

Supplementary Data

The wheat *Phs-A1* pre-harvest sprouting resistance locus delays dormancy loss during seed after-ripening and maps 0.3 cM distal to the *PM19* genes in UK germplasm.

Oluwaseyi Shorinola, Nicholas Bird, James Simmonds, Simon Berry, Tina Henriksson, Peter Jack, Peter Werner, Tanja Gerjets, Duncan Scholefield, Barbara Balcárková, Miroslav Valárik, Michael J Holdsworth, John Flintham, and Cristobal Uauy.

Fig S1: PHS resistance QTL on chromosome arm 4AL in the Alchemy x Robigus DH population.

Fig S2: After-ripening effect of *Phs-A1* in NILs grown at 13 °C post-anthesis.

Fig S3: Distribution of the sprouting percentage of Option x Claire F4 RILs in sprouting experiment 3.

Fig S4: Alignment of *PM19-A1* coding sequences of UK and Australian germplasm.

Fig S5: Alignment of *PM19-A2* coding sequences of UK and Australian germplasm.

Table S1: Statistical comparison of the GI and sprouting phenotype of Alchemy x Robigus NILs.

Table S2: Information on genes found in the syntenic *Phs-A1* intervals in wheat and *Brachypodium*.

Table S3: KASP SNP assays used to fine map *Phs-A1*.

Table S4: Statistical comparison of the sprouting scores of Option x Claire RILs in sprouting experiment 3.

Table S5: Statistical comparison of the sprouting score of Option x Claire RILs in sprouting experiment 4.

Table S6: Statistical comparison of the sprouting score of Alchemy x Robigus RILs in sprouting experiment 5.

