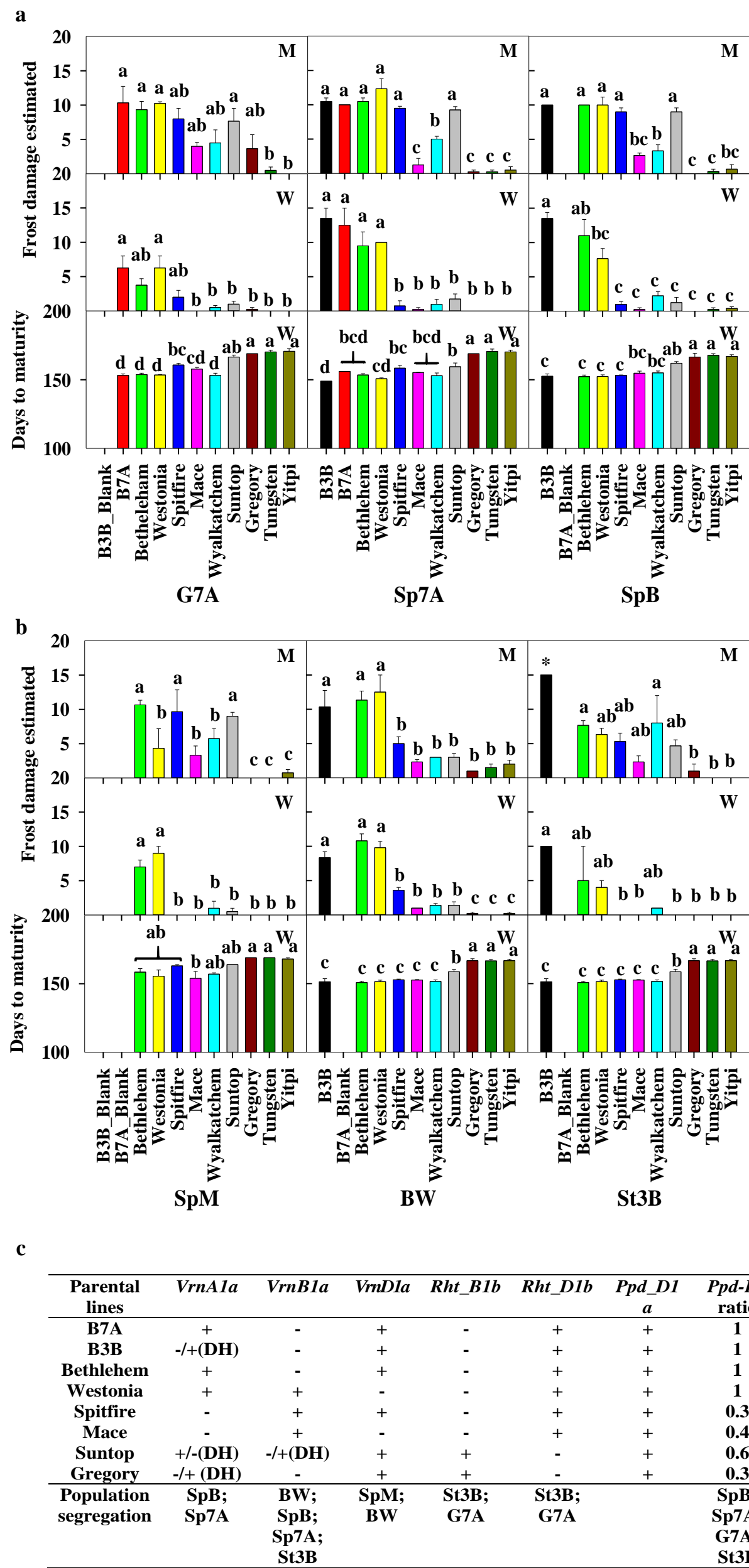


Fig. 1 Frost occurred 9-18 days before anthesis. **a**. Daily temperature below 2 degree presented in Muresk and Williams sites; **b**. Different types of frost damage occurred in both Williams and Muresk sites. A: Frost impacted on the lower part of spikes and the top of peduncles; B1 and B2 showed Bethlehem frost impacted spikes and seed settings, respectively; W1 and W2 showed Westonia frost impacted spikes and seed settings, respectively; **c**. Data of days to anthesis and days between last frost event and anthesis on each parental line and control varieties in two population areas of SpB and BW in Muresk (M) and Williams (W), respectively. Numbers represent days for different statistical classes; **d**: Number of days between the frost event and anthesis on different parental lines and control varieties. The vertical bars represent SE; values with the same letter are not different at $p = 0.05$.



