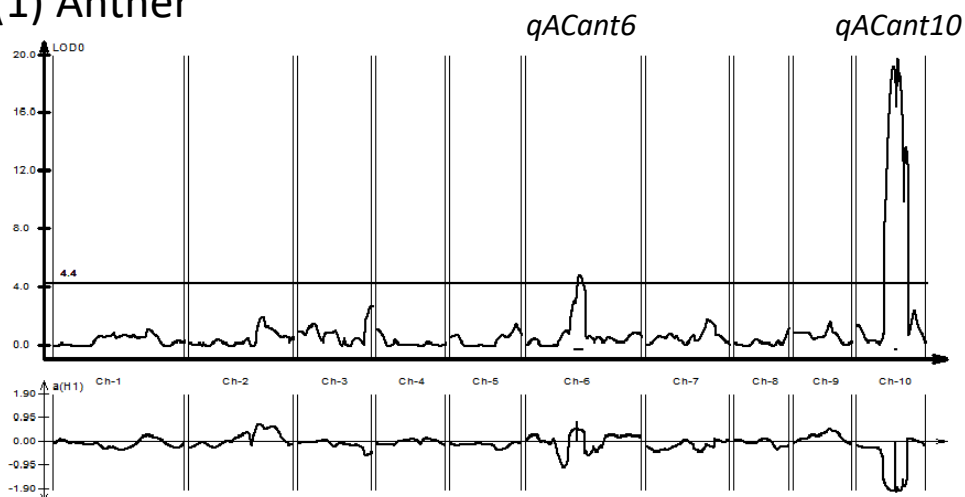
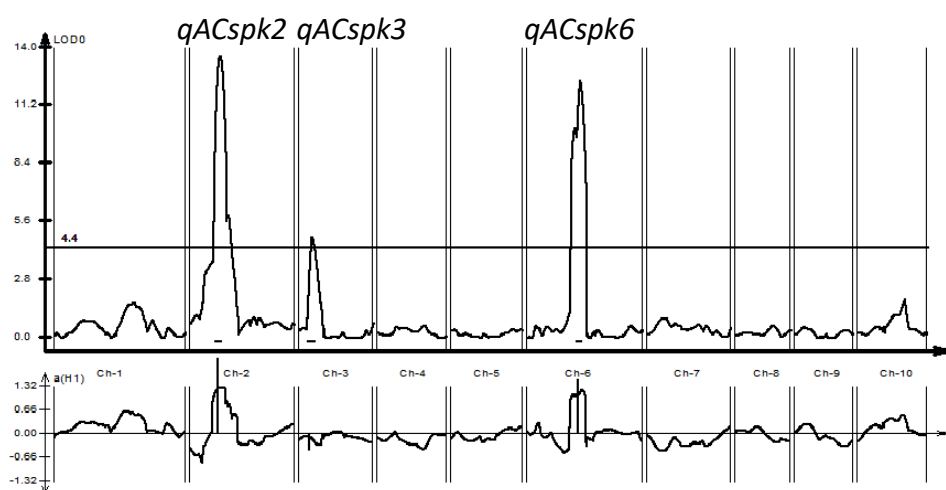