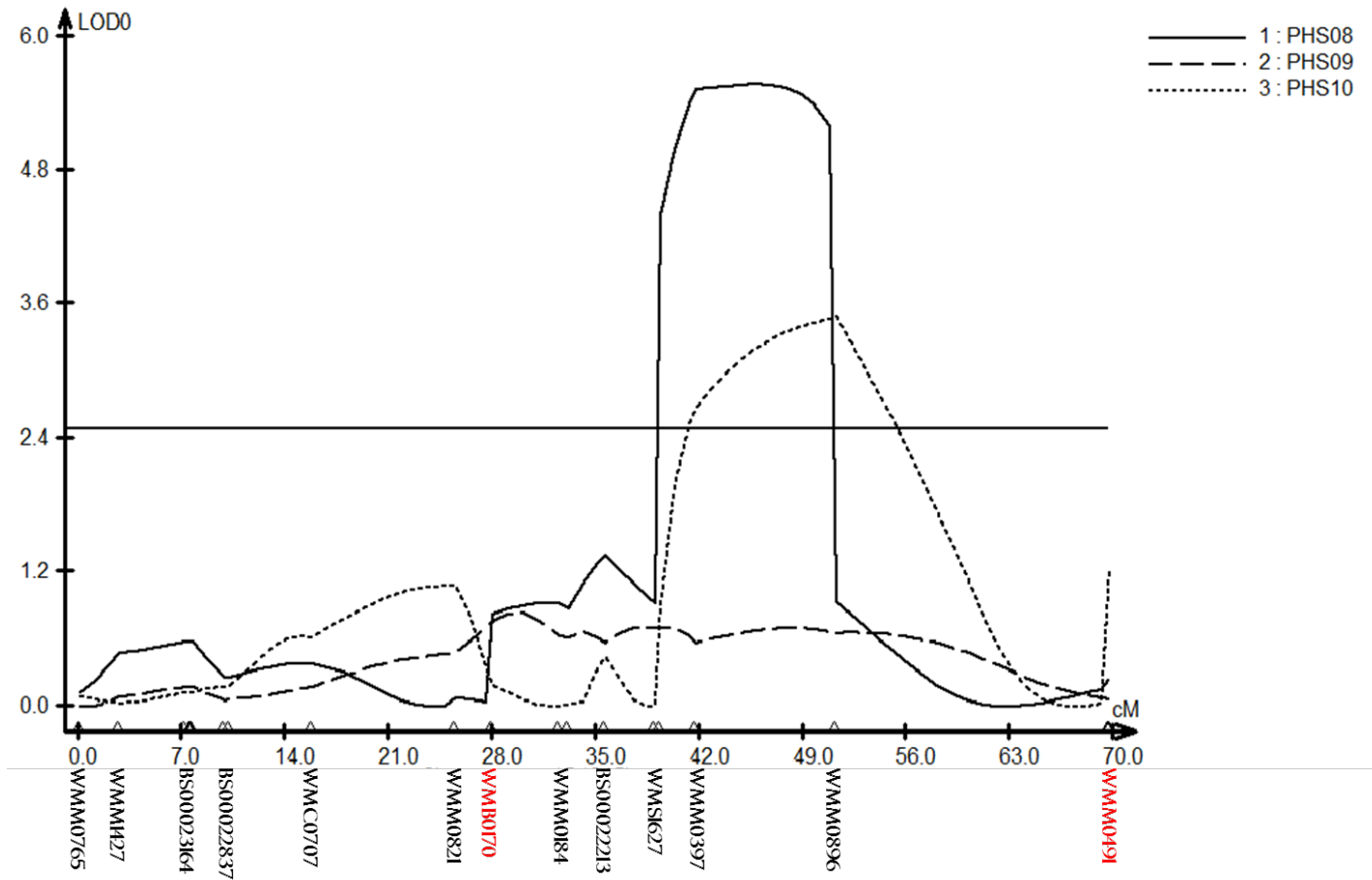


Fig S1: PHS resistance QTL on chromosome arm 4AL in the Alchemy x Robigus DH population. A QTL for PHS resistance was identified from composite interval mapping of the arcsin transformed sprouting percentage of DH lines phenotyped across three years of field trial (2008, 2009 and 2010). QTL was detected in 2008 and 2010 but not in 2009. The flanking markers used for selecting the QTL are highlighted in red.

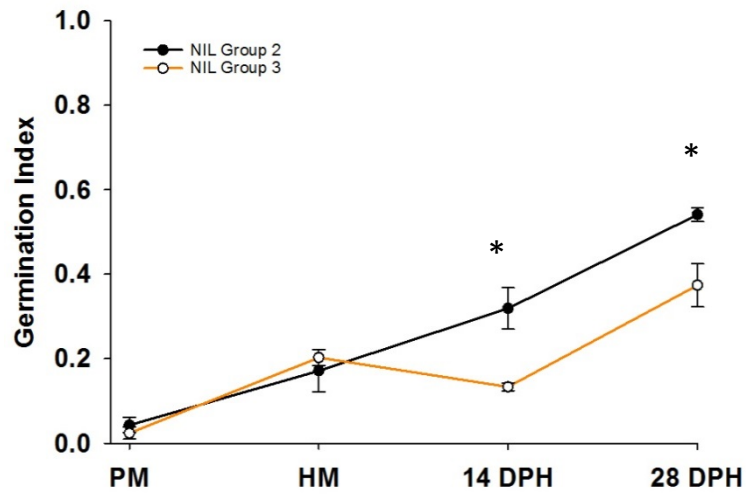


Fig S2: After-ripening effect of *Phs-A1* in NILs grown at 13 °C post-anthesis. The germination index of seeds harvested from NILs with either the recombinant haplotype (NIL Group 2) or Alchemy-type haplotype (NIL Group 3) between *barc170* and *wmc420* grown at 13 °C post-anthesis. Seeds were tested at Physiological Maturity (PM), Harvest Maturity (HM; 12 days after PM), 14 and 28 Days Post Harvest (DPH). Error bars represent SEM of 3 biological replications for each time point. Significant differences between NILs at $P < 0.05$ (*) is indicated

