i>TRITD5Bv1G249300</i>	692179316:692179690	Retrovirus-related Pol polyprotein from transposon TNT 1-94
<i>TRITD5Bv1G249310</i>	692180146:692180550	Retrovirus-related Pol polyprotein from transposon TNT 1-94
<i>TRITD5Bv1G249320</i>	692180838:692181200	Retrovirus-related Pol polyprotein from transposon TNT 1-94
<i>TRITD5Bv1G249330</i>	692190354:692191598	Myosin-10 G; ID=TRITD5Bv1G249330.1
<i>TRITD5Bv1G249340</i>	692197169:692197468	3-hydroxy-3-methylglutaryl-coenzyme A reductase G
<i>TRITD5Bv1G249350</i>	692257785:692271857	Methyl-CpG-binding domain-containing protein
<i>TRITD5Bv1G249360</i>	692280840:692283572	F-box family protein

Table S4. Predicted genes in the *SrPI94701* candidate region based on the genomic sequence of Chinese Spring (RefSeq v2.1). NBS-LRR (NLR) genes are highlighted in blue and protein kinases are highlighted in green. The expression levels of the candidate genes were based on published RNAseq studies compiled in the wheat expVIP database (<http://www.wheat-expression.com/>).

Gene ID in CS RefSeq v2.1	Start	END	Strand	Function description	Expression or not
<i>TraesCS5B03G1334300</i>	702.560373Mb	702.564756Mb	-	Disease resistance protein RPM1	Not
<i>TraesCS5B03G1334500</i>	702.61405Mb	702.616221Mb	+	Leucine-rich repeat receptor kinase-like protein	Not
<i>TraesCS5B03G1334600</i>	702.618368Mb	702.618688Mb	+	Protein kinase family protein	Not
<i>TraesCS5B03G1334700</i>	702.631769Mb	702.635441Mb	-	Disease resistance protein RPM1	Yes
<i>TraesCS5B03G1334900</i>	702.643865Mb	702.645383Mb	+	Receptor-like protein kinase	Not
<i>TraesCS5B03G1335000</i>	702.677875Mb	702.68294Mb	-	Disease resistance protein	Yes
<i>TraesCS5B03G1335100</i>	702.716212Mb	702.720447Mb	-	Disease resistance protein RPM1	Yes
<i>TraesCS5B03G1335200</i>	702.754213Mb	702.755609Mb	+	Werner Syndrome-like exonuclease	Not
<i>TraesCS5B03G1335300</i>	702.785489Mb	702.790804Mb	-	Disease resistance protein RPM1	Yes
<i>TraesCS5B03G1335500</i>	702.844686Mb	702.848323Mb	+	Receptor-like protein kinase	Yes
<i>TraesCS5B03G1335600</i>	702.852439Mb	702.8582Mb	-	Disease resistance protein (NBS-LRR class) family	Yes
<i>TraesCS5B03G1335800</i>	702.911476Mb	702.915825Mb	-	Disease resistance protein RPM1	Not
<i>TraesCS5B03G1335900</i>	703.642969Mb	703.644782Mb	-	Acyl-[acyl-carrier-protein] desaturase	Not
<i>TraesCS5B03G1336100</i>	703.808523Mb	703.81611Mb	+	Transducin/WD-like repeat-protein	Yes
<i>TraesCS5B03G1336800</i>	704.098827Mb	704.099421Mb	-	Hydroxyproline-rich glycoprotein family protein	Not
<i>TraesCS5B03G1337300</i>	704.194205Mb	704.194931Mb	+	Ethylene-responsive transcription factor	Not
<i>TraesCS5B03G1337400</i>	704.219804Mb	704.220353Mb	-	Hydroxyproline-rich glycoprotein family protein	Yes
<i>TraesCS5B03G1337600</i>	704.223674Mb	704.225128Mb	-	Pentatricopeptide repeat-containing protein, putative	Yes
<i>TraesCS5B03G1337700</i>	704.226305Mb	704.230813Mb	-	Derlin	Yes
<i>TraesCS5B03G1337800</i>	704.236306Mb	704.241341Mb	+	Nuclear factor Y, subunit C10	Yes
<i>TraesCS5B03G1338000</i>	704.242878Mb	704.245073Mb	+	Protein kinase family protein	Yes
<i>TraesCS5B03G1338200</i>	704.361881Mb	704.362863Mb	-	Hydroxyproline-rich glycoprotein	Yes
<i>TraesCS5B03G1338300</i>	704.387634Mb	704.391029Mb	+	Receptor-like protein kinase	Yes
<i>TraesCS5B03G1338400</i>	704.402336Mb	704.404802Mb	+	Ycf20-like protein	Yes
<i>TraesCS5B03G1338800</i>	704.414913Mb	704.416601Mb	+	Flavin-containing monooxygenase	Not
<i>TraesCS5B03G1339700</i>	704.517287Mb	704.525047Mb	-	Ankyrin repeat family protein	Yes
<i>TraesCS5B03G1340100</i>	704.695036Mb	704.699363Mb	+	Methyl-CpG-binding domain-containing protein 9	Not
<i>TraesCS5B03G1340200</i>	704.708346Mb	704.711203Mb	-	F-box family protein	Not

