

**Supplementary Information for “*Pm57* from ‘*Aegilops searsii*
encodes a novel tandem kinase protein conferring powdery
mildew resistance in bread wheat’ by Yue Zhao et al.**

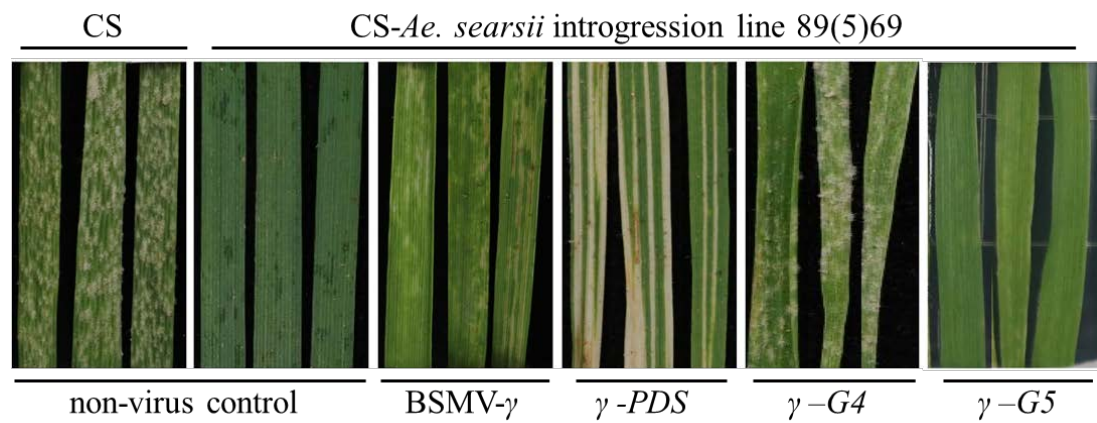


Fig. S1 Representative images showing the results of VIGS. γ -G4 (G4-VIGS) and γ -G5 (G5-VIGS) are two constructs targeting G4 and G5, respectively. γ -PDS (BSMV-TaPDS) targeting phytoene desaturase gene was used as a control to illustrate the effect of gene silencing, while BSMV- γ was used as the empty vector control.

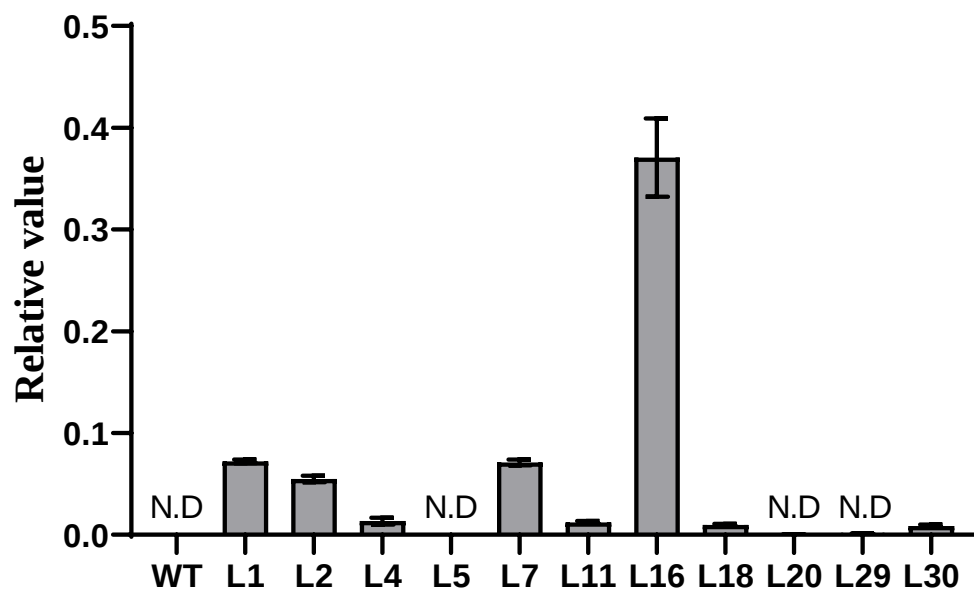


Fig. S2 Transcript levels of *WTK7-vWA* in the leaves of T_0 transgenic plants. Bars indicate standard deviations of three replicates. WT, non-transgenic control Fielder; N.D, Not Detected. There was no expression of *WTK7-vWA* gene in the positive transgenic lines L20 and L29, explaining why these two positive lines behaved susceptible to powdery mildew.

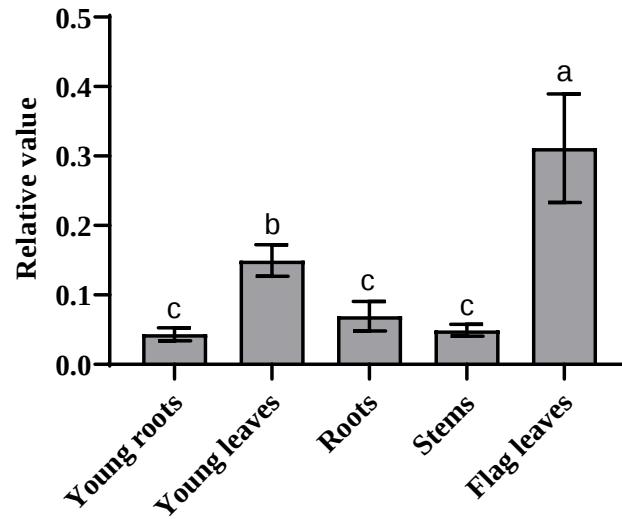


Fig. S3 *Pm57* expression in various tissues. Expression levels of *Pm57* in different organs including young roots (three-leaf period), young leaves (three-leaf period), roots (heading stage), stems (heading stage) and flag leaves (heading stage). The *TaActin1* gene was used as an internal reference. Data are mean $\pm$ SD for three replicates. Different lowercase letters above the bars denote significant differences at the $p < 0.05$ level.