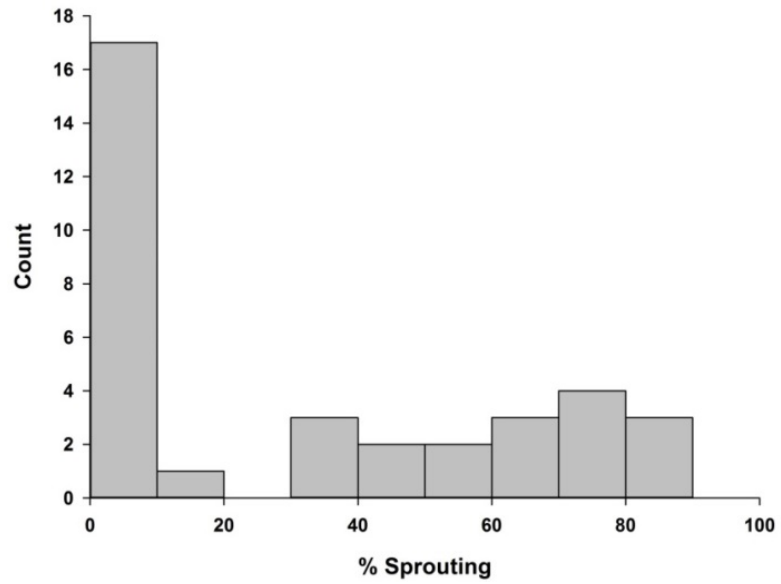


Fig S3: Distribution of the sprouting percentage of Option x Claire F4 RILs in sprouting experiment 3.

```

PM19-A1_Alchemy ATGGCGGGCGTGGGTGCGCAACATGGTGGCGCCGCTGCTGGTGTGAACCTCATCATGTACCTCATCGTCATCGGCTTCGCGAGCTGGAACCTCAACCCTTCATCAACGGCCTCACCAAC 120
PM19-A1_Option ATGGCGGGCGTGGGTGCGCAACATGGTGGCGCCGCTGCTGGTGTGAACCTCATCATGTACCTCATCGTCATCGGCTTCGCGAGCTGGAACCTCAACCCTTCATCAACGGCCTCACCAAC 120
PM19-A1_Yitpi ATGGCGGGCGTGGGTGCGCAACATGGTGGCGCCGCTGCTGGTGTGAACCTCATCATGTACCTCATCGTCATCGGCTTCGCGAGCTGGAACCTCAACCCTTCATCAACGGCCTCACCAAC 120
PM19-A1_Claire ATGGCGGGCGTGGGTGCGTAACATGGTGGCGCCGCTGCTGGTGTGAACCTCATCATGTACATCATCGTCATAGGGTTTCGCGAGCTGGAACCTCAACCCTTCATCAACGGCCTCACCAAC 120
PM19-A1_Robigus ATGGCGGGCGTGGGTGCGTAACATGGTGGCGCCGCTGCTGGTGTGAACCTCATCATGTACATCATCGTCATAGGGTTTCGCGAGCTGGAACCTCAACCCTTCATCAACGGCCTCACCAAC 120
PM19-A1_Chara ATGGCGGGCGTGGGTGCGTAACATGGTGGCGCCGCTGCTGGTGTGAACCTCATCATGTACATCATCGTCATAGGGTTTCGCGAGCTGGAACCTCAACCCTTCATCAACGGCCTCACCAAC 120
***** ** * * *****.*****.*****

PM19-A1_Alchemy CGCCCCGGCGTCGGCGGCAACGGCGCCACCTTCTACTTCTCCTCGTCTTCGCCATCCTCGCCGGGGTTCGTTGGGCGCCGCATCCAAGCTCGCCGGCGTGCACCACGTCGCGACCTGGCGGGC 240
PM19-A1_Option CGCCCCGGCGTCGGCGGCAACGGCGCCACCTTCTACTTCTCCTCGTCTTCGCCATCCTCGCCGGGGTTCGTTGGGCGCCGCATCCAAGCTCGCCGGCGTGCACCACGTCGCGACCTGGCGGGC 240
PM19-A1_Yitpi CGCCCCGGCGTCGGCGGCAACGGCGCCACCTTCTACTTCTCCTCGTCTTCGCCATCCTCGCCGGGGTTCGTTGGGCGCCGCATCCAAGCTCGCCGGCGTGCACCACGTCGCGACCTGGCGGGC 240
PM19-A1_Claire CGCCCCGGCGTCGGCGGCAACGGCGCCACCTTCTACTTCTCCTCGTCTTCGCCATCCTCGCCGGGGTTCGTTGGGCGCCGCATCCAAGCTCGCCGGCGTGCACCACGTCGCGACCTGGCGGGC 240
PM19-A1_Robigus CGCCCCGGCGTCGGCGGCAACGGCGCCACCTTCTACTTCTCCTCGTCTTCGCCATCCTCGCCGGGGTTCGTTGGGCGCCGCATCCAAGCTCGCCGGCGTGCACCACGTCGCGACCTGGCGGGC 240
PM19-A1_Chara CGCCCCGGCGTCGGCGGCAACGGCGCCACCTTCTACTTCTCCTCGTCTTCGCCATCCTCGCCGGGGTTCGTTGGGCGCCGCATCCAAGCTCGCCGGCGTGCACCACGTCGCGACCTGGCGGGC 240
*****

PM19-A1_Alchemy GACAGCCTCGCCACCTCCGCGTCCCTCCTCGCTGGTGGCCTGGGCGATCACCGCCTTGGCGTTCGGGCTGGCGTGAAGGAGATCCACATCGGCGGGTACCAGGGTGGCGCCTCCGGGTG 360