+: mutant; -: recessive; +/- (DH): mutant in DH population.

Fig. 2 Sensitivities of parental lines to frost impact associated with parental line maturity in different population areas in Muresk and Williams. **a.** Sensitivities in G7A, Sp7A and SpB area in both Muresk (M) and Williams (W); **b.** Sensitivities in SpM, BW and St3B area in both Muresk (M) and Williams (W). The vertical bars represent SE; values with the same letter are not different at $p = 0.05$; * represents no replicate. **c.** summarized table for parental lines with or without mutated *VRN1*, *Rht* and *Ppd_D1a* genes; *Ppd-B1*(*Ppd1_2B*) copy number ratio and the gene segregated populations.

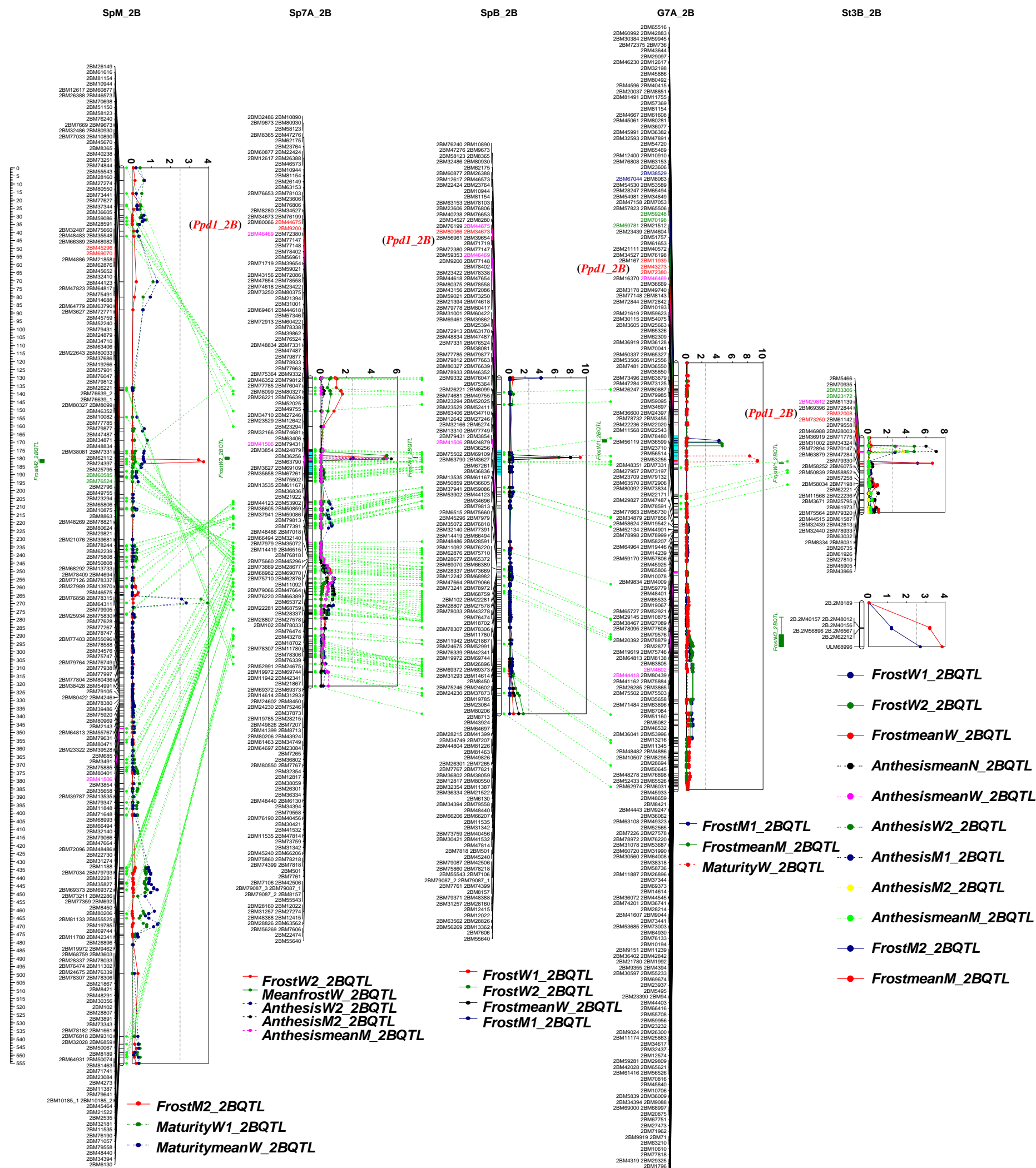


Fig. 3 Frost QTL were overlapped with anthesis QTL on the homologous region on 2B in five populations of Sp7A, SpB, G7A, St3B and SpM. The location of *Ppd1_2B* in High Confidence (HC) 1.0 physical map was indicated.