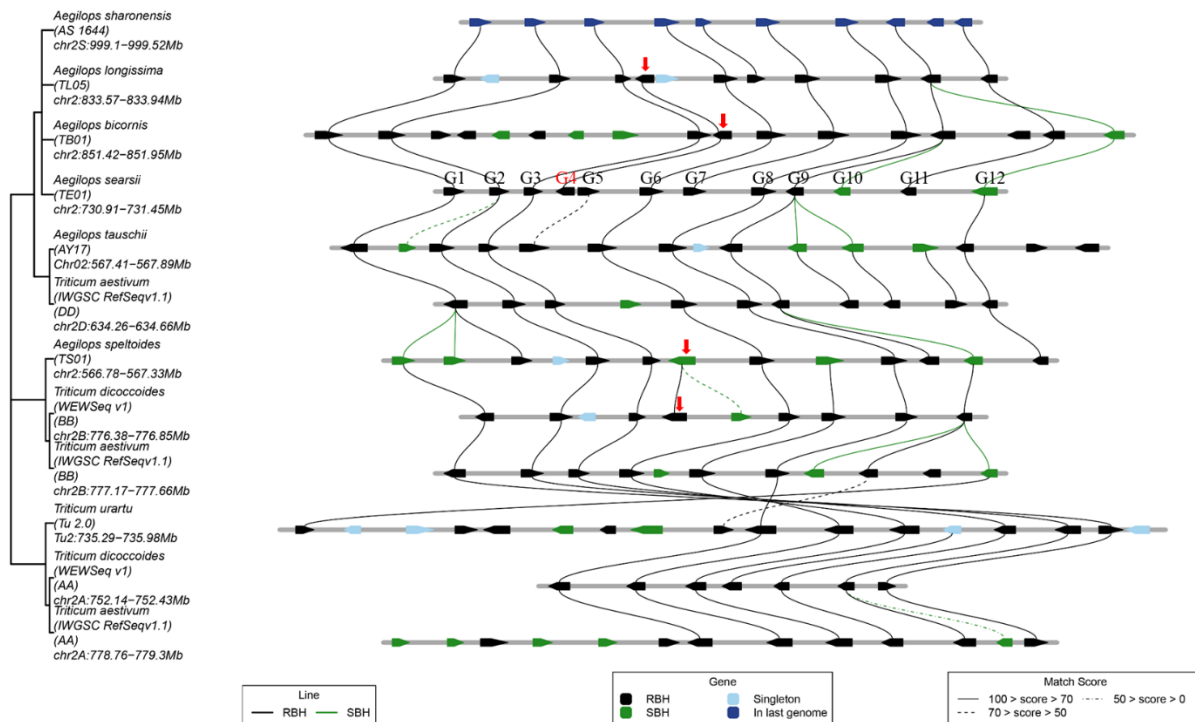


Fig. S4 Collinearity of the *Pm57* genomic regions in Triticeae and related species. Collinearity analysis was performed using the online tool Triticeae-GeneTribe²⁹. Orthologous genes are linked by lines, and *Pm57* (G4) orthologs are shown in red arrows. The *Pm57* orthologs were present only in *Aegilops bicornis* (TB01) (S^bS^b), *Ae. longissima* (TL05) (S^lS^l), *Ae. speltoides* (TS01) (SS), and B sub genome of *T. dicoccoides* (WEWSeq v1) (AABB).

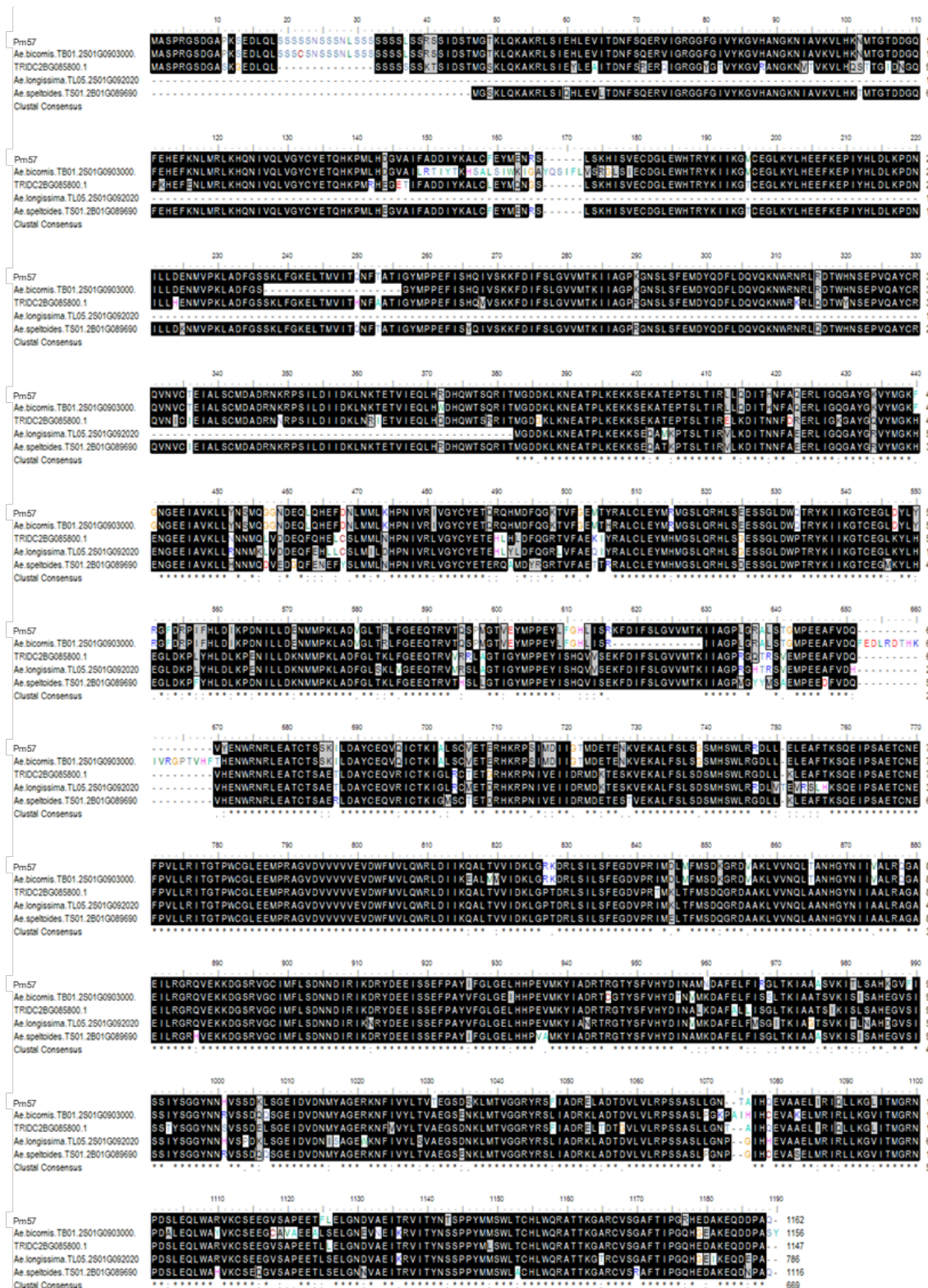


Fig. S5 Comparison of amino acid sequences of Pm57 and its orthologs. Amino acid residues conserved in all five sequences are marked in star.