PM19-A1_Option GACAGCCTCGCCACCTCCGCGTCCCTCCTCGCTGGTGGCCTGGGCGATCACCGCCTTGGCGTTCGGGCTGGCGTGAAGGAGATCCACATCGGCGGGTACCAGGGTGGCGCCTCCGGGTG 360
PM19-A1_Yitpi GACAGCCTCGCCACCTCCGCGTCCCTCCTCGCTGGTGGCCTGGGCGATCACCGCCTTGGCGTTCGGGCTGGCGTGAAGGAGATCCACATCGGCGGGTACCAGGGTGGCGCCTCCGGGTG 360
PM19-A1_Claire GACAGCCTCGCCACCTCCGCGTCCCTCCTCGCTGGTGGCCTGGGCGATCACCGCCTTGGCGTTCGGGCTGGCGTGAAGGAGATCCACATCGGCGGGTACCAGGGTGGCGCCTCCGGGTG 360
PM19-A1_Robigus GACAGCCTCGCCACCTCCGCGTCCCTCCTCGCTGGTGGCCTGGGCGATCACCGCCTTGGCGTTCGGGCTGGCGTGAAGGAGATCCACATCGGCGGGTACCAGGGTGGCGCCTCCGGGTG 360
PM19-A1_Chara GACAGCCTCGCCACCTCCGCGTCCCTCCTCGCTGGTGGCCTGGGCGATCACCGCCTTGGCGTTCGGGCTGGCGTGAAGGAGATCCACATCGGCGGGTACCAGGGTGGCGCCTCCGGGTG 360
*****

PM19-A1_Alchemy CTGGAGGCGTTCGTGATTGTTCTCATGTTACGCGAGCTGCTGTACGTGCTGGCGCTGCACTCGGGCCTCTTCGGGAACCAGTTTCGGTGGTAACCATGGTGGTGGGTATCCGGCGGAGCAC 480
PM19-A1_Option CTGGAGGCGTTCGTGATTGTTCTCATGTTACGCGAGCTGCTGTACGTGCTGGCGCTGCACTCGGGCCTCTTCGGGAACCAGTTTCGGTGGTAACCATGGTGGTGGGTATCCGGCGGAGCAC 480
PM19-A1_Yitpi CTGGAGGCGTTCGTGATTGTTCTCATGTTACGCGAGCTGCTGTACGTGCTGGCGCTGCACTCGGGCCTCTTCGGGAACCAGTTTCGGTGGTAACCATGGTGGTGGGTATCCGGCGGAGCAC 480
PM19-A1_Claire CTGGAGGCGTTCGTGATTGTTCTCATGTTACGCGAGCTGCTGTACGTGCTGGCGCTGCACTCGGGCCTCTTCGGGAACCAGTTTCGGTGGTAACCATGGTGGTGGGTATCCGGCGGAGCAC 480
PM19-A1_Robigus CTGGAGGCGTTCGTGATTGTTCTCATGTTACGCGAGCTGCTGTACGTGCTGGCGCTGCACTCGGGCCTCTTCGGGAACCAGTTTCGGTGGTAACCATGGTGGTGGGTATCCGGCGGAGCAC 480
PM19-A1_Chara CTGGAGGCGTTCGTGATTGTTCTCATGTTACGCGAGCTGCTGTACGTGCTGGCGCTGCACTCGGGCCTCTTCGGGAACCAGTTTCGGTGGTAACCATGGTGGTGGGTATCCGGCGGAGCAC 480
*****

PM19-A1_Alchemy GCGTACGGCGCAGGCGTCGGCGACCCGCACAACAAGGGCATGGGCATGGGCACCAG-----GGTCTGA 543
PM19-A1_Option GCGTACGGCGCAGGCGTCGGCGACCCGCACAACAAGGGCATGGGCATGGGCACCAG-----GGTCTGA 543
PM19-A1_Yitpi GCGTACGGCGCAGGCGTCGGCGACCCGCACAACAAGGGCATGGGCATGGGCACCAG-----GGTCTGA 543
PM19-A1_Claire GCGTACGGCGCAGGCGTCGGCGACCCGCACAACAAGGGCATGGGCATGGGCACCAGCGGGGTCGCCAGGGTCTGA 555
PM19-A1_Robigus GCGTACGGCGCAGGCGTCGGCGACCCGCACAACAAGGGCATGGGCATGGGCACCAGCGGGGTCGCCAGGGTCTGA 555
PM19-A1_Chara GCGTACGGCGCAGGCGTCGGCGACCCGCACAACAAGGGCATGGGCATGGGCACCAG-----GGTCTGA 543
*****