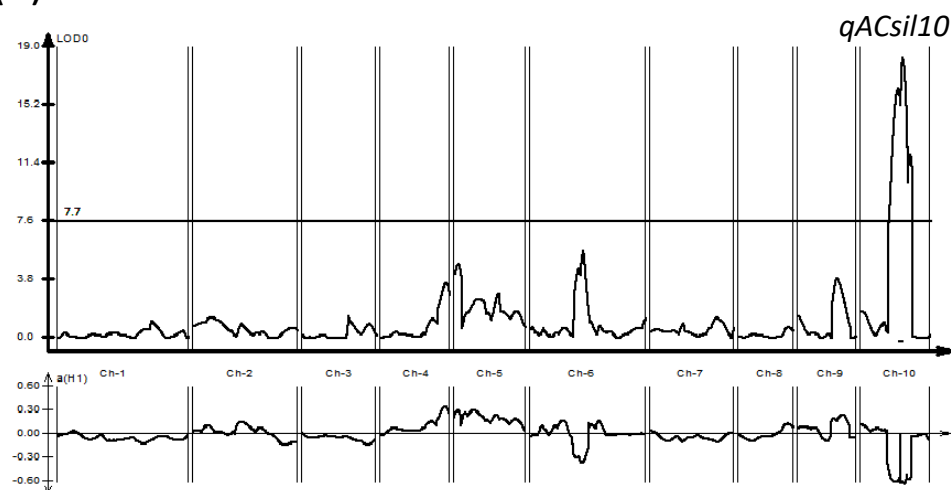
### (1) Anther



### (2) Spikelet



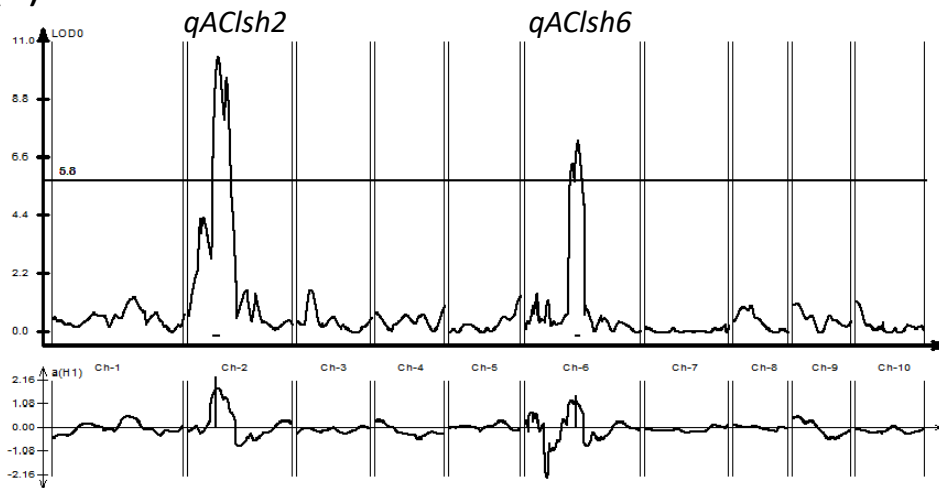
### (3) Silk



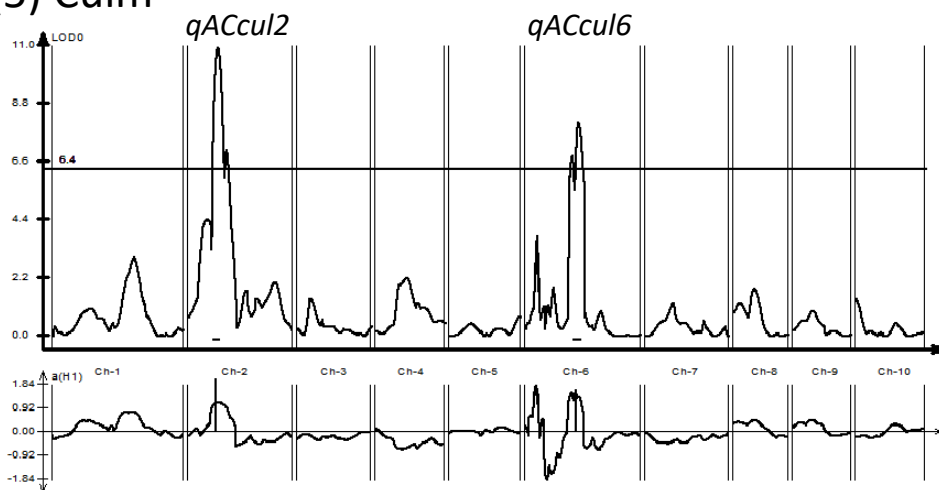
Supplemental Fig.1.

LOD scores (upper) and additive effects (lower) of QTLs for anthocyanin pigmentation in 11 maize organs. QTL names are shown above each LOD peak (continued on the next page).