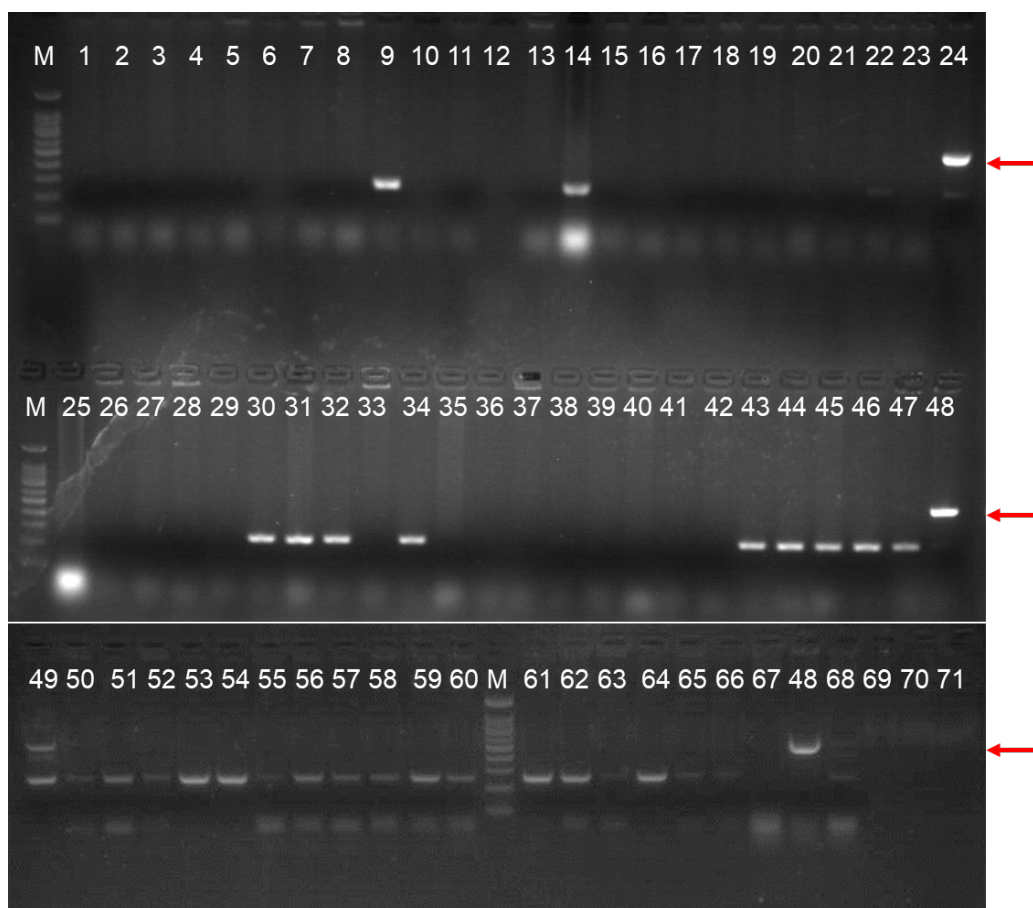


Fig. S6 Validation of sequence tagged site (STS) marker *STS-Pm57*. M, 1 kb ladder; 1-71 was listed in Table S6. Red arrows indicate the amplified fragment of *Pm57* gene.



Fig. S7 *Pm57* confers an all-stage resistant against powdery mildew. (a-b) Evaluation of the powdery mildew resistance in *WTK7-vWA* transgenic plants at the adult plant stage in the greenhouse. The '+' and '-' signs on each leaf designate the presence or absence of *WTK7-vWA* gene.

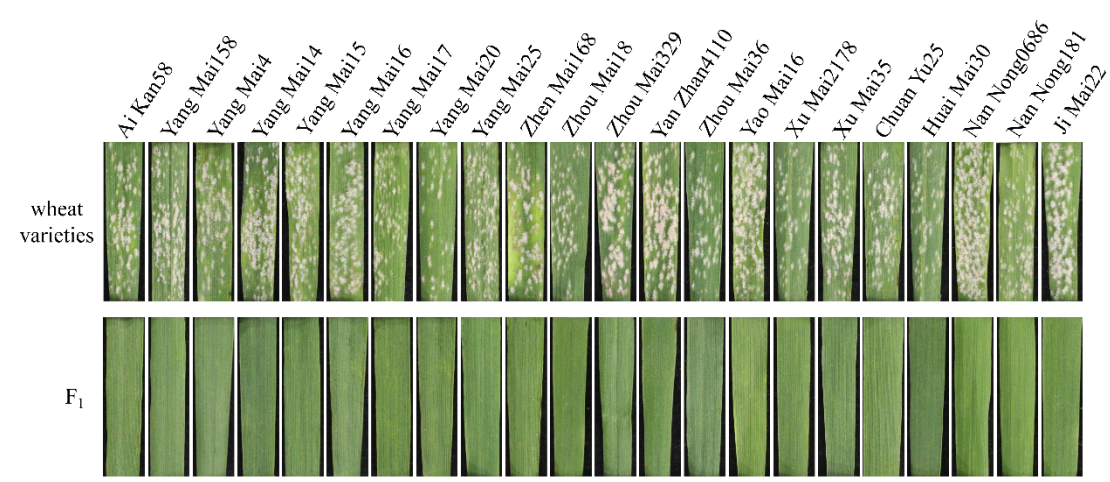


Fig. S8 Effect of genetic background on powdery mildew resistance of *Pm57*. *Pm57* was transformed to different wheat genetic background using introgression line with small alien segments containing *Pm57* as the female parent and 22 wheat varieties as the male parent, respectively. It was found that all of the F₁ plants showed high resistance to powdery mildew.