Table S5. Differentially expressed genes (DEGs) in the *SrPI94701* candidate region. TPM (transcripts per million) is used to measure expression levels. Differentially expressed genes (FDR < 0.05; *p*-value < 0.05; and |log2foldchange| > 1) are highlighted in bold.

Gene ID	Resistant groups			Susceptible groups			log2FoldChange	<i>p</i> -value	FDR	Annotation
	R32-1	R32-2	R32-3	S73-1	S73-2	S73-3				
<i>TraesCS5B03G1334700</i>	2.20	2.10	2.42	0.00	0.00	0.00	10.28	0.00	0.00	Disease resistance protein RPM1
<i>TraesCS5B03G1335000</i>	2.47	1.95	1.54	0.00	0.00	0.00	10.16	0.00	0.00	Disease resistance protein
<i>TraesCS5B03G1335100</i>	0.24	0.24	0.19	0.00	0.00	0.00	6.95	0.00	0.00	Disease resistance protein RPM1
<i>TraesCS5B03G1335500</i>	3.94	0.08	2.81	2.59	1.85	1.92	0.26	0.83	0.96	Receptor-like protein kinase
<i>TraesCS5B03G1335600</i>	1.24	1.49	0.95	0.30	0.44	0.33	1.55	0.00	0.00	Disease resistance protein (NBS-LRR class) family
<i>TraesCS5B03G1336100</i>	10.32	11.01	8.68	2.97	2.85	3.99	1.34	0.00	0.00	Transducin/WD-like repeat-protein
<i>TraesCS5B03G1337400</i>	1.04	2.82	2.37	0.00	1.14	0.25	2.09	0.06	0.33	Hydroxyproline-rich glycoprotein family protein
<i>TraesCS5B03G1337600</i>	0.40	0.77	0.41	0.00	0.08	0.02	3.82	0.00	0.01	Pentatricopeptide repeat-containing protein
<i>TraesCS5B03G1337700</i>	42.32	42.22	43.80	9.60	10.22	11.34	1.77	0.00	0.00	Derlin
<i>TraesCS5B03G1337800</i>	1.61	1.79	1.22	1.29	1.17	1.43	0.03	0.93	0.99	Nuclear factor Y, subunit C10
<i>TraesCS5B03G1338000</i>	0.47	0.18	0.18	0.08	0.13	0.00	1.67	0.16	0.54	Protein kinase family protein
<i>TraesCS5B03G1338200</i>	1.94	6.57	6.13	2.03	2.76	1.66	0.93	0.08	0.39	Hydroxyproline-rich glycoprotein
<i>TraesCS5B03G1338400</i>	6.65	7.25	8.52	7.97	7.07	7.60	0.30	0.36	0.76	Ycf20-like protein
<i>TraesCS5B03G1339700</i>	0.83	0.47	0.06	0.13	0.54	0.18	0.48	0.60	0.89	Ankyrin repeat family protein
<i>TraesCS5B03G1340200</i>	0.08	0.00	0.06	0.55	0.96	0.48	4.10	0.00	0.00	F-box family protein

Table S6. Genotyping results for markers *pku69124*, *pku69187*, *pku69211*, *pku69227*, and *pku69228*. A collection comprising 53 *T. dicoccon* accessions and 51 *T. aestivum* genotypes was used in this study. Wheat accessions carry the *SrPI94701* haplotype are highlighted in green. NT, not test.