```

Fig S4: Alignment of *PM19-A1* coding sequences of UK and Australian germplasm. The coding sequences of *PM19-A1* in Alchemy, Option, Robigus, Claire, Yitpi and Chara *PM19-A1* were aligned with Clustal Omega and the polymorphisms are shown in red.

```

PM19-A2_Claire      ATGGCGGGCGTGGGTCGCAACATGGTGGCGCCGCTGCTGGTGTGAACCTCATCATGTACCTCATCGTTCATCGGCTTCGCGAGCTGGAACCTCAACCCTTCATCAACGGCCTCACCAAC 120
PM19-A2_Robigus    ATGGCGGGCGTGGGTCGCAACATGGTGGCGCCGCTGCTGGTGTGAACCTCATCATGTACCTCATCGTTCATCGGCTTCGCGAGCTGGAACCTCAACCCTTCATCAACGGCCTCACCAAC 120
PM19-A2_Chara      ATGGCGGGCGTGGGTCGCAACATGGTGGCGCCGCTGCTGGTGTGAACCTCATCATGTACCTCATCGTTCATCGGCTTCGCGAGCTGGAACCTCAACCCTTCATCAACGGCCTCACCAAC 120
PM19-A2_Yitpi      ATGGCGGGCGTGGGTCGCAACATGGTGGCGCCGCTGCTGGTGTGAACCTCATCATGTACCTCATCGTTCATCGGCTTCGCGAGCTGGAACCTCAACCCTTCATCAACGGCCTCACCAAC 120
PM19-A2_Alchemy    ATGGCGGGCGTGGGTCGCAACATGGTGGCGCCGCTGCTGGTGTGAACCTCATCATGTACCTCATCGTTCATCGGCTTCGCGAGCTGGAACCTCAACCCTTCATCAACGGCCTCACCAAC 120
PM19-A2_Option     ATGGCGGGCGTGGGTCGCAACATGGTGGCGCCGCTGCTGGTGTGAACCTCATCATGTACCTCATCGTTCATCGGCTTCGCGAGCTGGAACCTCAACCCTTCATCAACGGCCTCACCAAC 120
*****. **

PM19-A2_Claire      CGCCCCGGCGTCGGCGGCAACGGCGCCACCTTCTACTTCTCCTCGTCTTCGCCATCCTCGCCGGGGTTCGTTGGGCGCCGATCCAAGCTCGCCGGCGTGCACCACGTCCGCACCTGGCGGGC 240
PM19-A2_Robigus    CGCCCCGGCGTCGGCGGCAACGGCGCCACCTTCTACTTCTCCTCGTCTTCGCCATCCTCGCCGGGGTTCGTTGGGCGCCGATCCAAGCTCGCCGGCGTGCACCACGTCCGCACCTGGCGGGC 240
PM19-A2_Chara      CGCCCCGGCGTCGGCGGCAACGGCGCCACCTTCTACTTCTCCTCGTCTTCGCCATCCTCGCCGGGGTTCGTTGGGCGCCGATCCAAGCTCGCCGGCGTGCACCACGTCCGCACCTGGCATGGG 240
PM19-A2_Yitpi      CGCCCCGGCGTCGGCGGCAACGGCGCCACCTTCTACTTCTCCTCGTCTTCGCCATCCTCGCCGGGGTTCGTTGGGCGCCGATCCAAGCTCGCCGGCGTGCACCACGTCCGCACCTGGCATGGG 240
PM19-A2_Alchemy    CGCCCCGGCGTCGGCGGCAACGGCGCCACCTTCTACTTCTCCTCGTCTTCGCCATCCTCGCCGGGGTTCGTTGGGCGCCGATCCAAGCTCGCCGGCGTGCACCACGTCCGCACCTGGCATGGG 240
PM19-A2_Option     CGCCCCGGCGTCGGCGGCAACGGCGCCACCTTCTACTTCTCCTCGTCTTCGCCATCCTCGCCGGGGTTCGTTGGGCGCCGATCCAAGCTCGCCGGCGTGCACCACGTCCGCACCTGGCATGGG 240