Pm57
 Lr9
 Pm24
 Sx62
 Rgp1
 WTK4
 Yr15
 Un8
 Sx60

1
 1
 100
 1
 23
 22
 1
 1
 1

Pm57
 Lr9
 Pm24
 Sx62
 Rgp1
 WTK4
 Yr15
 Un8
 Sx60

67
 71
 187
 38
 122
 103
 42
 45
 36

Mut223

G78D

Pm57
 Lr9
 Pm24
 Sx62
 Rgp1
 WTK4
 Yr15
 Un8
 Sx60

167
 171
 286
 136
 221
 202
 132
 133
 134

I

II

III

Pm57
 Lr9
 Pm24
 Sx62
 Rgp1
 WTK4
 Yr15
 Un8
 Sx60

265
 269
 381
 233
 318
 299
 221
 219
 228

Mut141

G177E

Mut51

G193R

Vla

Catalytic loop

Mut210

Vib

D209N

VII

Activation loop

VIII

Pm57
 Lr9
 Pm24
 Sx62
 Rgp1
 WTK4
 Yr15
 Un8
 Sx60

361
 365
 471
 321
 408
 388
 314
 312
 328

IX

Pm57
 Lr9
 Pm24
 Sx62
 Rgp1
 WTK4
 Yr15
 Un8
 Sx60

411
 415
 546
 403
 429
 397
 349
 374
 428

Mut92

G424D

Pm57
 Lr9
 Pm24
 Sx62
 Rgp1
 WTK4
 Yr15
 Un8
 Sx60

500
 504
 643
 499
 517
 487
 413
 443
 501

I

II

III

Pm57
 Lr9
 Pm24
 Sx62
 Rgp1
 WTK4
 Yr15
 Un8
 Sx60

584
 588
 729
 585
 600
 568
 512
 516
 589

Vla

Vib

VII

Catalytic loop

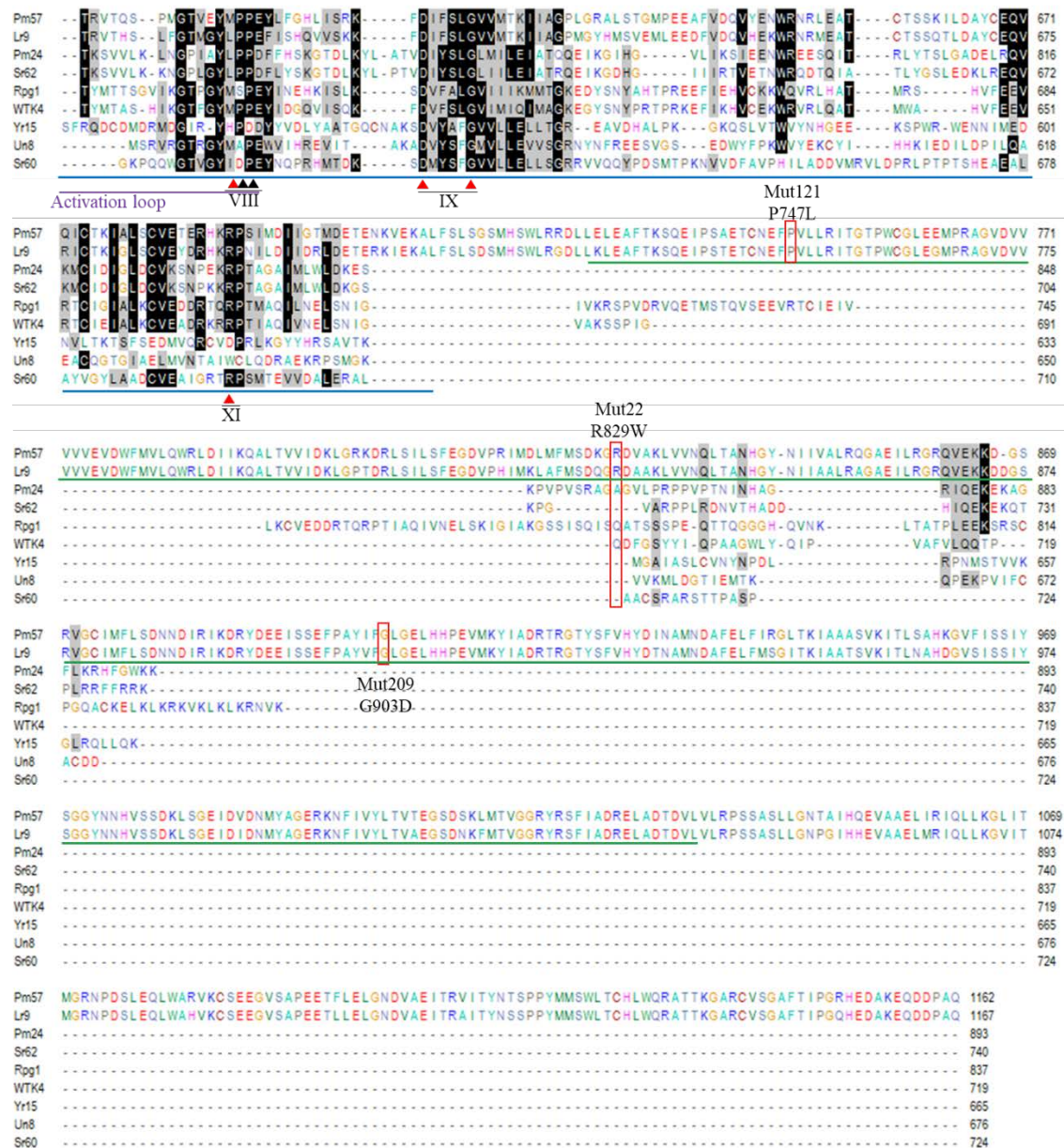


Fig. S9 Sequence alignment of WTK Proteins. Based on the sequence conservation of the key amino acid residues in the two kinase domains, the Pm57 Kin I (orange line) is classified as a non-RD kinase and a serine/ threonine protein kinase. The Pm57 Kin II (blue line) is a putative pseudokinase. vWA domain is shown in green line. Black triangles indicate ATP binding site; red triangles indicate key conserved residues; and green triangles positions determining RD or non-RD kinase. The catalytic loop and the activation loop are indicated by light blue and purple colors, respectively. EMS missense mutations that resulted in loss of Pm57 function are indicated by red boxes.