Accessions	Species	Markers					Pgt race
		<i>pku69124</i> (<i>SspI</i>)	<i>pku69187</i> (<i>BbvCI</i>)	<i>pku69211</i> (<i>HpyCH4IV</i>)	<i>pku69227</i> (<i>Pvu II</i>)	<i>pku69228</i> (<i>Hpy188III</i>)	
PI 94701	<i>T. durum</i>	A	A	A	A	A	1+/2-
Rusty	<i>T. durum</i>	B	B	B	B	B	3+
CItr 12214	<i>T. dicoccon</i>	A	A	A	A	A	1+
CItr 14621	<i>T. dicoccon</i>	A	A	H	A	A	2/2+
CItr 14637	<i>T. dicoccon</i>	A	A	A	A	A	1+
CItr 14919	<i>T. dicoccon</i>	A	A	H	A	A	1-
CItr 14970	<i>T. dicoccon</i>	A	A	A	A	A	1+
PI 94615	<i>T. dicoccon</i>	A	B	B	A	A	0;/1-
PI 94616	<i>T. dicoccon</i>	A	B	A	A	A	0
PI 94626	<i>T. dicoccon</i>	A	B	A	A	A	0;
PI 94631	<i>T. dicoccon</i>	A	A	A	A	A	1+/2
PI 94638	<i>T. dicoccon</i>	A	B	A	A	A	0
PI 94656	<i>T. dicoccon</i>	A	A	A	A	A	1/1+
PI 94657	<i>T. dicoccon</i>	B	B	A	A	A	0
PI 94664	<i>T. dicoccon</i>	A	A	A	A	A	1+
PI 94666	<i>T. dicoccon</i>	A	B	A	A	A	1+
PI 94674	<i>T. dicoccon</i>	A	B	A	A	A	1/1+
PI 94675	<i>T. dicoccon</i>	A	B	A	A	A	1
PI 154582	<i>T. dicoccon</i>	B	B	B	B	A	1/1+
PI 168679	<i>T. dicoccon</i>	A	B	A	A	A	1/1+
PI 193877	<i>T. dicoccon</i>	A	A	A	A	A	1-
PI 193879	<i>T. dicoccon</i>	A	A	A	A	A	1-
PI 193880	<i>T. dicoccon</i>	A	A	A	A	A	1-
PI 193882	<i>T. dicoccon</i>	A	A	A	A	A	1
PI 194042	<i>T. dicoccon</i>	A	A	A	A	A	1+
PI 194375	<i>T. dicoccon</i>	A	A	A	A	A	1+
PI 197259	<i>T. dicoccon</i>	A	A	A	A	A	1+/2
PI 197260	<i>T. dicoccon</i>	A	A	A	A	A	1/1+
PI 197481	<i>T. dicoccon</i>	A	A	A	A	A	1+/2
PI 197485	<i>T. dicoccon</i>	A	A	A	A	A	1-
PI 197489	<i>T. dicoccon</i>	A	A	A	A	A	2+/3
PI 197495	<i>T. dicoccon</i>	A	A	A	A	A	1
PI 217637	<i>T. dicoccon</i>	A	A	A	A	A	1+
PI 217639	<i>T. dicoccon</i>	A	B	A	A	A	1-/1
PI 221400	<i>T. dicoccon</i>	B	B	A	A	A	0
PI 225332	<i>T. dicoccon</i>	B	B	A	A	A	3