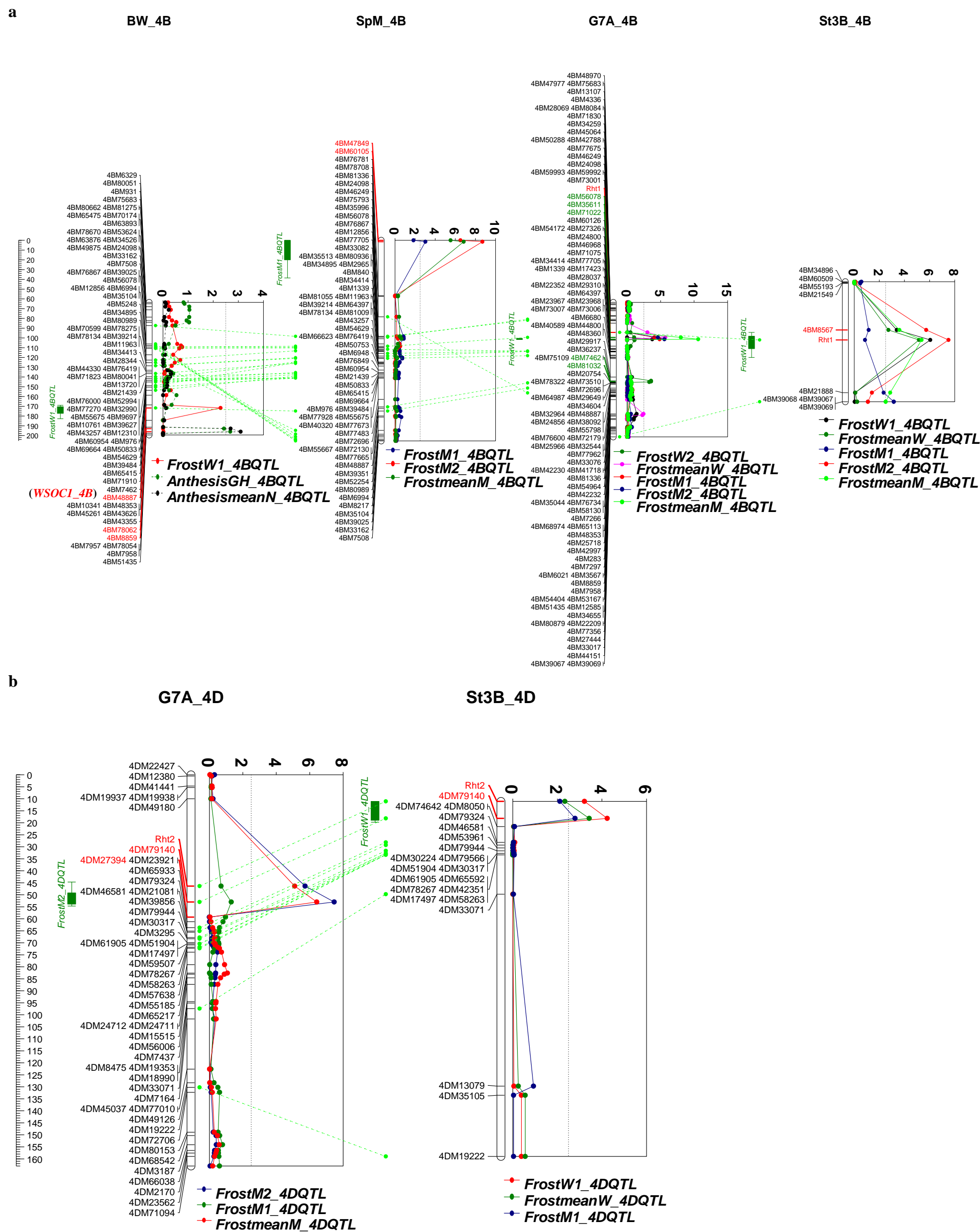


Fig. 4 Significant frost QTL were detected on the *Rht1* and *Rht2* regions. **a.** Frost QTL on *Rht1* regions in the populations of G7A and St3B while the frost QTL in BW and SpM were on the distal down stream and upstream, respectively. A new gene of *WSOC1_4B* may close to the frost QTL on 4B in BW population; **b.** Significant frost QTL were detected on the *Rht2* regions in the populations of G7A and St3B.