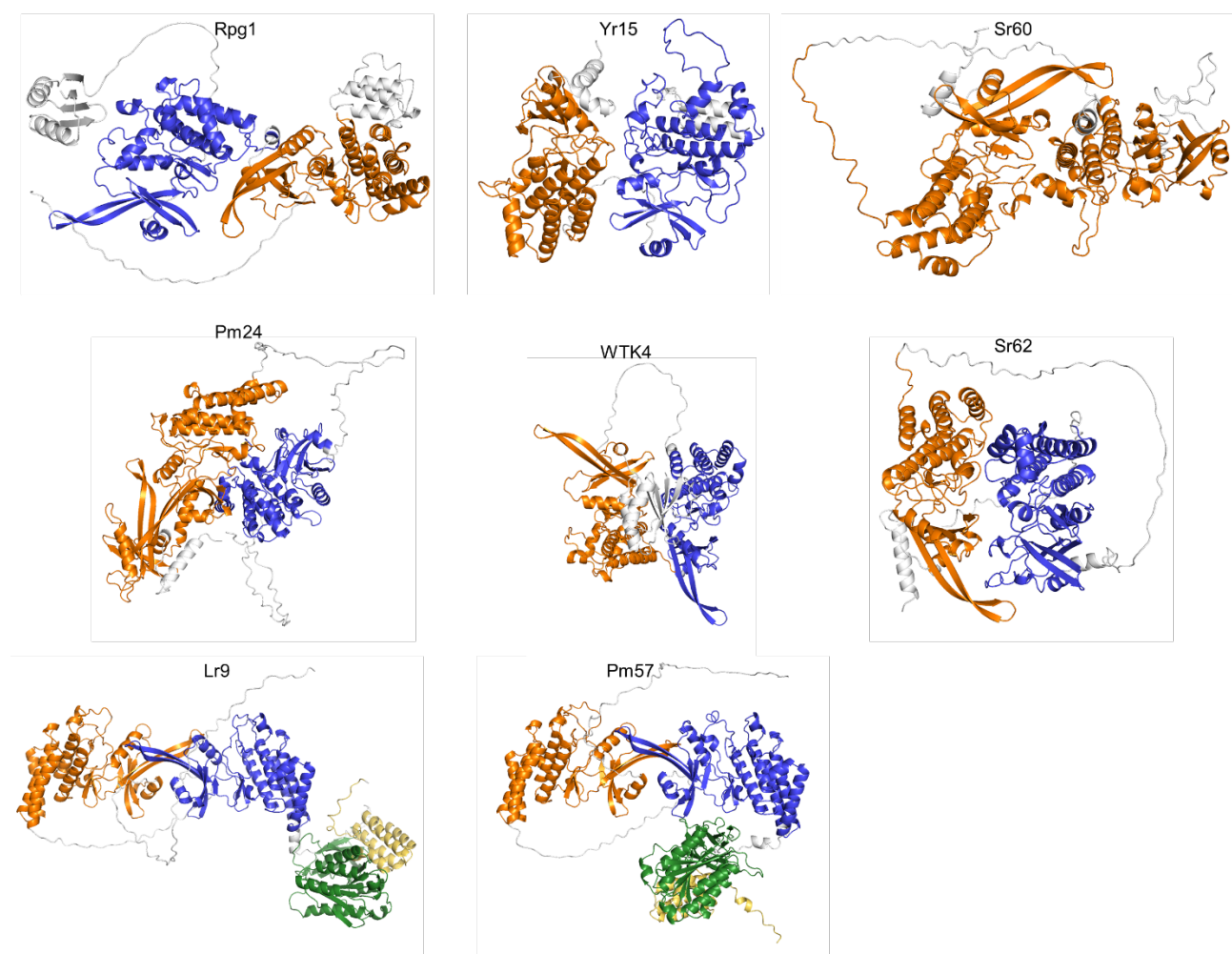


Fig. S10 Protein structure prediction of eight cloned WTKs. Three-dimensional model of eight WTKs is predicted by AlphaFold. Orange, kinase domain; blue, pseudokinase domain; Green, vWA domain; Yellow, putative Vwaint domain. The first kinase domain (Kin I) for each protein is shown to the left of that protein structure.

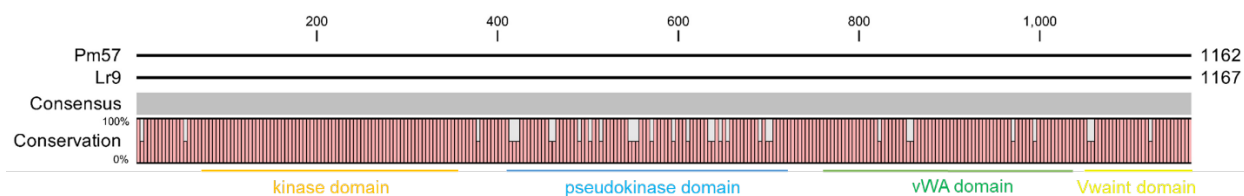


Fig. S11 Alignment of amino acid sequences of Pm57 and Lr9. The position of the underscore denotes the location of different structural domains. The sequences of Pm57 and Lr9 were compared using CLC Sequence Viewer 7 software.

Supplementary Table S1 Primers used in this study.

Name	Forward primer	Reverse primer	Application
X1	TTCGATTTACATGTTGGGTTAC	AATGACCACCGGCAGTAGTACA	Fine mapping, STS marker
X2	CCTCATGTGCCACAACAAGT	AAGCTCACTGTTAGAAGGTCGA	Fine mapping, STS marker
X3	TCAGCGCACCAGACACTTGT	AGCTCAAAGGGGACGACTGTG	Fine mapping, STS marker
X4	CTTACTTGCCAGACCGTTGCT	GTTACACGGGGTGGAGAGTC	Fine mapping, STS marker
X5	CCGACGCTTATCAGAATCATC	ACCCGACTAAGGTTGATCTCTA	Fine mapping, STS marker
X6	GCTTGTCTCAAGGTCTATTC	CCCTATACTTGTGGGTTATCAATC	Fine mapping, STS marker
X7	GGCGGACAAAACACTACTCAGC	GCCTAAGCGCCTCGTATCAC	Fine mapping, STS marker
X8	CGAACCTTGACTTGGCTGCT	GCCGTTGAGAATCTTCCATG	Fine mapping, STS marker
X9	AGGGCACGGAAGAGACATGT	CGCTGTGTCTCCTGGAAGTG	Fine mapping, STS marker
X10	GAGGATCTCCTCGGCCGA	TGCCGTAGATGATGGGGATT	Fine mapping, STS marker
X11	CGTTTTGATGCCTTGAGAGC	GTGATGATGTGATGTGGCATG	Fine mapping, STS marker
X12	GCTGATTCGAGTCTTGAGCCA	GGTCAGTGCACCATTCCCAT	Fine mapping, STS marker
X13	CAACATCATCTTCAACATCGGTG	TGCACACGAGCACGTCGAGA	Fine mapping, STS marker
X14	AGTCGTCCGCATCATCATGT	TGGTATGTGCCACTGTTCAA	Fine mapping, STS marker
X15	GCCCACGACTTTCAGCC	TCCAATGCAGGGTTTCCTATA	Fine mapping, STS marker
X16	CGACATCGATCAGGTCATTG	GGTGTCCCCTCTAGTATGTACG	Fine mapping, STS marker
1F/1R	GTGAAGCACAGGGACGATTG	CATCCGCACACCTACAGTTAC	Mutants analysis
2F/2R	ACAAGCAGGTGAGAACATCCT	CGGGAAACTCGTTACATGTC	Mutants analysis
3F/3R1	AAGTACCGGAATGCCTGAAG	ATACTATTGTGCTGGGTCGT	Mutants analysis
2F2/2R2	GGACACATGGCACAATTCTG	GCCAACAATCCGTACAATGT	Mutants analysis
1F/3R1	GTGAAGCACAGGGACGATTG	ATACTATTGTGCTGGGTCGT	Gene cloning and sequencing
G4-VIGS	CATTTTTTTTTTTTTTTAGCTAGCTCATCCGGATCCAGCTTCTC	GATGATTCTTCTTCCGTTGCTAGCCTGCCACAGGTGACAAGTCA	BSMV-VIGS assay
G5-VIGS	CATTTTTTTTTTTTTTTAGCTAGCCGTCCGACTGCTGCTCAATT	GATGATTCTTCTTCCGTTGCTAGCTGGCTCCAGAGGTAAGGCTAC	BSMV-VIGS assay

