

### Supplementary materials

Table S1. Pt-code for the 20 differential hosts of *Puccinia triticina* in ordered sets of four and additional set five.

Pt-code <sup>a</sup>	Infection type produced on near isogenic Lr lines				
	Host set 1:	1	2a	2c	3
	Host set 2:	9	16	24	26
	Host set 3:	3ka	11	17	30
	Host set 4:	10	18	21	2b
	Host set 5:	14b	15	36	42
B		Low	Low	Low	Low
C		Low	Low	Low	High
D		Low	Low	High	Low
F		Low	Low	High	High
G		Low	High	Low	Low
H		Low	High	Low	High
J		Low	High	High	Low
K		Low	High	High	High
L		High	Low	Low	Low
M		High	Low	Low	High
N		High	Low	High	Low
P		High	Low	High	High
Q		High	High	Low	Low
R		High	High	Low	High
S		High	High	High	Low
T		High	High	High	High

<sup>a</sup>Pt-code consists of the designation for set 1 followed by that for set 2, etc. L = Low infection type (avirulent pathogen); H = High infection type (virulent pathogen).

**Table S2. Wheat leaf rust infection types used in disease assessment for seedling stage according to Johnston and Browder [31].**

<b>Host response (class)</b>	<b>Infection type</b>	<b>Disease symptoms</b>
<b>Immune</b>	0	No uredia or other macroscopic sign of infection.
<b>Nearly immune</b>	0;	No uredia but hypersensitive necrotic or chlorotic flecks present.
<b>Very resistant</b>	1	Small uredia surrounded by necrosis.
<b>Moderately resistant</b>	2	Small to medium uredia surrounded by chlorosis or necrosis.
<b>Moderately susceptible</b>	3	Medium-sized uredia that may be associated with chlorosis.
<b>Very susceptible</b>	4	Large uredia without chlorosis or necrosis or rarely necrosis.
<b>Heterogeneous</b>	X	Random distribution of different variable sized uredia on single leaf.

**Table S3. Code, nucleotide sequence and G+C (%) of primers used in the random amplified polymorphic DNA (RAPD) reactions.**

<b>Primer</b>	<b>Sequence</b>	<b>(G+C) %</b>
1	5'- GGTGCGGGAA- 3'	70
2	5'- GTTTCGCTCC- 3'	60
3	5'- GTAGACCCGT- 3'	60

**Table S4. The pedigree list of the monogenic lines (*Lr* genes) used in this study.**

<b>No.</b>	<b><i>Lr</i> gene</b>	<b>Origin of seed resource</b>
1	<i>Lr1</i>	TC*6/Centenatrio (RL6003)
2	<i>Lr2a</i>	TC*6/Webster (RL6016)
3	<i>Lr2b</i>	TC*6/Carine (RL6016)
4	<i>Lr2c</i>	TC*6/Lorous (RL6047)
5	<i>Lr3</i>	TC*6/Democrat (RL6002)
6	<i>Lr3ka</i>	Bage/TC*6 (RL6042)
7	<i>Lr9</i>	Transefer/8*TC (RL6010)
8	<i>Lr10</i>	TC*6/Exchange (RL6004)
9	<i>Lr11</i>	Kussar (W976)
10	<i>Lr14b</i>	TC*6/Maria Escobar (RL6006)
11	<i>Lr15</i>	TC*6/Kenya 1483 (RL6052)
12	<i>Lr16</i>	TC*6/Exchange (RL6005)
13	<i>Lr17</i>	Klein Lucero/6*TC (RL6008)
14	<i>Lr18</i>	TC*6/Africa 43 (RL6009)
15	<i>Lr19</i>	TC*7/Tr (RL6040)
16	<i>Lr21</i>	TC*6/RL5406 (RL6043)
17	<i>Lr24</i>	TC*6/Agent (RL6064)
18	<i>Lr26</i>	TC*6/St-1-25 (RL6078)
19	<i>Lr28</i>	CS2D-2M
20	<i>Lr30</i>	TC*6/Terenz10(RL6049)
21	<i>Lr36</i>	E84018
22	<i>Lr42</i>	<i>T. tauchii</i>

**Table S5. Primer names, sequences, annealing temperatures and references from *Lr* genes associated markers used in this study.**

<b>Gene</b>	<b>Name</b>	<b>Primer sequences (5'-3')</b>	<b>Annealing temperatures</b>
<i>Lr19</i>	SCS73719-1	TCG TCC AGA TCA GAA TGT G	55
	SCS73719-2	CTC GTCGATTAGCAGTGAG	
<i>Lr28</i>	<i>Lr</i> 28-01	CCC GGC ATA AGT CTA TGG TT	50
	<i>Lr</i> 28-02	CAA TGA ATG AGA TAC GTG AA	