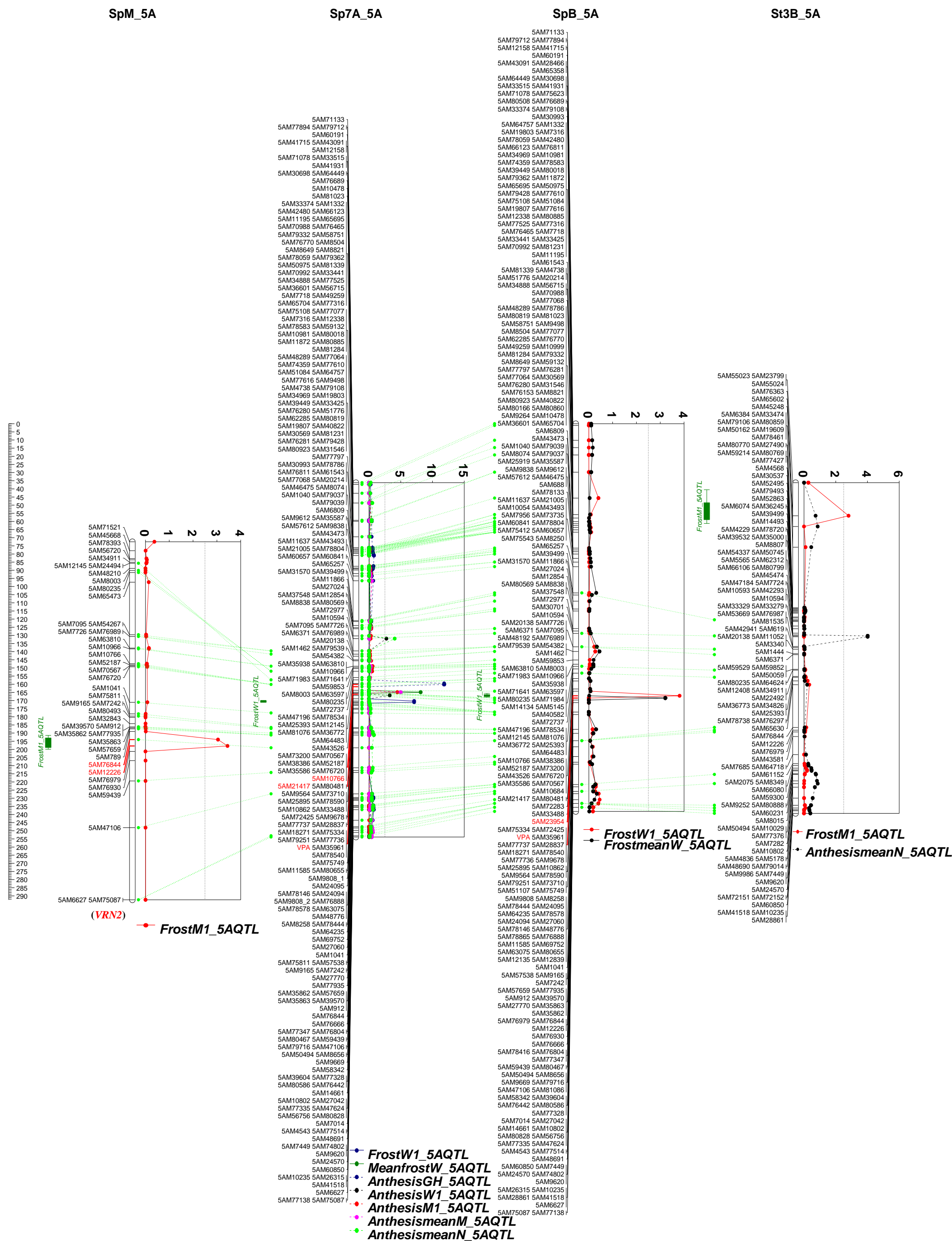


Fig. 5 Significant frost QTL were overlapped with anthesis QTL where *Vrn1_5A* (VPA) tightly linked in Sp7A and SpB populations. The frost QTL on SpM_5A was about 25 cM below the *Vrn1_5A* and 90 cM above *VRN2* loci while it was on the upstream on St3B_5A.

