

Table S1. Primers used for identification of *Lr* genes in wheat cultivar “Klein Proteo”.

<i>Lr</i> Gene	Primer name	Primer sequence (5'-3')	Product size (bp)	Annealing T. (°C)
<i>Lr3</i>	Xmwg798F	GGCTGTCTACATCTTCTGCA	365	58
	Xmwg798R	CAAGTGTGAGAAGGAGAGT		
<i>Lr10</i>	Fl.2245	GTGTAATGCATGCAGGTTCC	310	60
	Lr10-6/r2	AGGTGTGAGTGAGTTATGTT		
<i>Lr13</i>	HBAU-Lr13 F	TGCACATGGATATGCGGAGA	431 ^a	55
	HBAU-Lr13 R	GCTTTGAGTTGCCCATGCTC		
<i>Lr13</i> (CDS ¹)	Lr13F1	GTGTACTTATTAATTCAGACATCATAAGG	3555	55
	Lr13R1	ACCATACAGCTATCTCAGGATA		
<i>Lr13</i> (CDS ²)	Lr13F5	GCTCGGTCCTGTTGTGCCA	453	62
	Lr13R6	GAGCAATTATCCGGCATTCTG		

^a the expected PCR product size before digestion, PCR products of the *HBAU-Lr13* marker were digested using restriction enzyme *HindIII*.

Table S2. Segregation of seedling reactions to the *Pt* pathotype PHQS in “Klein Proteo”, “Zhengzhou 5389”, and their selected F_{3:4} lines.

Material	Total	Infection types			Chi-square tests
		Homozygous Resistance	Heterozygous	Homozygous Susceptible	
Klein Proteo	20	20			
Zhengzhou 5389	20			20	
KPZ-30 F _{3:4} lines	114	30	55	29	$\chi^2_{1:2:1} = 0.158$

Table S3. Information of designated *Lr* genes on chromosome 2BS

Gene	Origen	Marker	Reference
<i>Lr13</i>	<i>T. aestivum</i>	<i>HBAU-Lr13</i> (diagnostic marker)	Yan et al. [7]
<i>Lr16</i>	<i>T. aestivum</i>	<i>2BS-5175914_kwm849</i> (co-segregating marker)	Kassa et al. [30]
<i>Lr23</i>	<i>T. durum</i>	<i>sun471</i> (co-segregating marker)	Chhetri et al.[31]
<i>Lr35</i>	<i>Ae. speltoides</i>	<i>BCD260F1/35R2</i> (co-segregating marker)	Seyfarth et al. [32]
<i>Lr48</i>	<i>T. aestivum</i>	<i>IWB36920</i> (co-segregating marker)	Nsabiyea et al. [33]
<i>Lr73</i>	<i>T. aestivum</i>	<i>XwPt8760</i> and <i>wPt-4453</i> (flanking markers)	Park et al. [34]

Table S4. Information of 12 DEGs in the 114-168 Mb interval on chromosome 2B

Gene ID (CS RefSeq v1.1)	Reads Counts		Gene Description
	R-bulk	S-bulk	
TraesCS2B02G148500	76	2	Lectin receptor kinase
TraesCS2B02G181900	70.01400236	7.00210906	3-isopropylmalate dehydratase large subunit
TraesCS2B02G182800	2222	690	NBS-LRR disease resistance protein
TraesCS2B02G152300	212.3721414	1243.90742	Haloacid dehalogenase-like hydrolase domain-containing protein 3
TraesCS2B02G156100	17.35019282	161.9945552	N-alpha-acetyltransferase
TraesCS2B02G160900	0	48.35694742	ARM repeat superfamily protein
TraesCS2B02G161000	0	108	ARM repeat superfamily protein
TraesCS2B02G163300	0	393	Protein DETOXIFICATION
TraesCS2B02G163800	3.174273137	114.6136807	Calcium-binding protein 39
TraesCS2B02G164100	7.361561896	66.42063856	Mitochondrial inner membrane translocase subunit Tim44
TraesCS2B02G164200	40	223	BSD domain-containing protein 1
TraesCS2B02G184100	11.07687143	99.36795167	GTPase obg