PI 244341	<i>T. dicoccon</i>	A	A	A	A	A	1+
PI 254147	<i>T. dicoccon</i>	A	A	A	A	A	1+
PI 254164	<i>T. dicoccon</i>	B	A	A	A	A	3
PI 254165	<i>T. dicoccon</i>	B	A	A	A	A	3
PI 254190	<i>T. dicoccon</i>	A	B	A	A	A	1-/1
PI 272531	<i>T. dicoccon</i>	A	B	A	A	A	1+
PI 273978	<i>T. dicoccon</i>	A	A	A	A	A	1+
PI 273980	<i>T. dicoccon</i>	A	A	A	A	A	4
PI 273981	<i>T. dicoccon</i>	A	A	A	A	A	1+
PI 275996	<i>T. dicoccon</i>	A	A	A	A	A	1+/2
PI 276013	<i>T. dicoccon</i>	No PCR product	B	A	B	A	3/3+
PI 298582	<i>T. dicoccon</i>	A	A	A	A	A	1/1+
PI 298586	<i>T. dicoccon</i>	A	A	A	A	A	1+
PI 324076	<i>T. dicoccon</i>	A	A	A	A	A	1+
PI 349043	<i>T. dicoccon</i>	A	B	A	A	A	1
PI 355477	<i>T. dicoccon</i>	A	A	A	A	A	1-
PI 355507	<i>T. dicoccon</i>	A	B	B	A	A	0
PI 362696	<i>T. dicoccon</i>	H	B	A	A	A	0
PI 377657	<i>T. dicoccon</i>	B	B	A	A	A	1
ISr8a-Ra	<i>T. aestivum</i>	A	No PCR product	A	A	A	3
ISr9a-Ra	<i>T. aestivum</i>	A	No PCR product	A	A	A	4
Avocet-S	<i>T. aestivum</i>	A	H	B	B	A	4
ISr5-Ra	<i>T. aestivum</i>	A	H	A	A	A	4
Jinan17	<i>T. aestivum</i>	A	H	A	B	A	4
Jimai229	<i>T. aestivum</i>	A	H	A	B	A	NT
Jimai24	<i>T. aestivum</i>	A	H	A	B	A	NT
Jimai44	<i>T. aestivum</i>	A	No PCR product	A	B	No PCR product	NT
Yannong19	<i>T. aestivum</i>	A	A	A	B	H	NT
Huaimai40	<i>T. aestivum</i>	A	A	A	A	A	4
Huaimai22	<i>T. aestivum</i>	A	H	A	A	A	NT
Huaimai44	<i>T. aestivum</i>	A	A	A	B	No PCR product	NT
Luyuan502	<i>T. aestivum</i>	A	A	A	A	A	4
Zhongmai895	<i>T. aestivum</i>	A	H	A	B	H	NT
Zhongmai578	<i>T. aestivum</i>	A	No PCR product	A	B	A	NT
Yumai70	<i>T. aestivum</i>	A	No PCR product	A	B	B	NT
Fielder	<i>T. aestivum</i>	H	B	B	B	A	4
Ningchun4	<i>T. aestivum</i>	A	H	A	A	A	4
Xiaoyan22	<i>T. aestivum</i>	A	A	A	A	A	NT
PI 660060	<i>T. aestivum</i>	H	B	B	B	A	NT
PI 600064	<i>T. aestivum</i>	H	A	A	B	A	NT
PI 679621	<i>T. aestivum</i>	A	No PCR product	A	A	A	NT
PI 648417	<i>T. aestivum</i>	A	A	A	A	A	NT
PI 442904	<i>T. aestivum</i>	A	A	A	B	A	NT
PI 603918	<i>T. aestivum</i>	A	A	A	B	A	NT

PI 189747	<i>T. aestivum</i>	H	B	H	B	A	NT
PI 660057	<i>T. aestivum</i>	A	A	A	B	A	NT
PI 182527	<i>T. aestivum</i>	B	B	H	B	A	NT
PI 600683	<i>T. aestivum</i>	A	A	A	B	A	NT
PI 660056	<i>T. aestivum</i>	A	A	B	B	A	NT
PI 679605	<i>T. aestivum</i>	A	A	A	B	No PCR product	NT
GSTR409	<i>T. aestivum</i>	A	A	B	B	A	NT
PI 675564	<i>T. aestivum</i>	H	B	B	B	A	NT
PI 672538	<i>T. aestivum</i>	A	A	A	B	A	NT
PI 277012	<i>T. aestivum</i>	A	A	A	A	A	NT
PI 596533	<i>T. aestivum</i>	A	A	A	A	A	NT
PI 679598	<i>T. aestivum</i>	A	A	B	B	A	NT
PI 679603	<i>T. aestivum</i>	H	B	H	B	A	NT
GSTR437	<i>T. aestivum</i>	A	A	B	B	A	NT
GSTR441	<i>T. aestivum</i>	A	A	A	A	A	NT
PI 638738	<i>T. aestivum</i>	A	A	A	A	A	NT
Taichang29	<i>T. aestivum</i>	A	A	A	B	A	NT
GSTR425	<i>T. aestivum</i>	A	A	B	B	A	NT
Xinong511	<i>T. aestivum</i>	A	A	A	B	A	NT
CItr15082	<i>T. aestivum</i>	A	A	No PCR product	B	A	NT
GSTR434	<i>T. aestivum</i>	A	A	B	B	A	NT
GSTR429	<i>T. aestivum</i>	A	A	B	B	A	NT
GSTR428	<i>T. aestivum</i>	A	A	B	B	A	NT
GSTR420	<i>T. aestivum</i>	A	A	B	B	A	NT
GSTR501	<i>T. aestivum</i>	A	No PCR product	A	A	A	NT
GSTR522	<i>T. aestivum</i>	A	A	A	B	A	NT