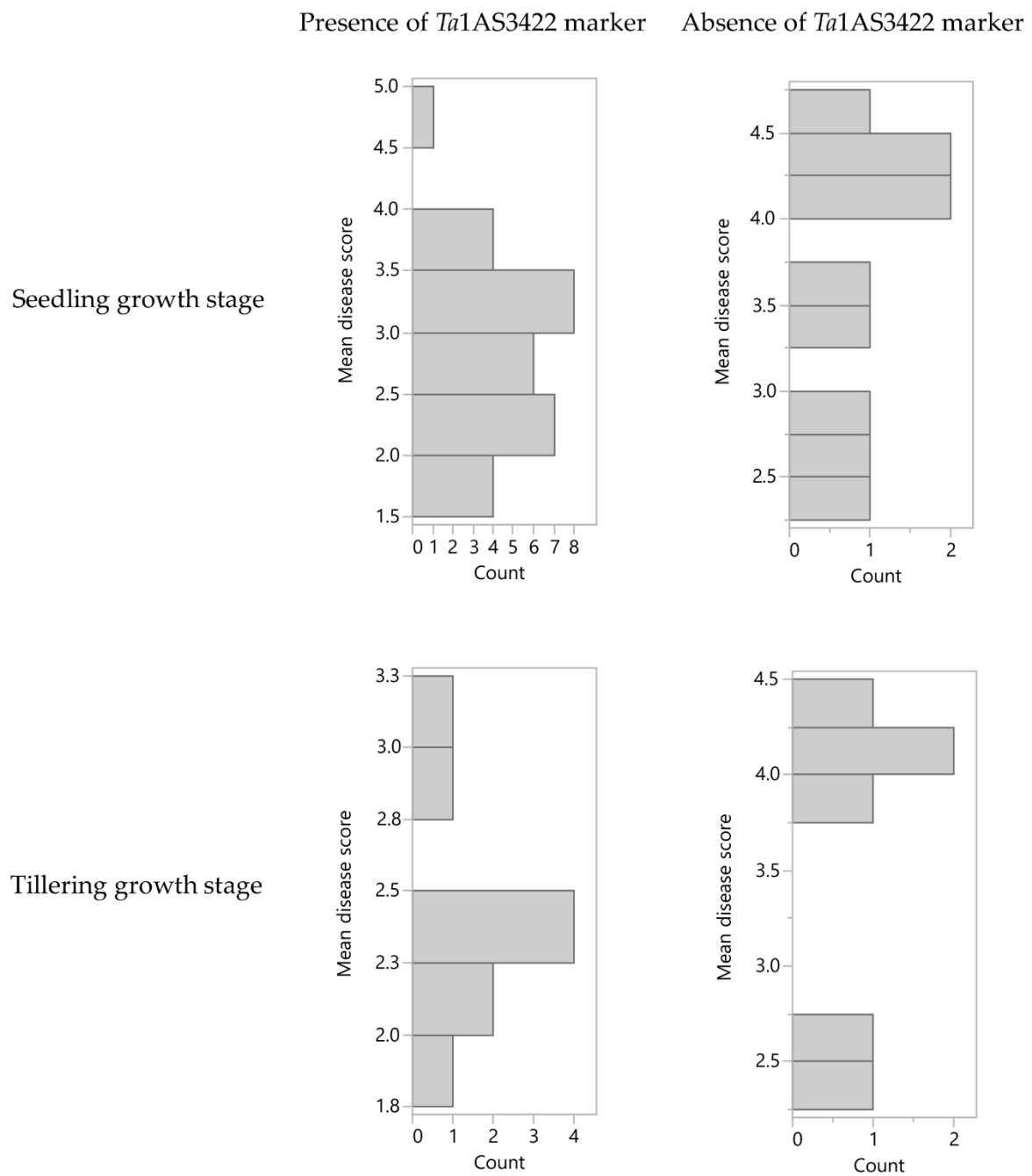


**Table S1.** Published significant QTL markers associated with tan spot disease susceptibility on wheat chromosome 1AS.

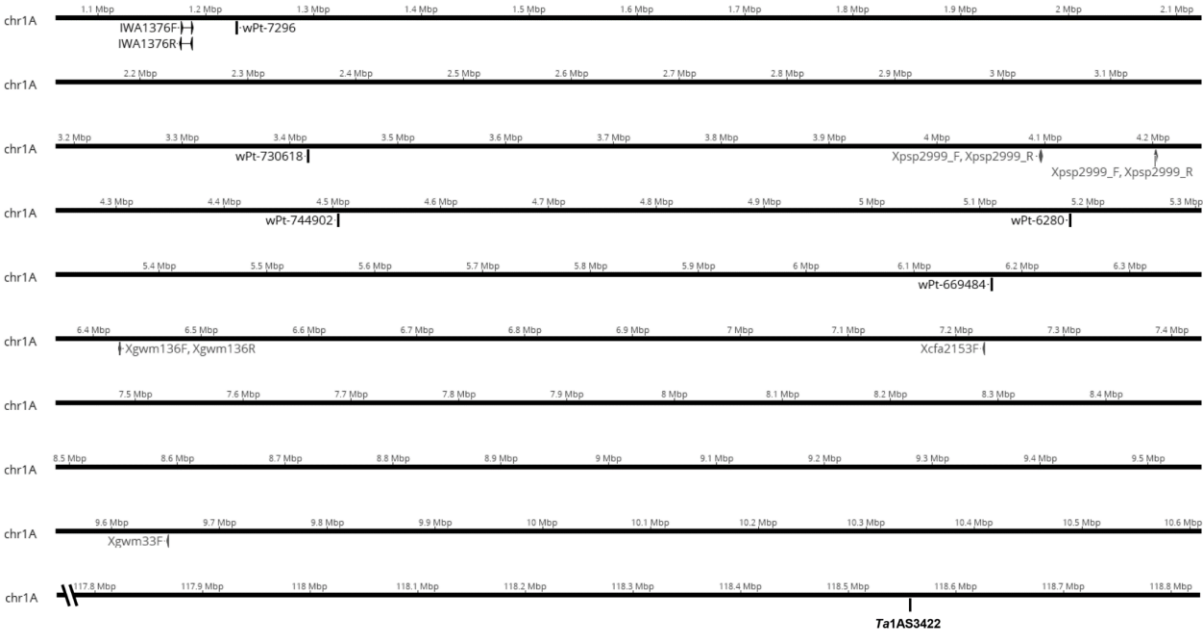
Marker Loci/Flanking markers	Marker type	Source
<i>Xgwm136</i>	SSR	Faris et al. 1997
<i>Xgwm33</i>	SSR	Sun et al. 2010
<i>Xcfa2153</i>	SSR	Sun et al.2010
<i>Xiwa6644 - Xpsp2999</i>	SNP and SSR	Kariyawasam et al. 2016
IWA1367	SNP	Liu et al. 2017
<i>wPt-2527 - wPt-744902</i>	DArT	Shankar et al. 2017
<i>wPt-7296 - wPt-6280</i>	DArT	Shankar et al. 2017
<i>wPt-730618 - wPt-669484</i>	DArT	Kalia et al. 2018

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**Figure S1.** Distribution of mean disease scores of hexaploid wheat varieties following infection with the *Atoxa* Ptr mutant at seedling and tillering growth stages.



**Figure S2.** Genomic location on wheat chromosome 1A of previously reported QTL markers related to tan spot disease resistance (Table S2). DArT marker probes and primer sets targeting the marker loci are aligned to the wheat Chinese Spring genomic sequence. The position of *Ta1AS3422* is marked at the nucleotide position of 118,557,370 bp – 118,557,586 bp. Diagonal lines represent a break at the nucleotide sequence of approximately 100 Mbp.



**Figure S3.** Location of *Ta1AS3422* on the Chinese Spring 1A chromosome. The TraesCS1A02G114400.1 gene is adjacent to *Ta1AS3422*, while another annotated gene (TraesCS1A02G114300.2) is located 48 Mbp from *Ta1AS3422*.