G4-OE	AGGTCGACTCTAGAG <u>GATCC</u> ATGGCGTCTCCTCGCG	AGCTCGGTACCCGGG <u>GATCC</u> CTATTGTGCTGGGTCGTC	<i>ProUbi:WTK7-vWA</i> construction
3F/2R	AAGTACCGGAATGCCTGAAG	CGGGAAACTCGTTACATGTC	Examination of transgenic plants
eGFP-IF1-F/R	GGCTCGAGAAGCTT <u>GATCC</u> ATGGCGTCTCCTCGC	TTATCTAGATCCGGT <u>GATCC</u> CTATTGTGCTGGGTC	Subcellular localization
SSF2/SSR2	TCATCCGGATCCAGCTTCTC	CTGCCACAGGTGACAAGTCA	qRT-PCR
PR1	CTGGAGCACGAAGCTGCAG	CGAGTGCTGGAGCTTGCAGT	qRT-PCR
PR2	CTCGACATCGGTAACGACCAG	GCGGCGATGTACTTGATGTTC	qRT-PCR
PR3	AGAGATAAGCAAGGCCACGTC	GGTTGCTCACCAGGTCCTTC	qRT-PCR
PR4	CGAGGATCGTGGACCAGTG	GTCGACGAACTGGTAGTTGACG	qRT-PCR
PR9	GAGATTCCACAGATGCAAACGAG	GGAGGCCCTTGTTTCTGAATG	qRT-PCR
TaActin1	GTTGGTGATGAGGCCCAATC	GTGCTACACGGAGCTCATTG	qRT-PCR
STS-F/R	AGGGAGATATGCTTTGGTTACAT	CTCGTTGCTGAGAACACCACTT	Gene-specific primers for MAS

Supplementary Table S2 Read counts of the twelve genes within the *Pm57* mapping interval in the *Pm57* mutants.

Type	Gene	ID	209-1	51-3	216-2	141-3	60-3	89(5)69
gene_count	G1	Asea EVM0036665	0	0	0	0	0	0
gene_count	G2	Asea EVM0051586	371	432	151	369	285	348
gene_count	G3	Asea EVM0012740	0	0	0	0	0	0
gene_count	G4	Asea EVM0016946	943	1710	1133	826	1268	1340
gene_count	G5	Asea EVM0041895	45	77	18	66	64	21
gene_count	G6	Asea EVM0018635	166	2	2	27	18	50
gene_count	G7	Asea EVM0050643	92	190	112	61	102	73
gene_count	G8	Asea EVM0056562	639	1077	475	772	635	788
gene_count	G9	Asea EVM0002576	104	85	51	26	57	92
gene_count	G10	Asea EVM0023928	136	115	34	7	35	59
gene_count	G11	Asea EVM0051934	18	47	2	22	8	18
gene_count	G12	Asea EVM0049887	0	2	1	0	0	0

Supplementary Table S3 Powdery mildew evaluation of the T₁ transgenic plants to *Bgt* isolate E09.

T ₁ transgenic family	Trangenic positive plants			Trangenic negative plants	
	No. of positive plants	No. of resistant plants	No. of susceptible plants	No. of negative plants	No. of susceptible plants
L1	11	11	0	1	1
L2	12	12	0	0	0
L3	9	9	0	3	3
L4	8	8	0	4	4
L5	0	0	0	12	12
L6	12	12	0	0	0
L7	8	8	0	4	4
L8	9	9	0	3	3
L9	11	11	0	0	0
L10	10	10	0	1	1
L11	10	10	0	1	1
L12	8	8	0	4	4
L13	9	9	0	2	2
L14	9	9	0	3	3
L15	11	11	0	0	0
L16	12	12	0	0	0
L17	9	9	0	2	2
L18	9	9	0	3	3
L19	11	11	0	0	0
L20	10	0	10	1	1
L21	11	11	0	1	1
L22	12	12	0	0	0
L23	0	0	0	12	12
L24	9	9	0	2	2
L25	10	10	0	2	2
L26	8	8	0	2	2
L27	0	0	0	11	11
L28	9	9	0	3	3
L29	12	0	12	0	0
L30	10	10	0	2	2
L31	12	12	0	0	0
L32	11	11	0	0	0
L33	8	8	0	4	4
L34	12	12	0	0	0
L35	10	10	0	2	2
L36	9	9	0	3	3

Supplementary Table S4 The proteins with the tandem kinase -vWA domains or a single kinase domain followed by a vWA domain in plants.

Accession name	Tandem kinase -vWA	Genomic positions	Single kinase-vWA
Chinese Spring	-	-	TraesCS1B03G0954800.1
			TraesCS2D03G0134600.1
			TraesCS3D03G0964900.2
			TraesCS4B03G0790000.1
			TraesCS6B03G0135900.1
			TraesCS7B03G1156100.1
			TraesCS7D03G1191500.1
Fielder	Fielder-2A: manually annotated gene	chr2A_Fielder:768778667-768796762	TraesFLD1B01G382300.1
	Fielder-2B: manually annotated gene	chr2B_Fielder:779548621-779573097	TraesFLD2D01G082600.1
Zang1817	Zang1817-2B: manually annotated gene	chr2B_Zang1817:772202987-772212893	TraesFLD3D01G477300.1
			TraesFLD4B01G329400.1
Attraktion	Attraktion-chr2A: manually annotated gene	chr2A_Attraktion:767654376-767672471	Not Available
	Attraktion-chr2B: manually annotated gene	chr2B_Attraktion:752184148-752192672	
ArinaLrFor	ArinaLrFor-2A: manually annotated gene	chr2A_ArinaLrFor:764538079-764555160	TraesARI1B01G376000.1
	ArinaLrFor-2B: manually annotated gene	chr2B_ArinaLrFor:783149651-783174127	TraesARI2D01G076100.1
CDC Landmark	CDC_Landmark-2B: manually annotated gene	chr2B_CDC_Landmark:771311714-771320369	TraesARI3D01G465000.1
			TraesARI4B01G323100.1
			TraesLDM1B01G373600.1
			TraesLDM2D01G078400.1
CDC Stanley	CDC_St Stanley-2B: manually annotated gene	chr2B_CDC_St Stanley:773551786-773560523	TraesLDM3D01G471200.1
			TraesLDM4B01G328300.1
			TraesSTA1B01G375600.1
			TraesSTA2D01G078100.1
CDC Stanley	CDC_St Stanley-2B: manually annotated gene	chr2B_CDC_St Stanley:773551786-773560523	TraesSTA3D01G489500.1
			TraesSTA4B01G323200.1

