

Fig. S1 Frequency distribution of PT index in the DH population. Scores are averaged across testing environments for DH population.

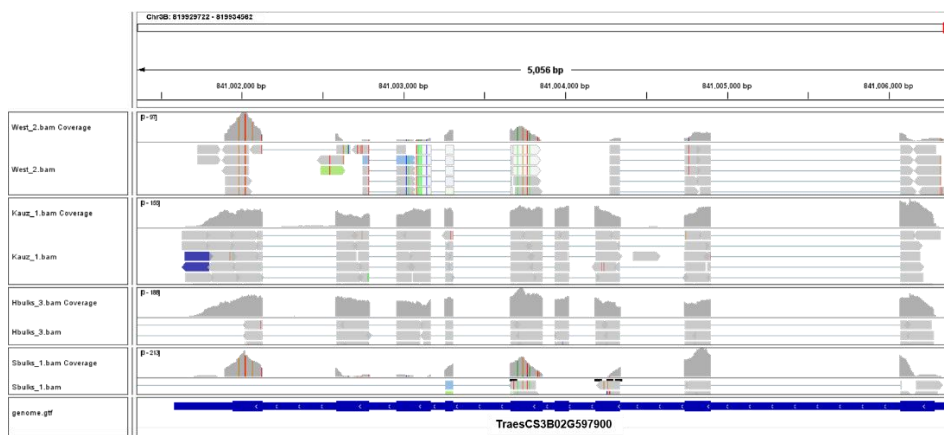


Fig.S2 Visualization of the mRNA sequence of candidate gene using IGV.


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Kauz_VPE-b-P      GTGATAGAGTTTTCCCTGTAGTGTGCTTTCATCGTTAAATAGTATATTAAMTTTGTGTGCACTTATCATGTAATAGCACCTCGAGGCAGAAATGTTTATGCGGTGAATCC 120
Westonia_VPE-b-P GTGATAGAGTTTTCCCTGTAGTGTGCTTTCATCGTTAAATAGTATATTAAMTTTGTGTGCACTTATCATGTAATAGCACCTCGAGGCAGAAATGTTTATGCGGTGAATCC 120
Consensus        gtgtataaggttttccct gttagtgatgcttccatggttaattagtagtatataaa tttgtgtg aaccttatcgttaattagcacctcgaggacaaaatggt ttat ggtgaatcc

Kauz_VPE-b-P      TCACTGGTATAGTTTTTGGTGAACAGCCACCCAGGATTCARGTCCTAATCTGAAATGTGTGCGCTCAGTATCTTGGCAATTTCATAGGGATAAGTGTATGTTTCATAGAAA 240
Westonia_VPE-b-P TCACTGGTATAGTTTTTGGTGAACAGCCACCCAGGATTCARGTCCTAATCTGAAATGTGTGCGCTCAGTATCTTGGCAATTTCATAGGGATAAGTGTATGTTTCATAGAAA 239
Consensus        tcca agttaggtttttt tgggtgaacccagccaccaggttaacagtcctaaacttg aat gtgctggctcagtagtcttga gatt tcatagggataag tgotatgtccatagaaa

Kauz_VPE-b-P      TGAATTAATGTGCATATATAACCATCTCGCGCTTTACACACACTAAAAGAGAATGTTCTTATTTGGACCGGTACTTAAGCTAATTTTGTTCGATCTCTCTTTTGAATGTTGTGGCC 360
Westonia_VPE-b-P TGAATTAATGTGCATATATAACCATCTCGCGCTTTACACACACTAAAAGAGAATGTTCTTATTTGGACCGGTACTTAAGCTAATTTTGTTCGATCTCTCTTTTGAATGTTGTGGCC 359
Consensus        tgatt tatgtgc tatatataaccatctgcgctttacaacactaaaagaagaatttctcttatgtggaccggtact taagctat tttgttcgatctctcttttgatggtgtggc

Kauz_VPE-b-P      TGCAGTCCGCTCCTAGTCCGCTGCAATTAATTCGTCGCGCTGGTTTTTCTCCGCAATTTGTTAGGGCCACTCTCTAATTTGGTCCGATAAGTTTGGTAATTTTGTGCA 480
Westonia_VPE-b-P TGCAGTCCGCTCCTAGTCCGCTGCAATTAATTCGTCGCGCTGGTTTTTCTCCGCAATTTGTTAGGGCCACTCTCTAATTTGGTCCGATAAGTTTGGTAATTTTGTGCA 479
Consensus        tgacgtccctcctactgcctgcaaaattt cgtccaggt gctttttctccgcaattgttttagggccactcctcataaattggtccaataaagtttggtaagtttggctgca

