

1 **Supplementary Material**

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3 Table S1. Primer sequences, amplicon size and optical read temperatures for Quantitative

4 RT-PCR assays.

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Assay	Primers 5' to 3' sequences	Product size	Optical read temp.	Reference
18s rRNA	18S_F: atacgtgcaacaaccc 18S_R: ctacctccccgtgtca	288bp	81°C	Beales et al (2007)
<i>TaCO1</i>	HvCO1MidF1 : ggggcagagcaggtgcctc HvCO1MidR1: tggcttctctctccttgagc	207bp	81°C	from barleyAF490467 Griffiths et al (2003)
<i>TaGI</i>	Gi_F: caattgccacaccaagtgcta Gi_R: tgatgaattcagaggtacaacca	497bp	81°C	Beales et al (2007)
2A <i>PRR</i> gene	TaPRR72_AgF7: gtggtcaccaagcccgcc TaPRR72_AgR6: gctgcggtgctccatta	356 bp	81°C	This paper
2B <i>PRR</i> gene	TaPRR72_BgF1: agacgattcattccgctcc HvPRR72_R6_2: agcagcaccatttgagagg	659 bp	81°C	Beales et al (2007)
<i>TaFT1</i>	JD_TaFT_F3 cagcagcccagggttgag JD_TaFT_R3 atctgggtctaccatcacgagtg	68 bp (In DQ890162)	81°C	Yan et al (2006)

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1 Table S2. Phenotypic measurements of parental lines grown in 10h of natural light
 2 (experiment 1). Days to 50% ear emergence from the flag leaf.

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Line	Type	Photoperiod insensitive parent	Days to ear emergence from 1st May	SD	Days difference in flowering
GS-100	In	Westbred 881	70.8	± 1.7	
GS-101	S		106.5	± 1.7	35.8
GS-102	S		109.8	± 3.2	36.3
GS-103	In	Westbred 881	73.5	± 0.7	
GS-104	S		105.0	± 1.4	29.3
GS-105	In	Corm 'S'-Rufo 'S'	75.8	± 2.2	
GS-106	In	Nile	75.2	± 1.3	
GS-107	S		108.0	± 3.5	32.8
GS-108	In	not specified	76.0	± 1.4	
GS-109	S		108.3	± 5.7	32.3

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5 Each pair has a photoperiod sensitive (S) and insensitive (In) line. For the 'GS-104'/'GS-105'
 6 and 'GS-108'/'GS-109' pairs the classification is the reverse of that given in Clarke et al.
 7 (1998).

1 Table S3. Phenotypic measurements of F₂ plants grown in 10h of natural light (experiment
 2 2). Days to 50% ear emergence from the flag leaf, days to anthesis and number of fertile
 3 spikelets were recorded from the leading tiller of each plant. Genotype was determined by
 4 PCR assays for the 1027 or 1117 bp A genome deletions.

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Genotype	Type	Number of plants	Days to 50% ear emergence.	Days to anthesis	Fertile spikelet number
GS-100 parent	E	5	75.0	82.0	20.6
GS-101 parent	L	5	117.0	116.0	22.6
GS-100/GS-100 F ₂	E	32	76.7	83.2	19.6
GS-100/GS-101 F ₂	H	75	83.5	89.0	21.9
GS-101/GS-101 F ₂	L	31	117.8	118.6	22.5
L - E F ₂			41.1 **	34.4 **	2.9 **
H - L F ₂			34.3 **	29.6 **	0.6 ns
H - E F ₂			6.8 **	5.8 **	2.3 **
GS-105 parent	E	5	80.0	86.0	20.2
GS-104 parent	L	5	125.0	125.0	26.0
GS-105/GS-105 F ₂	E	29	80.1	86.8	19.8
GS-104/GS-105 F ₂	H	68	88.5	93.4	22.7
GS-104/GS-104 F ₂	L	42	118.6	120.0	25.0
L - E F ₂			38.5 **	33.2 **	5.2 **
H - L F ₂			30.1 **	26.6 **	2.3 **
H - E F ₂			8.4 **	6.6 **	2.9 **

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7 ** significant at $p < 0.01$; (Fisher's LSD); ns, not significant at $p < 0.05$

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1 Table S3

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Genotype	<i>Ppd</i> alleles	Days to 50% ear emergence in short days
GS-100	<i>Ppd-A1a</i> ; <i>Ppd-B1b</i>	67.5 ± 1.0
Chinese Spring	<i>Ppd-A1b</i> ; <i>Ppd-B1a</i> ; <i>Ppd-D1b</i>	89.0 ± 2.2
Chinese Spring (Marquis 2B)	<i>Ppd-A1b</i> ; <i>Ppd-B1b</i> ; <i>Ppd-D1b</i>	did not flower
Opata 85	<i>Ppd-A1b</i> ; <i>Ppd-B1b</i> ; <i>Ppd-D1a</i>	72.5 ± 3.1
Paragon	<i>Ppd-A1b</i> ; <i>Ppd-B1b</i> ; <i>Ppd-D1b</i>	did not flower
Sonora 64	<i>Ppd-A1b</i> ; <i>Ppd-B1a</i> ; <i>Ppd-D1a</i>	56.8 ± 0.5

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5 **Supplementary Figure Legends**
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7 **Fig. S1** Alignment of predicted PRR protein sequences from the 2A, 2B and 2D genes of
8 various wheat genotypes and the 2H chromosome of barley. Tetraploid 2A sequences ('GS-
9 100', 'GS-101', 'GS-104' and 'GS-105') are described in this paper. Hexaploid sequences are
10 CS_A, CS_B and CS_D from 'Chinese Spring' (DQ885753, DQ885757 and DQ885766) and
11 Chey_B from 'Cheyenne' (DQ885760). The barley (H) sequence is from 'Igri' (AY970701).
12 Two conserved regions, the pseudo-receiver domain and CCT domain, are marked by
13 brackets. Red arrows show variant amino-acids distinguishing the tetraploid wheat
14 genotypes. Blue arrows show variant amino-acids distinguishing the tetraploid and hexaploid
15 wheats. The adjacent coloured numbers refer to polymorphisms listed in Table 1 in the main
16 text.

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18 **Fig. S2** Sequence homology of a promoter region identified by alignment of wheat A, B and
19 D genome sequences with barley ('Morex' AY943294), *Brachypodium sylvaticum* (previously
20 analysed by Turner et al. 2005) and rice (AP005199). 6x and 4x refer to hexaploid and
21 tetraploid sequences, respectively. This conserved region of about 100 bp lies in the centre of
22 the minimum region defined by the three deletions and was the only region in the wheat
23 promoter with significant homology to rice identified using BLAST (<http://www.NCBI.org>).
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26 **References cited in Supplementary Information**
27

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