Julius	-	-	TraesJUL1B01G375400.1 TraesJUL2D01G077700.1 TraesJUL3D01G475200.1 TraesJUL4B01G323500.1
LongReach Lancer	-	-	TraesLAC1B01G378900.1 TraesLAC2D01G078200.1 TraesLAC3D01G473200.1 TraesLAC4B01G324700.1
Mace	Mace-2A: manually annotated gene	chr2A_Mace:763414514-763432288	TraesMAC2D01G081000.1 TraesMAC3D01G458600.1 TraesMAC4B01G324900.1
Norin61	chr2B_Norin61: manually annotated gene	chr2B_Norin61: 777899697-777929002	TraesNOR2D01G078100.1 TraesNOR3D01G471500.1 TraesNOR4B01G328400.1
<i>Triticum spelta</i> _PI190962	-	-	Not Available
SY Mattis	SY_Mattis-2A: manually annotated gene	chr2A_SY_Mattis:765940564-765957716	TraesSYM1B01G370400.1 TraesSYM2D01G079500.1 TraesSYM3D01G462100.1 TraesSYM4B01G323000.1
Renan	Renan-2A: manually annotated gene Renan-2B: manually annotated gene	chr2A_Renan:768921120-768939207 chr2B_Renan:783078687-783087198	TraesRN1B0100974400.1 TraesRN2D0100150400.1 TraesRN3D0101007100.1
Kariega	-	-	TraesKAR1B01G0042160.1 TraesKAR1B01G0379500LC.1 TraesKAR2D01G0025780.1 TraesKAR3B01G0487400.1 TraesKAR3D01G0398130.1 TraesKAR4B01G0395050.1

Svevo (tetraploid durum wheat)	-	-	TRITD1Bv1G016880.1
			TRITD1Bv1G185910.1
			TRITD2Av1G015640.1
			TRITD3Bv1G244120.1
			TRITD5Bv1G244810.2
Zavitan (tetraploid wild emmer wheat)	TRIDC2BG085800.1	chr2B_Wild_emmerV2:797534515-797558995	TRIDC1BG056560.6
<i>Triticum urartu</i> _G1812	-	-	-
<i>Aegilops bicornis</i> _TB01	Ae.bicornis.TB01.2S01G0903000.1	chr2S_ae.bicornis.TB01:851590434-851600918	Ae.bicornis.TB01.2S01G0102900.1
			Ae.bicornis.TB01.2S01G0015300.1
			Ae.bicornis.TB01.Un01G0378900.1
<i>Aegilops longissima</i> _TL05	-	-	Ae.longissima.TL05.2S01G0024000.1
			Ae.longissima.TL05.2S01G0920200.1
			Ae.longissima.TL05.3S01G0689100.1
<i>Aegilops searsii</i> _TE01	WTK7: manually annotated gene base on Ae.searsii.TE01.2S01G0858700 (Previous_id: Asea EVM0016946) and RNA-seq data	chr2S_ae.searsii.TE01: 730956195-730965667	Ae.searsii.TE01.2S01G0908600.1
			Ae.searsii.TE01.4S01G0582500.1
			Ae.searsii.TE01.5S01G0802700.4
<i>Aegilops sharonensis</i> _TH02	-	-	Ae.sharonensis.TH02.2S01G0098400.1
			Ae.sharonensis.TH02.3S01G0682100.1
<i>Aegilops speltoides</i> _TS01	Ae.speltoides.TS01.2B01G0896900.1	chr2B_ae.speltoides.TS01:566961159-566972987	Ae.speltoides.TS01.1B01G0150800.1
			Ae.speltoides.TS01.1B01G0531500.1
<i>Aegilops tauschii</i> _AY17	-	-	AetAY17_2Dv1G097200.1
			AetAY17_3Dv1G747300.1
<i>Thinopyrum intermedium</i>	-	-	Thint.05G0470400.1
			Thint.02G0441600.1
			Thint.08G0530700.1
			Thint.V0435300.1
<i>Ceratodon purpureus</i> _R40	-	-	CepurR40.VG339300.1
			CepurR40.2G134200.1
			CepurR40.6G128600.1
			CepurR40.2G134300.1
<i>Eleusine coracana</i>	-	-	ELECO.r07.9BG0699310.1
			ELECO.r07.9AG0670800.1

Supplementary Table S5 Infection type of CS-*Ae. searsii* chromosome 2S^s introgression line 89(5)69 and transgenic plants to divergent *Bgt* isolates.

<i>Bgt</i>	CS	89(5)69	Fielder	Transgenic plants
GY-KDZ-1	4	0	4	0
HB-XX-WXZ-1	3	0	4	0
SQ-YC-YJZ	3	0	4	0
ZK-CHQ-LHZ-2	4	0	4	0
SL-FS-5	4	0	4	0
SQ-YC-CGS	3	0	4	0
ZK-HY-QLZ-1	4	0;	4	0
ZK-HY-QLZ-2	3	0	4	0
KF-YLH	4	0	4	0
Y01	4	0	4	0
Y02	4	0	4	0
Y03	3	1	4	0
Y04	4	0	4	0
Y06	4	0	4	0
Y07	4	0	4	0
Y08	4	0	4	0
Y09	4	0	4	0
Y10	4	0	4	0
Y11	4	0	4	0
Y14	4	0;	4	0
Y15	4	0	4	0
Y16	4	0	4	0
Y17	4	0	4	0
Y18	3	0	4	0
Y21	4	0	4	0
B18	4	0	4	0
E05	4	0	4	0
E09	4	0	4	0
E26	4	0	4	0

Supplementary Table S6 Wild and cultivated wheat accessions used in this study.