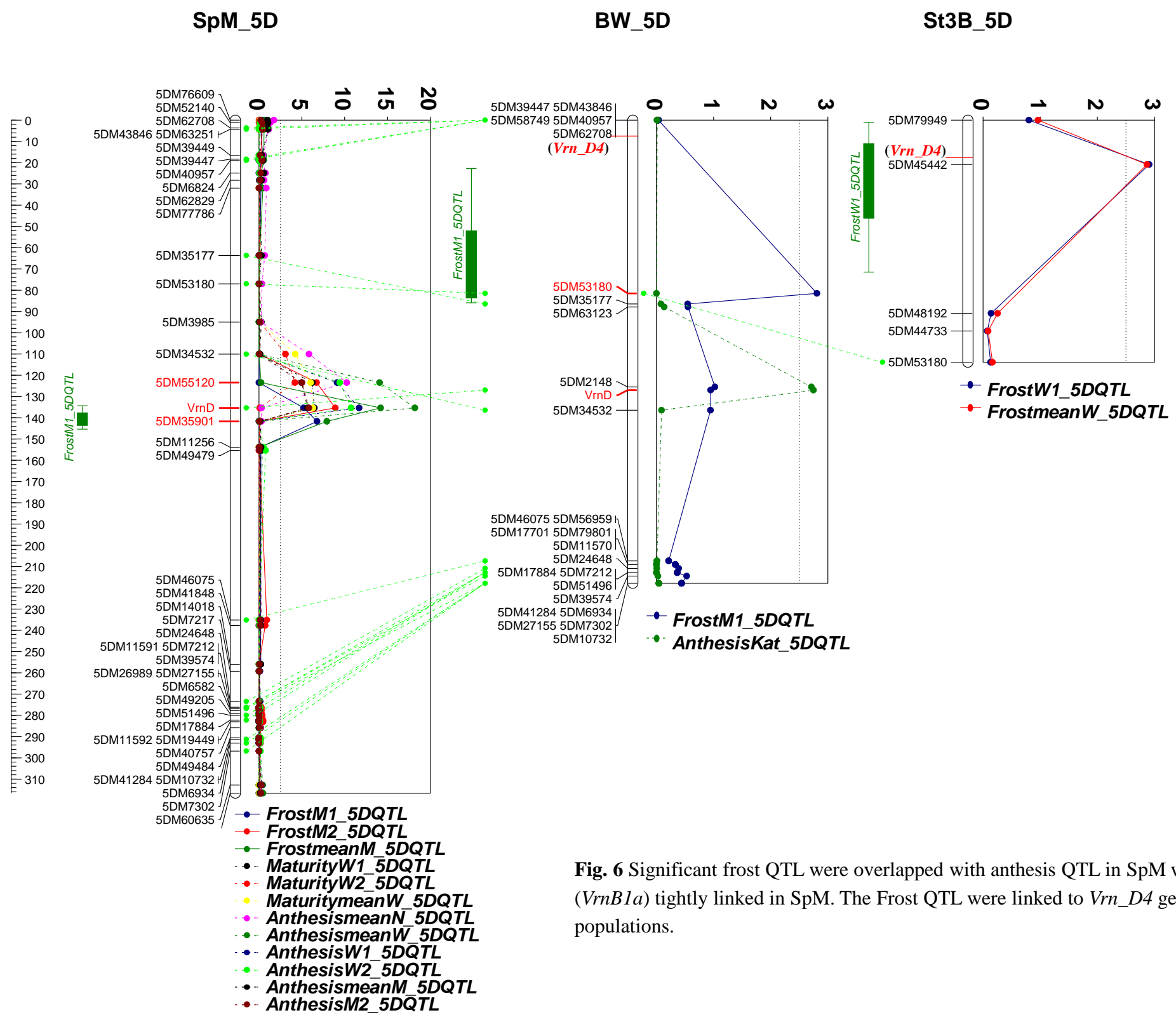


Fig. 6 Significant frost QTL were overlapped with anthesis QTL in SpM where *Vrn1_5D* (*VrnB1a*) tightly linked in SpM. The Frost QTL were linked to *Vrn_D4* gene in BW and St3B populations.