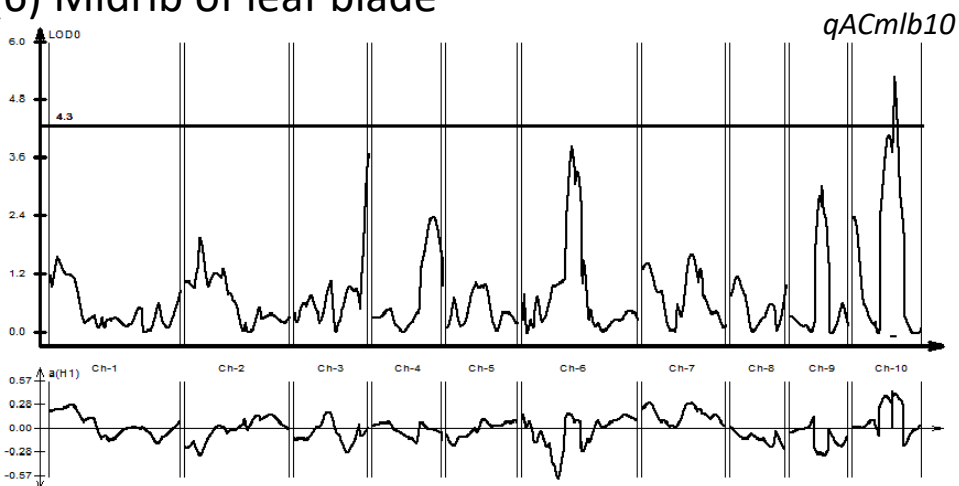
#### (4) Leaf sheath



#### (5) Culm

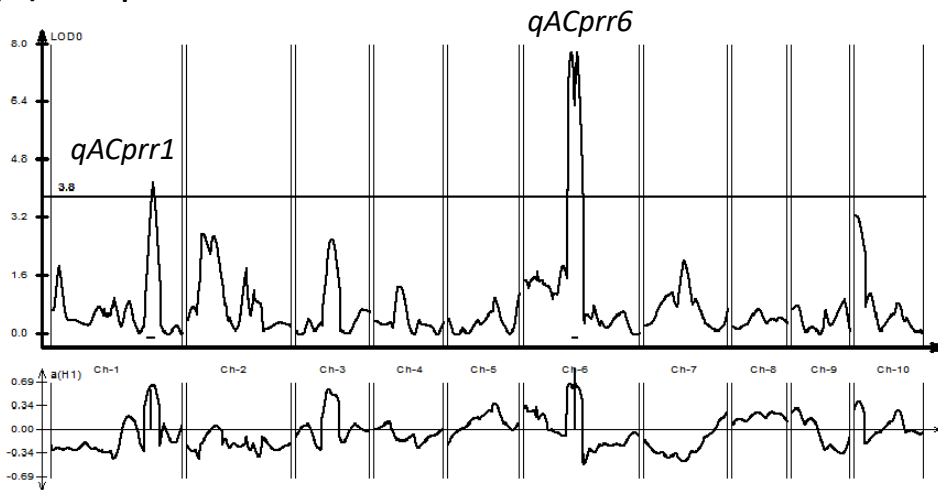


#### (6) Midrib of leaf blade

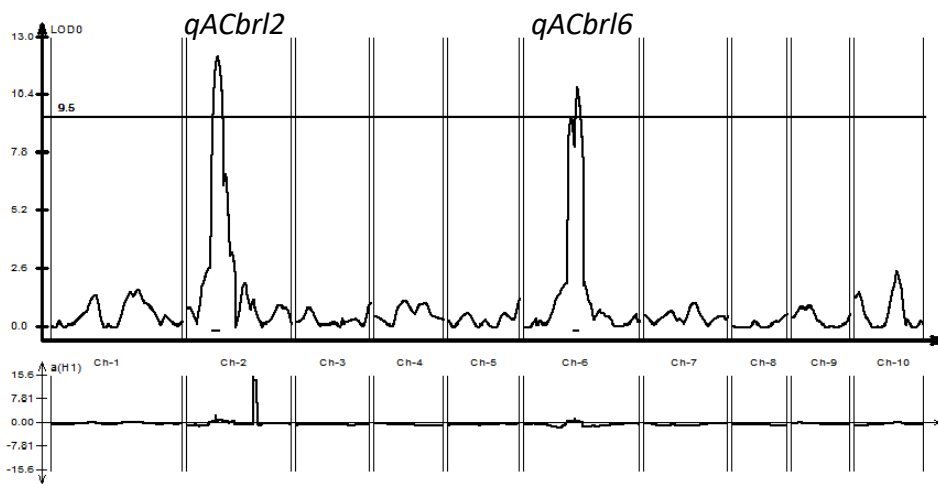


Supplemental Fig.1 (Continued from previous page)