*****. **

PM19-A2_Claire      GACAGCCTCGCCACCTCCGCGTCCCTCCTCGCTGGTGGCCTGGGCGATCACCGCCTTGGCGTTCGGGCTGGCGTGAAGGAGATCCACATCGCCGGGTACCGAGGGTGGCGCCTCCGGGTG 360
PM19-A2_Robigus    GACAGCCTCGCCACCTCCGCGTCCCTCCTCGCTGGTGGCCTGGGCGATCACCGCCTTGGCGTTCGGGCTGGCGTGAAGGAGATCCACATCGCCGGGTACCGAGGGTGGCGCCTCCGGGTG 360
PM19-A2_Chara      GACAGCCTCGCCACCTCCGCGTCCCTCCTCGCTGGTGGCCTGGGCGATCACCGCCTTGGCGTTCGGGCTGGCGTGAAGGAGATCCACATCGCCGGGTACCGAGGGTGGCGCCTCCGGGTG 360
PM19-A2_Yitpi      GACAGCCTCGCCACCTCCGCGTCCCTCCTCGCTGGTGGCCTGGGCGATCACCGCCTTGGCGTTCGGGCTGGCGTGAAGGAGATCCACATCGCCGGGTACCGAGGGTGGCGCCTCCGGGTG 360
PM19-A2_Alchemy    GACAGCCTCGCCACCTCCGCGTCCCTCCTCGCTGGTGGCCTGGGCGATCACCGCCTTGGCGTTCGGGCTGGCGTGAAGGAGATCCACATCGCCGGGTACCGAGGGTGGCGCCTCCGGGTG 360
PM19-A2_Option     GACAGCCTCGCCACCTCCGCGTCCCTCCTCGCTGGTGGCCTGGGCGATCACCGCCTTGGCGTTCGGGCTGGCGTGAAGGAGATCCACATCGCCGGGTACCGAGGGTGGCGCCTCCGGGTG 360
*****

PM19-A2_Claire      CTGGAGGCGTTCGTATCATCCTGGCCTTACGCGAGTGTCTACGTGTGGCGTGCCTCTGGGCTGTTTGGCAACCAGTTTGGTAACCATGCTGGTGGATAACGGCGGGAGCACGGC 480
PM19-A2_Robigus    CTGGAGGCGTTCGTATCATCCTGGCCTTACGCGAGTGTCTACGTGTGGCGTGCCTCTGGGCTGTTTGGCAACCAGTTTGGTAACCATGCTGGTGGATAACGGCGGGAGCACGGC 480
PM19-A2_Chara      CTGGAGGCGTTCGTATCATCCTGGCCTTACGCGAGTGTCTACGTGTGGCGTGCCTCTGGGCTGTTTGGCAACCAGTTTGGTAACCATGCTGGTGGATAACGGCGGGAGCACGGC 480
PM19-A2_Yitpi      CTGGAGGCGTTCGTATCATCCTGGTCTTACGCGAGTGTCTACGTGTGGCGTGCCTCTGGGCTGTTT-----GGTAACCATGCTGGTGGATAACGGCGGGAGCACGGC 468
PM19-A2_Alchemy    CTGGAGGCGTTCGTATCATCCTGGTCTTACGCGAGTGTCTACGTGTGGCGTGCCTCTGGGCTGTTT-----GGTAACCATGCTGGTGGATAACGGCGGGAGCACGGC 468
PM19-A2_Option     CTGGAGGCGTTCGTATCATCCTGGTCTTACGCGAGTGTCT-----GGTAACCATGCTGGTGGATAACGGCGGGAGCACGGC-----401
*****

PM19-A2_Claire      GGGTATGGCGCCGGCGATCCGCACAATAAGGGCATGGGCACCGGGCGGCGTCCGAGGGTCTGA 543
PM19-A2_Robigus    GGGTATGGCGCCGGCGATCCGCACAATAAGGGCATGGGCACCGGGCGGCGTCCGAGGGTCTGA 543
PM19-A2_Chara      GGGTATGGCGCCGGCGATCCGCACAATAAGGGCATGGGCACCGGGCGGCGTCCGAGGGTCTGA 543
PM19-A2_Yitpi      GGGTATGGCGCCGGCGATCCGCACAATAAGGGCATGGGCACCGGGCGGCGTCCGAGGGTCTGA 531
PM19-A2_Alchemy    GGGTATGGCGCCGGCGATCCGCACAATAAGGGCATGGGCACCGGGCGGCGTCCGAGGGTCTGA 531
PM19-A2_Option     -----401