Kauz_VPE-b-P      TTCTTATTGATTTTTTCAACTTATCTTATAGCATAGCACTTATTAGCATAGCACTTATTAGCTATACGTAACAGGATTATCCATGTGAATGTGAGTGGCGGAGGGACGATTTAGTCTCTCTTGTGAACA 600
Westonia_VPE-b-P TTCTTATTGATTTTTTCAACTTATCTTATAGCATAGCACTTATTAGCTATACGTAACAGGATTATCCATGTGAATGTGAGTGGCGGAGGGACGATTTAGTCTCTCTTGTGAACA 599
Consensus        ttcttactgatttttcaacttatctttag atggacttattaga atacgtaaaacgattatccatgtgaatgt gagtggcgcgagggcag a ttagtctctctttt tgaaca

Kauz_VPE-b-P      CGATTAAGACCGATGATCAAGGACTCGTACATACACTCAATTTTGTGAACATCTTGAGATTTACGAAGTCATCATAGACATCTGTAAGTTACGGGAAGACTCTCTACTGAACGAAC 720
Westonia_VPE-b-P CGATTAAGACCGATGATCAAGGACTCGTACATACACTCAATTTTGTGAACATCTTGAGATTTACGAAGTCATCATAGACATCTGTAAGTTACGGGAAGACTCTCTACTGAACGAAC 719
Consensus        cgata agag agatgat atggactcgacatacactca ttttatgaacatcttgagattacgaagtcatcatagacatctcgtagttaacgggaagactctctactgaaacgaac

Kauz_VPE-b-P      AATGCCGAAAGTCGAATATAAATTAAGAAAATTCAGCTTACTCTCCCTAG..... 777
Westonia_VPE-b-P AATGCCGAAAGTCGAATATAAATTAAGAAAATTCAGCTTACTCTCCCTAG..... 839
Consensus        at gccgaaaagctgaaataataaatt agaaaatg gacttactgtccc tag

Kauz_VPE-b-P      TTATTACAACAAAAGTTTGCCTGCCATGAAGAGGGGGCATGACGGCGAGCGGGCTTTGACTCGCTTACTGCTTTAGTCTGCTCGCTAGTGGTTTCATGATCTGGTTGTAAT 777
Westonia_VPE-b-P TTATTACAACAAAAGTTTGCCTGCCATGAAGAGGGGGCATGACGGCGAGCGGGCTTTGACTCGCTTACTGCTTTAGTCTGCTCGCTAGTGGTTTCATGATCTGGTTGTAAT 959
Consensus

Kauz_VPE-b-P      ...TCTTACCAAGGTTGTTTGGGCGCCCAT...AATTACCGAGTATGCTGTGACGGTACGTGAACGGCCGAGAGAGATTCCAGCCACCGTATGGGCGGAGCGGCC 891
Westonia_VPE-b-P ACACGCTTACCAAGGTTGTTTGGGCGCCCAT...AATTACCGAGTATGCTGTGACGGTACGTGAACGGCCGAGAGAGATTCCAGCCACCGTATGGGCGGAGCGGCC 1199
Consensus        a a c agg cg gc g ccccat aattacy agtatgctgtgacggtgacgtgaacggccgagagagattccaagccagcctagggccggagcgcgc

Kauz_VPE-b-P      AGCCAACGACAAACAGCTTCGAATTGACGGCGGATATTTCTCCGAGGACACCCACACGTAAGTGGTGGCAGAAAGCGCAGCCAAATCGGCCATGCACAGCTGATGAATCATTAGTGG 1011
Westonia_VPE-b-P AGCCAACGACAAACAGCTTCGAATTGACGGCGGATATTTCTCCGAGGACACCCACACGTAAGTGGTGGCAGAAAGCGCAGCCAAATCGGCCATGCACAGCTGATGAATCATTAGTGG 1319
Consensus        agccaacgacaacacagcttc gaattgacggcgatatttctccgaggacacccacacgtagtaggtggcagaaagcgcagccaaatcggccatgcacagctgactgaaatcattagtg