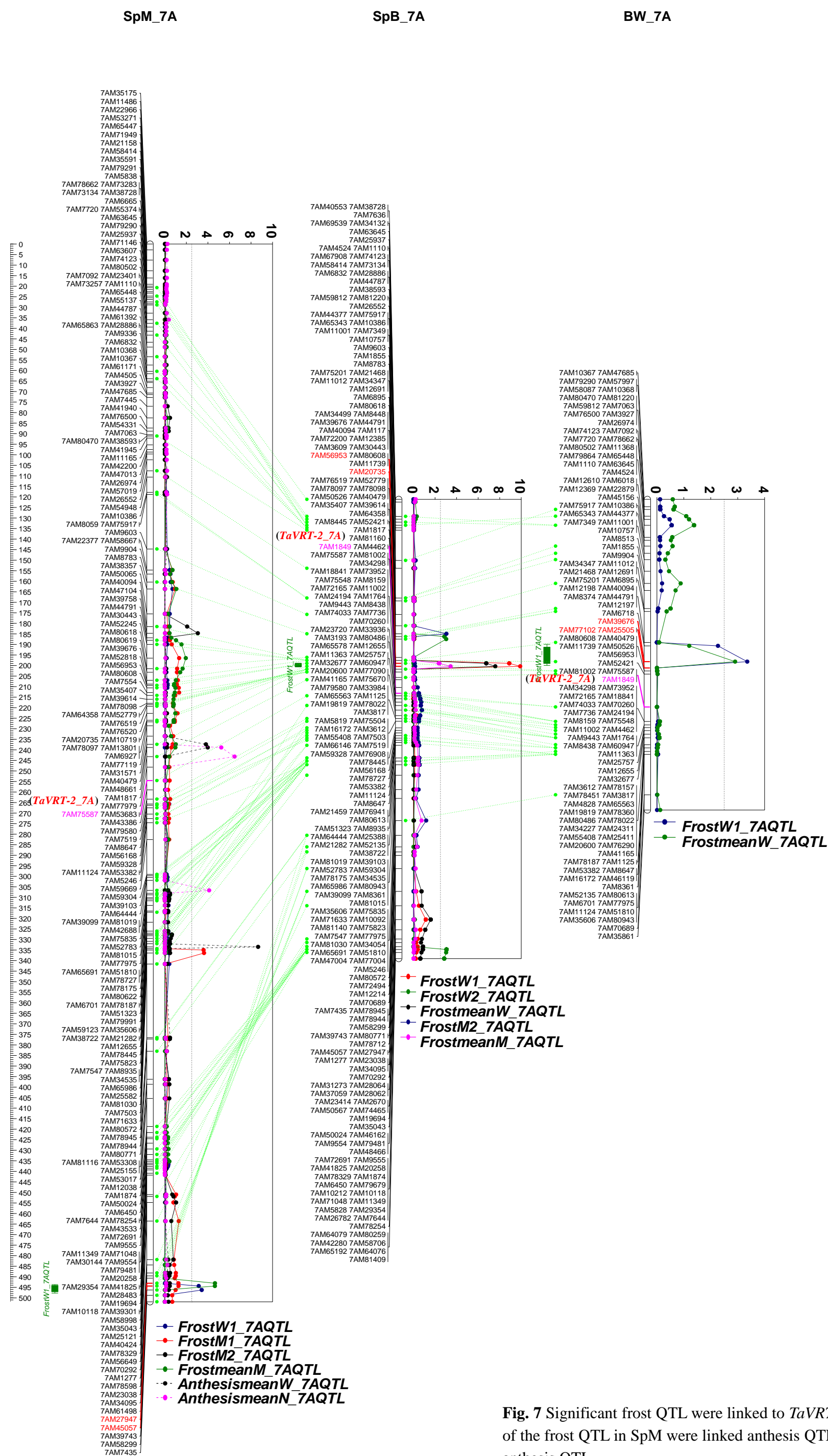
