



7B	65.6	IWA3437	A/ <u>G</u>	0.59	306, 3438, 3691, 3812, 4250, 507, 6712	-	-	-	-	1.8	1.9
7B	99.0	IWA4701	T/ <u>C</u>	0.65	1345, 1346, 4160, 4701	-	1.4	-	-	<b>2.5</b>	<b>2.2</b>

<sup>a</sup> Scaled position from the hexaploid wheat consensus map (Cavanagh et al. 2013)

<sup>b</sup> SNP indexes from the Illumina iSelect 9K wheat assay (Cavanagh et al. 2013). **Bold**: QTL with Bonferroni P<0.1.

\* Eleven SNPs that are also identified using all 875 accessions.

<sup>c</sup> SNP variant associated to the resistant response is underlined.

<sup>d</sup> Frequency of the favorable SNP variant.

<sup>e</sup> SNP loci in LD with the representative SNP and significantly associated to the *Pst* response.

<sup>f</sup> IT= infection type, SEV= disease severity. IT-ALL and SEV-ALL, best linear unbiased estimates (BLUEs) over all environments.

<sup>g</sup> Significances are reported as -log (P value) as follows: ‘-’ = not-significant, 1.3 = P=0.05, values > 2 are in **bold**, and value ≥ 4 (experiment-wise significant at α = 0.10) are in **bold underlined**.

<sup>h</sup> Additional associated SNPs: IWA1092, 919, 920, 7992, 8322, 3893, 846, 1791, 724, 7892, 6831

<sup>i</sup> Additional associated SNPs: IWA1102, 1127, 1128, 1129, 1130, 1131, 1177, 1188, 1229, 1237, 4604, 4606, 771, 776, 777, 829, 869, 874