Kauz_VPE-b-P      GTSSTTGGTTTTTCCTTTCGGGCGCATATAAAGAGAGAGCTTTCTTTCCTTATTTGGAATGCAACAGCGAGCGCTC 1096
Westonia_VPE-b-P GTSSTTGGTTTTTCCTTTCGGGCGCATATAAAGAGAGAGCTTTCTTTCCTTATTTGGAATGCAACAGCGAGCGCTC 1404
Consensus        gttgta gctttccctttgcccggcacaataaaaaggag agtttct cgttatctggatccaacaccggacccttc

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Fig.S5 Sequence alignment for promoters of *TraesCS3B02G597900* in Westonia and Kauz. Sequences on blue lines represent a 309 bp insertion.

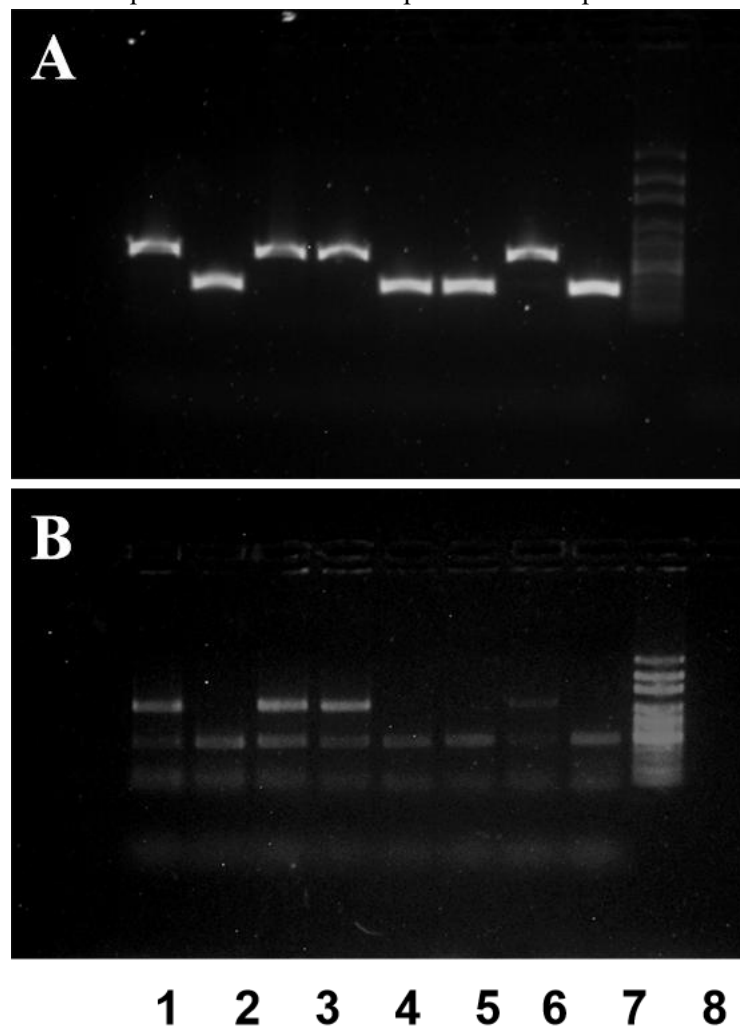


Fig.S6 Genotyping of *TaVPE3cB* in different wheat cultivars.

(A) PCR with *Qpt3B-F2/R2*;

(B) PCR with *Qpt3B-F1/R1*. Lanes: M, molecular weight markers (Axygen® DNA LADDER 100BP), the bands are 3,000, 2,000, 1,000, 800, 700, 600, 500, 400, 300, 200 and 100bp, respectively; 1, 'Westonia' (*TaVPE3cB.b*), 2, 'Kauz' (*TaVPE3cB.a*), 3, 'Lancer' (*TaVPE3cB.b*), 4, 'Janz' (*TaVPE3cB.b*), 5, 'Chinese spring' (*TaVPE3cB.a*), 6, 'Stanley' (*TaVPE3cB.a*), 7, 'Landmark' (*TaVPE3cB.b*), 8, 'Filder' (*TaVPE3cB.a*).