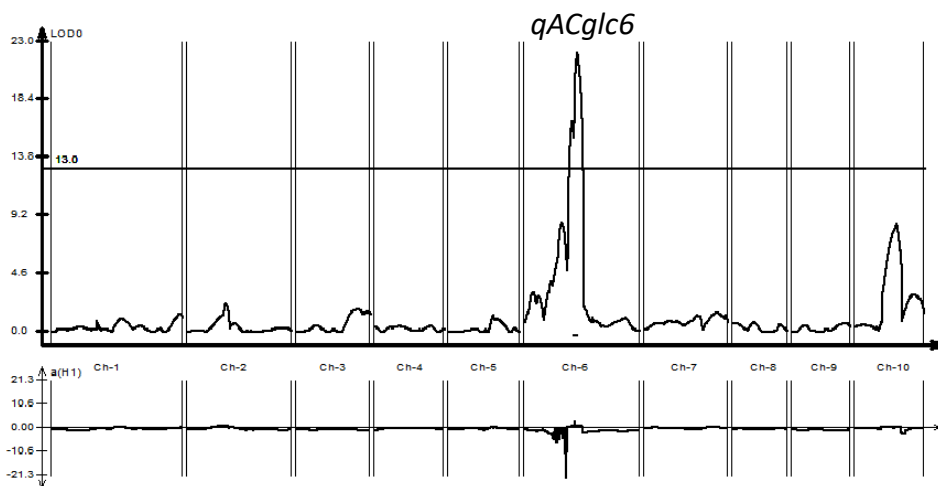
### (7) Prop root



### (8) Bract leaf

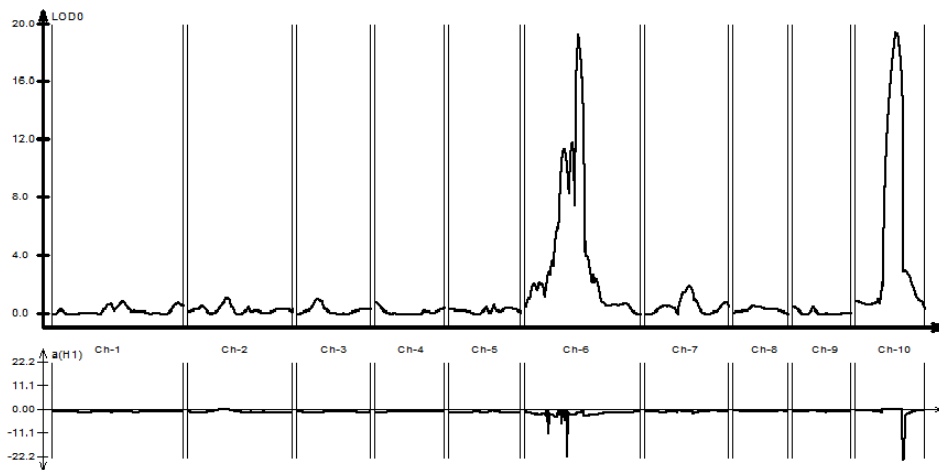


### (9) Glumes of cob

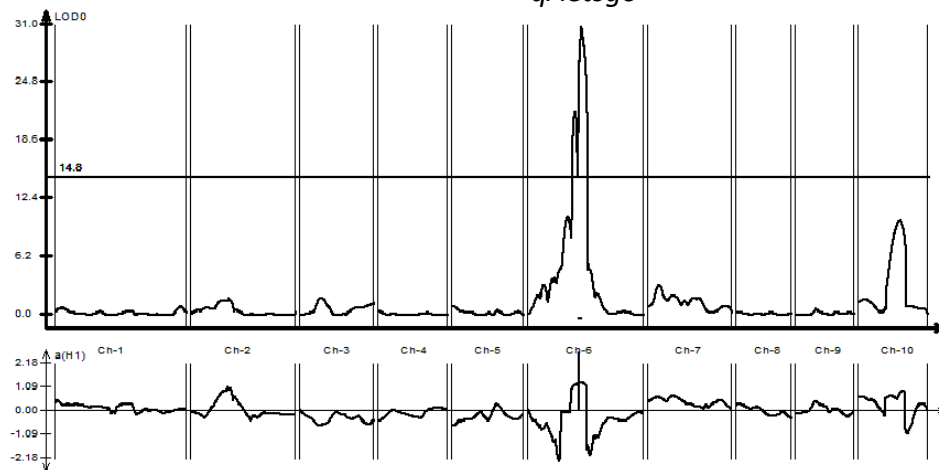


Supplemental Fig.1 (Continued from previous page)

## (10) Dorsal side of grain



## (11) Top side of grain



Supplemental Fig.1 (Continued from previous page)

JC072A : ATGGGCAGGAGGGCGTGCTGCGCCAAGGAAGGGGTGAAGAGAGGGGCGTGGACGGCCAAG : 60  
Ki68 : ATGGGCAGGAGGGCGTGCTGCGCCAAGGAAGGGGTGAAGAGAGGGGCGTGGACGGCCAAG : 60

JC072A : GAAGACGATACCTTGGCCGCCTACGTCAAGGCCACCGCGAAGGCCAAATGGAGAGAGGTG : 120  
Ki68 : GAAGACGATACCTTGGCCGCCTACGTCAAGGCCACCGCGAAGGCCAAATGGAGAGAGGTG : 120

JC072A : CCCCAGAAAGCCGGTAAATAAATTTGTTGATTAGCTTTTCTTTTCAGATTTTCGTTTTGGGAT : 180  
Ki68 : CCCCAGAAAGCCGGTAAATAAATTTGTTGATTAGCTTTTCTTTTCAGATTTTCGTTTTGGGAT : 180

JC072A : CAGCATATCATATATATATACCAAGACAAGAT --CGACGACGCGGCTGATG --GTGTGT : 235  