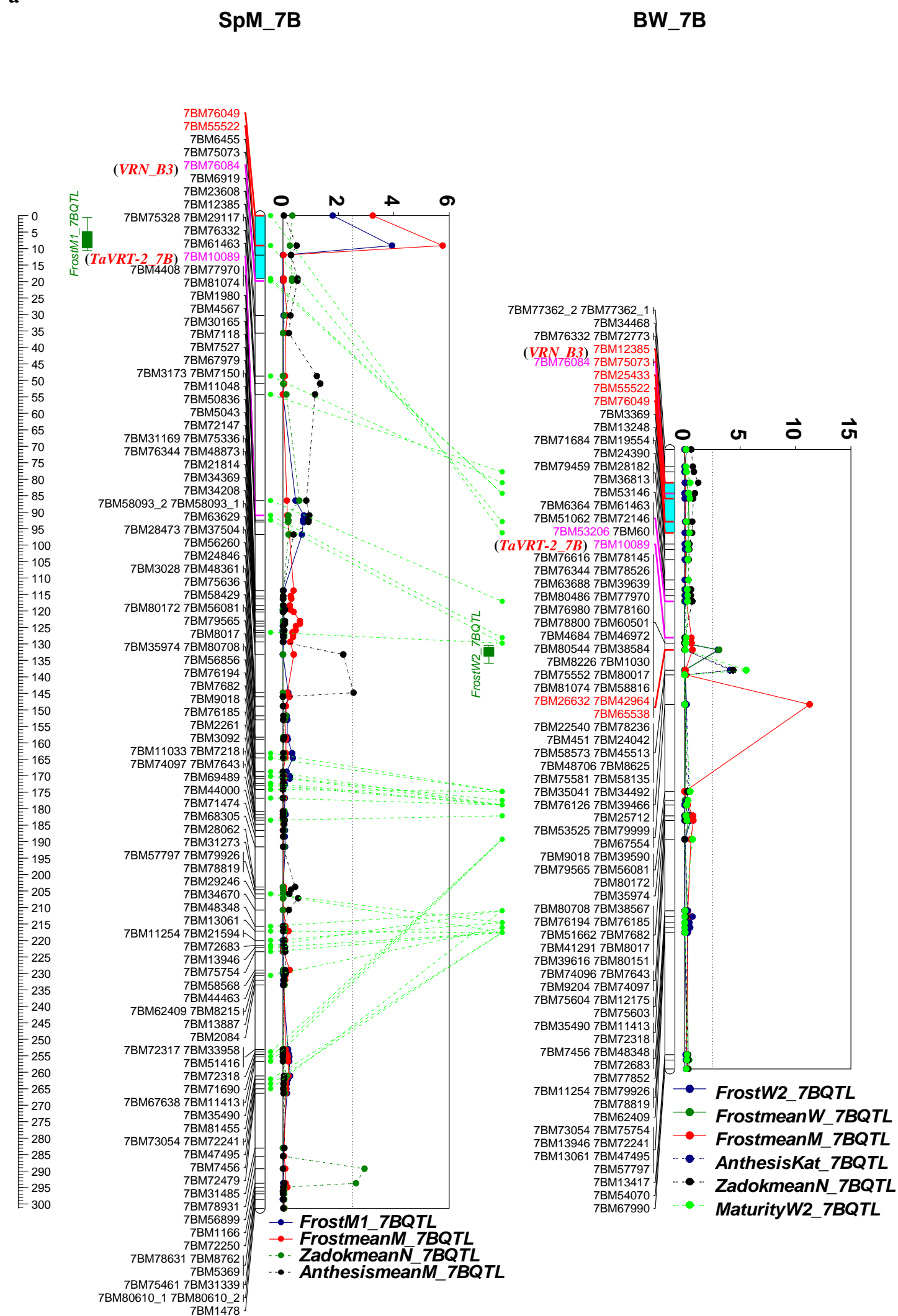