```

Fig S5: Alignment of *PM19-A2* coding sequences of UK and Australian germplasm.The coding sequences of *PM19-A2* in Alchemy, Option, Robigus, Claire, Yitpi and Chara were aligned with Clustal omega and the polymorphisms are shown in red. Partial *PM19-A2* sequence was obtained for Option.

Table S1: Statistical comparison of GI and sprouting phenotype of Alchemy x Robigus NILs

Test	Lines	Mean	Std Error	Sig (P) against Alchemy	Sig (P) against Robigus	Phenotype Classification
GI	Alchemy	0.1	0.01	NA	< 0.001	Low
	Robigus	0.9	0.02	< 0.001	NA	High
	Group 1	0.8	0.06	< 0.001	0.895	High
	Group 2	0.9	0.01	< 0.001	0.998	High
	Group 3	0.4	0.05	< 0.001	< 0.001	Moderate
	Group 4	0.9	0.01	< 0.001	0.994	High
	Group 5	0.8	0.05	< 0.001	0.908	High
	Group 6	0.7	0.04	< 0.001	0.009	Moderate
Group 7	0.9	0.02	< 0.001	0.895	High	
% Sprouting Arcsin	Alchemy	9.0	1.68	-	0.002	Low
	Robigus	27.9	2.21	0.002	-	High
	Group 1	39.7	3.52	< 0.001	0.044	High
	Group 2	27.0	2.41	< 0.001	1	High
	Group 3	7.5	0.98	1	< 0.001	Low
	Group 4	49.8	3.14	< 0.001	< 0.001	High
	Group 5	27.5	2.27	< 0.001	1	High
	Group 6	29.1	3.30	< 0.001	1	High
Group 7	31.5	2.18	< 0.001	0.92	High	

Table S2: Information on genes found in the syntenic *Phs-A1* intervals in wheat and *Brachypodium*.

	<i>Brachypodium</i> genes	IWGSC CSS Contigs	Gene model ID	Gene Names
1	<i>Bradi1g00600</i>	4AL_7123764	Traes_4AL_BFAB568BF	<i>Plasma Membrane Protein 19-A2 (PM19-A1)</i>
		4AL_7174272	Traes_4AL_F99FCB25F	<i>Plasma Membrane Protein 19-A2 (PM19-A2)</i>
2	<i>Bradi1g00607</i>	4AL_7174272	Traes_4AL_DD1B27086*	<i>Myosin-J heavy chain protein</i>
		4AL_7093716		
3	<i>Bradi1g00620</i>	4AL_7074626	M28059 [#]	<i>Ubiquitin Conjugating Enzyme (UBC)</i>
4	Non-collinear	4AL_7074626	Traes_4AL_65DF744B71	<i>1 Aminocyclopropane carboxylate Oxidase-1-like (ACC – Oxidase-1)</i>
5	<i>Bradi1g00670</i>	4AL_7095843	Traes_4AL_F18648C49	<i>Ethylene Responsive Factor 1B (ERF-1B)</i>
6	<i>Bradi1g00677</i>	4AL_6230861	Traes_4AL_02AE47773*	<i>Activating Signal Co-integrator 1 Like (ASC1-Like)</i>
		4AL_5621077		
7	<i>Bradi1g00690</i>	4AL_7159962	Traes_4AL_2EBB63DBA	<i>Serine threonine Protein Phosphatase 1-like (PP1-Like)</i>
8	<i>Bradi1g00700</i>	4AL_7162562	Traes_4AL_C56125840	<i>Phosphate Transporter</i>
9	<i>Bradi1g00710</i>	4AL_7177172	Traes_4AL_DD344FC87	<i>Hypothetical protein</i>
10	<i>Bradi1g00720</i>	4AL_7172877	Traes_4AL_F00707FAF	<i>OTU cysteine Protease</i>

*Gene model is split across two contigs.

[#] NCBI gene model used as no suitable gene model was found on EnsemblPlant

Table S3: KASP SNP assays used to fine map *Phs-A1*

Gene	Robigus/Claire Specific Primer	Alchemy/Option Specific Primer	Common Primer
<i>PM19_A2</i>	GCACTCTGGGCTGTTGGc	GCACTCTGGGCTGTTGGt	TATCAGCCTGTCACTGTCGC
<i>ACC Oxidase-1</i>	CTCGTTGAAGCGCCGGAt	CTCGTTGAAGCGCCGGAc	CCAGGTGACGAACCACGA
<i>PP1-like</i>	GTCCTAGAGTTGAGACACTAATTTTAa	GTCCTAGAGTTGAGACACTAATTTTAg	AGACTTAACCAAGTCTCAGTCA
<i>OTU Cysteine Protease</i>	ACCGTTTCGGTTTCTTGTTc	ACCGTTTCGGTTTCTTGTTg	TTGAAGAAAAATGTTTCGCAGA
<i>STW17</i>	TTGCAGTCATGGTGTGATAAc	TTGCAGTCATGGTGTGATAAt	GCTAGCCACACACCGTCT

Table S4: Statistical comparison of the sprouting scores of Option x Claire RILs in sprouting experiment 3.