No.	genome	Label	Species	Origin	Accession no.
1	A ^m A ^m	3AA4	<i>T. monococcum</i>	N/A	N/A
2	A ^b A ^b	3AA5	<i>T. boeoticum</i>	Japan	KU-104-1
3	A ^m A ^m	3AA6	<i>T. monococcum</i>	United States	KU-104-2
4	A ^m A ^m	3AA28	<i>T. monococcum</i>	Lebanon	KU-199-15
5	BBAA	IW106	<i>T.dicoccoides</i>	Israel	TZ-108
6	BBAA	Kronos	<i>T.durum</i>	United States	PI 576168
7	BBAA	Langdon	<i>T.durum</i>	United States	CItr 13165
8	BBAA	JY8	<i>T.durum</i>	N/A	N/A
9	BBAADD	YT-2	<i>T. aestivum</i> ssp. <i>yunnanese</i>	China	N/A
10	BBAADD	YT-6	<i>T. aestivum</i> ssp. <i>yunnanese</i>	China	N/A
11	BBAADD	YT-19	<i>T. aestivum</i> ssp. <i>yunnanese</i>	China	N/A
12	BBAADD	YT-31	<i>T. aestivum</i> ssp. <i>yunnanese</i>	China	N/A
13	BBAADD	YT-32	<i>T. aestivum</i> ssp. <i>yunnanese</i>	China	N/A
14	GGAA	AR1	<i>T. araraticum</i> Jakubz.	N/A	N/A
15	BBAADD	MA1	<i>T. aestivum</i> ssp. <i>macha</i>	N/A	N/A
16	BBAADD	MA2	<i>T. aestivum</i> ssp. <i>macha</i>	N/A	N/A
17	BBAADD	MA3	<i>T. aestivum</i> ssp. <i>macha</i>	N/A	N/A
18	BBAADD	Altgold	<i>T. aestivum</i> ssp. <i>spelta</i>	N/A	Altgold
19	BBAADD	Hubel	<i>T. aestivum</i> ssp. <i>spelta</i>	Switzerland	Hubel
20	BBAADD	3418	<i>T. aestivum</i> ssp. <i>spelta</i>	N/A	N/A
21	BBAADD	S11-7	<i>T. aestivum</i> ssp. <i>spelta</i>	N/A	N/A
22	BBAADD	S11-8	<i>T. aestivum</i> ssp. <i>spelta</i>	N/A	N/A
23	BBAADD	S11-9	<i>T. aestivum</i> ssp. <i>spelta</i>	N/A	N/A
24	N/A	89(5)69	<i>CS-Ae. searsii</i> chromosome 2Ss introgression line	China	TA5109
25	BBAADD	S11-10	<i>T. aestivum</i> ssp. <i>spelta</i>	N/A	S11-10
26	BBAADD	S11-11	<i>T. aestivum</i> ssp. <i>spelta</i>	N/A	S11-11
27	BBAADD	S11-12	<i>T. aestivum</i> ssp. <i>spelta</i>	N/A	S11-12
28	BBAADD	S11-13	<i>T. aestivum</i> ssp. <i>spelta</i>	N/A	S11-13
29	BBAADD	S11-14	<i>T. aestivum</i> ssp. <i>spelta</i>	N/A	S11-14
30	BBAADD	S11-16	<i>T. aestivum</i> ssp. <i>spelta</i>	N/A	S11-16
31	BBAADD	S11-17	<i>T. aestivum</i> ssp. <i>spelta</i>	N/A	S11-17
32	BBAADD	S11-18	<i>T. aestivum</i> ssp. <i>spelta</i>	N/A	S11-18
33	BBAADD	S11-19	<i>T. aestivum</i> ssp. <i>spelta</i>	N/A	S11-19
34	BBAADD	S11-22	<i>T. aestivum</i> ssp. <i>spelta</i>	N/A	S11-22
35	BBAADD	S12-2	<i>T. aestivum</i> ssp. <i>spelta</i>	N/A	S12-2
36	BBAADD	S12-3	<i>T. aestivum</i> ssp. <i>spelta</i>	N/A	S12-3
37	BBAADD	S12-7	<i>T. aestivum</i> ssp. <i>spelta</i>	N/A	S12-7
38	BBAADD	S12-10	<i>T. aestivum</i> ssp. <i>spelta</i>	N/A	S12-10
39	BBAADD	S12-13	<i>T. aestivum</i> ssp. <i>spelta</i>	N/A	S12-13
40	BBAADD	XM001303	<i>T. aestivum</i> ssp. <i>tibetanum</i>	China	XM001303

41	BBAADD	AS1772	<i>T. aestivum</i> ssp. <i>tibetanum</i>	China	AS1772
42	BBAADD	XM001202	<i>T. aestivum</i> ssp. <i>tibetanum</i>	China	XM001202
43	BBAADD	XM001203	<i>T. aestivum</i> ssp. <i>tibetanum</i>	China	XM001203
44	BBAADD	XM001231	<i>T. aestivum</i> ssp. <i>tibetanum</i>	China	XM001231
45	BBAADD	XM001237	<i>T. aestivum</i> ssp. <i>tibetanum</i>	China	XM001237
46	BBAADD	XM001238	<i>T. aestivum</i> ssp. <i>tibetanum</i>	China	XM001238
47	BBAADD	XM001264	<i>T. aestivum</i> ssp. <i>tibetanum</i>	China	XM001264
48	S ^s S ^s	TE01	<i>Ae. searsii</i>	N/A	N/A
49	BBAADD	WL711	<i>T. aestivum</i>	China	WL711
50	BBAADD	TM198	<i>T. aestivum</i>	China	Tian Min198
51	BBAADD	JM20	<i>T. aestivum</i>	China	Ji Mai20
52	BBAADD	TM369	<i>T. aestivum</i>	China	Tian Min369
53	BBAADD	BN207	<i>T. aestivum</i>	China	Bai Nong207
54	BBAADD	XN979	<i>T. aestivum</i>	China	Xi Nong979
55	BBAADD	KN199	<i>T. aestivum</i>	China	Ke Nong199
56	BBAADD	Y49-198	<i>T. aestivum</i>	China	Yu Mai49-198
57	BBAADD	Z7698	<i>T. aestivum</i>	China	Zheng Mai7698
58	BBAADD	AK58	<i>T. aestivum</i>	China	Ai Kang58
59	BBAADD	FDC5	<i>T. aestivum</i>	China	Feng De Cun5
60	BBAADD	Z18	<i>T. aestivum</i>	China	Zhou Mai18
61	BBAADD	PA0518	<i>T. aestivum</i>	China	Ping An0518
62	BBAADD	PA602	<i>T. aestivum</i>	China	Ping An602
63	BBAADD	YZ411	<i>T. aestivum</i>	China	Yan Zhan411
64	BBAADD	Z22	<i>T. aestivum</i>	China	Zhou Mai22
65	BBAADD	Fielder	<i>T. aestivum</i>	United States	CItr 17268
66	BBAADD	CB037	<i>T. aestivum</i>	China	CB037
67	BBAADD	CS	<i>T. aestivum</i>	China	Chinese Spring
68	A ^u A ^u	TMU38	<i>T. urartu</i>	Israel	TMU38
69	A ^b A ^b	TMB02	<i>T. boeoticum</i>	Israel	TMB02
70	DD	TQ27	<i>Ae. tauschii</i>	N/A	TQ27
71	DD	Y2282	<i>Ae. tauschii</i>	N/A	Y2282