Fig. 7 Significant frost QTL were linked to *TaVRT-2_7A* gene in SpB and BW populations. One of the frost QTL in SpM were linked anthesis QTL on 7A while *TaVRT-2_7A* closely linked two anthesis QTL.

a



b

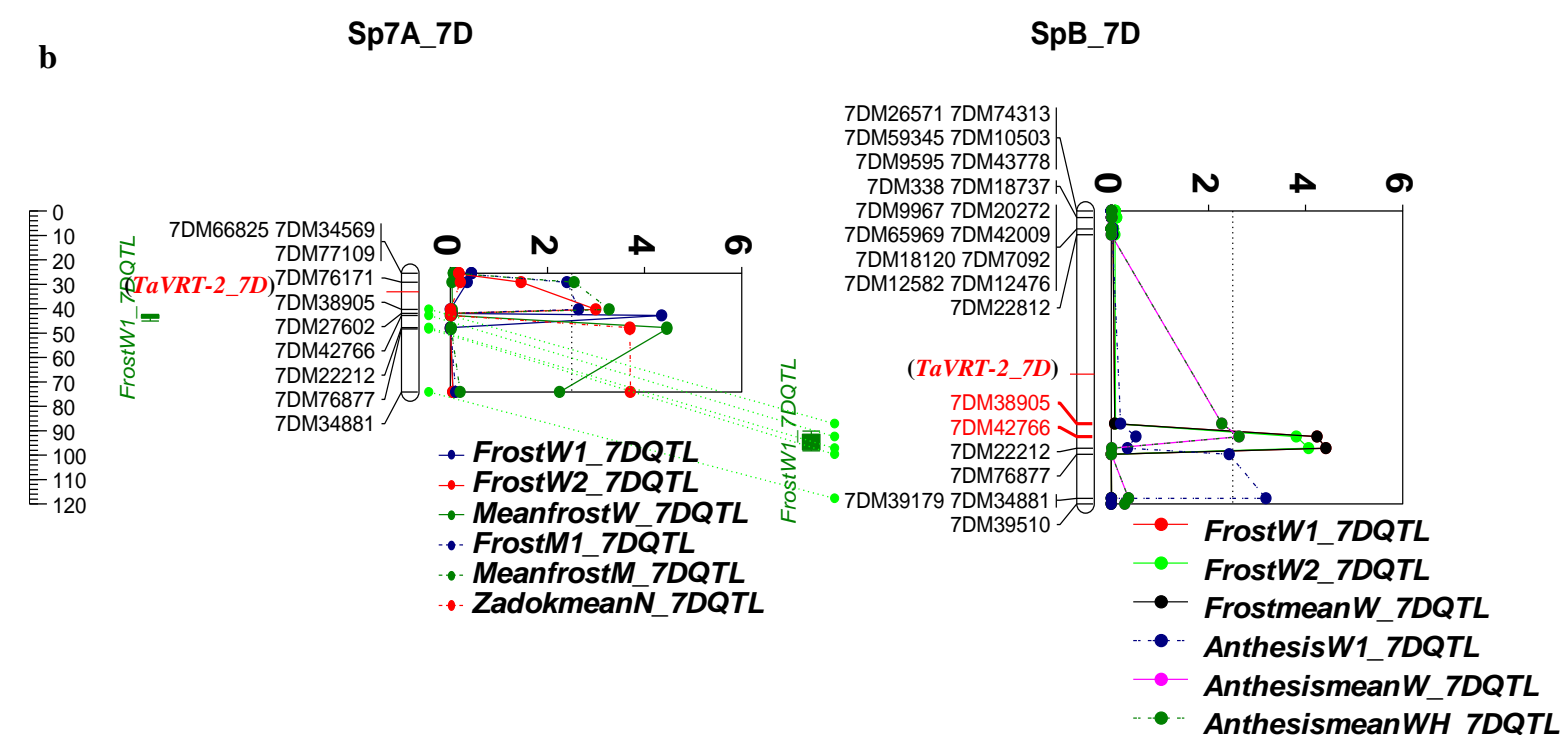


Fig. 8 Significant frost QTL were linked to *VRN_B3* and *TaVRT-2* genes. **a.** Significant frost QTL were linked to *VRN_B3* and *TaVRT-2_7B* gene in SpM and BW populations, respectively; **b.** Significant frost and anthesis QTL were linked to *TaVRT-2_7D* gene in Sp7A and SpB populations.

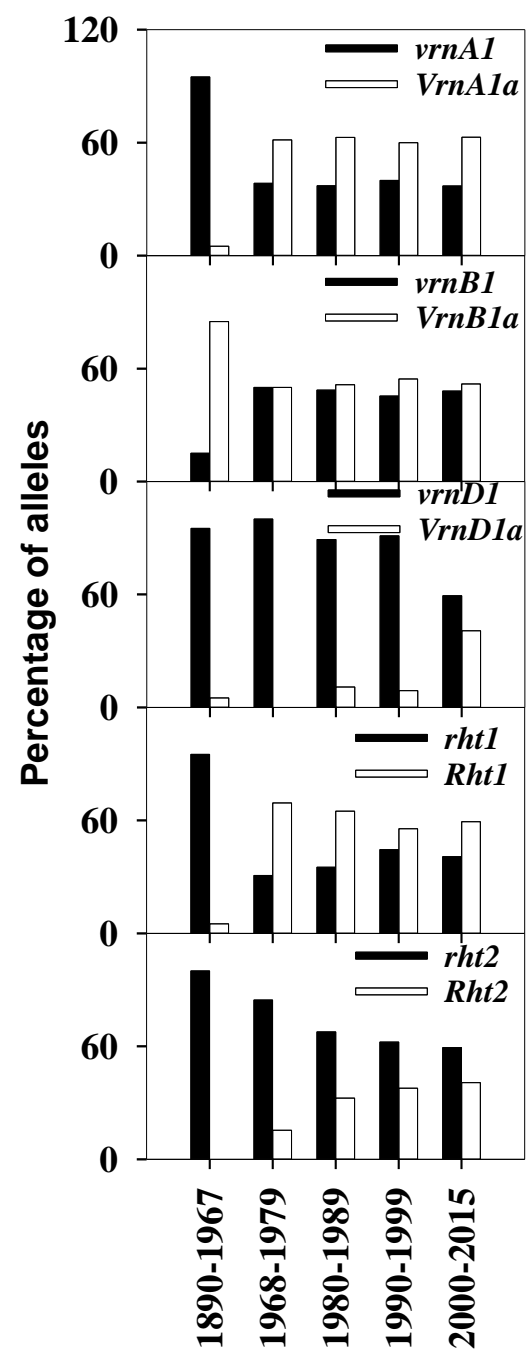


Fig. 9 The proportion of mutated *VrnA1a*, *VrnB1a*, *VrnD1a*, and *Rht1* and *Rht2* gene utilization in historical lines collected in Australia.