Groups	line	% Sprouting	Std Error	Sig (P) against Option	Sig (P) against Claire	Phenotype Classification
Susceptible Parent	Claire	70.6	8.3	< 0.001	NA	High
Resistant Parent	Option	2.4	2.0	NA	< 0.001	Low
Claire Control RIL	-	65.0	3.7	< 0.001	1.000	High
Option Control RIL	-	4.0	0.6	0.992	< 0.001	Low
RIL Group 11	4/204	0.0	0.0	1.000	< 0.001	Low
RIL Group 12	20/24	60.0	4.4	< 0.001	0.800	High
	24/28	75.0	7.9	< 0.001	1.000	High
	25/58	36.2	4.1	< 0.001	0.004	Moderate
	4/95	74.5	5.3	< 0.001	1.000	High
RIL Group 13	21/46	4.6	1.0	0.856	< 0.001	Low
RIL Group 14	20/42	49.4	8.4	< 0.001	0.235	High
	21/19	34.2	3.9	< 0.001	0.002	Moderate
	22/57	73.5	4.3	< 0.001	1.000	High
	26/8	37.2	7.2	< 0.001	0.005	Moderate
RIL Group 15	5/189	88.1	3.3	< 0.001	0.640	High

Table S5: Statistical comparison of the sprouting score of Option x Claire RILs in sprouting experiment 4.

Groups	Line	% Sprouting	Std Error	Sig (P) against Option	Sig (P) against Claire	Phenotype Classification
Susceptible Parent	Claire	89.9	2.6	< 0.001	NA	High
Resistant Parent	Option	0.7	0.2	NA	< 0.001	Low
RIL Group 11	27/8	32.1	4.6	< 0.001	< 0.001	Moderate
	4/204	50.7	7.6	< 0.001	0.001	Moderate
RIL Group 12	20/24	93.6	1.0	< 0.001	1	High
	24/28	95.4	0.8	< 0.001	0.982	High
	25/58	97.8	0.2	< 0.001	0.917	High
	4/95	96.4	1.2	< 0.001	0.884	High
RIL Group 13	21/46	49.8	7.3	< 0.001	0.024	Moderate
	26/37	69.6	5.7	< 0.001	0.472	High
RIL Group 14	20/42	97.4	0.5	< 0.001	0.596	High
	21/19	72.0	6.8	< 0.001	0.375	High
	22/57	95.0	0.9	< 0.001	0.969	High
	26/8	91.1	1.6	< 0.001	1	High

Table S6: Statistical comparison of the sprouting score of Alchemy x Robigus RILs in sprouting experiment 5.

Groups	Line	% Sprouting	Std Error	Sig (P) against Option	Sig (P) against Claire	Phenotype Classification
Susceptible Parent	Robigus	84.4	3.3	0	NA	High
Resistant Parent	Alchemy	18.5	7.8	NA	0	Low
RIL Group 21	3/70/3/27	15.9	0.8	0.982	0.005	Low
	3/101/6/31	9.0	0.9	1	0.001	Low
RIL Group 22	3/63/1/22	86.4	0.9	0	1	High
	3/70/2/94	77.5	5.6	0.001	1	High
	3/72/3/54	76.6	5.8	0.001	1	High
	3/72/4/41	88.1	4.1	0	1	High
	3/101/9/23	78.4	5.8	0.001	1	High
	3/101/9/73	90.5	3.1	0	1	High
	3/124/6/81	84.2	6.0	0	1	High
	3/158/1/82	92.2	2.2	0	0.992	High
	3/158/2/67	93.3	1.7	0	0.984	High
	3/175/1/60	89.7	1.1	0	1	High
RIL Group 23	3/101/6/48	2.6	0.9	0.92	0	Low
RIL Group 24	3/148/2/4	5.4	0.3	1	0	Low
	3/172/10/92	11.4	7.5	0.986	0	Low
RIL Group 25	3/106/9/2	81.7	4.2	0	1	High
	3/124/6/24	80.6	7.7	0.001	1	High
	3/124/6/74	93.9	1.6	0	0.617	High
	3/149/9/55	90.1	3.9	0	0.87	High
	3/158/1/38	88.5	5.7	0	1	High
	3/175/1/50	88.9	2.3	0	1	High