Ki68 : CAGCATATCATATATATATATACCAAGACAAGATCGACGACGCGGCTGATG GTGTGTGT : 240

JC072A : GCAGGTTTGCCTCGGTGCGGCAAGAGCTGCCGGCTGCGGTGGCTGAACTACCTCCGGCCC : 295  
Ki68 : GCAGGTTTGCCTCGGTGCGGCAAGAGCTGCCGGCTGCGGTGGCTGAACTACCTCCGGCCC : 300

JC072A : AACATCAAGCGCGGCAACATCTCCTACGACGAGGAGGATCTCATCGTCCGGCTCCACAAG : 355  
Ki68 : AACATCAAGCGCGGCAACATCTCCTACGACGAGGAGGATCTCATCGTCCGGCTCCACAAG : 360

JC072A : CTCCTCGGCAACAGGTTACATGAGCTGACGACGAGCAGCCATCTGCTACGAATTCATCCG : 415  
Ki68 : CTCCTCGGCAACAGGTTACATGAGCTGACGACGAGCAGCCATCTGCTACGAATTCATCCG : 420

JC072A : TTCCGGTGTGTTGTCTACTCCTTTACATACGTACGTACGTACGTACGTTGTGTTGGCATGC : 475  
Ki68 : TTCCGGTGTGTTGTCTACTCCTTTACATACGTACGTACGTACGTACGTTGTGTTGGCATGC : 477

JC072A : AGGTGGTCGCTGATTGCAGGCAGGCTGCCGGGCCGAACAGACAATGAAATCAAGAACTAC : 535  
Ki68 : AGGTGGTCGCTGATTGCAGGCAGGCTGCCGGGCCGAACAGACAATGAAATCAAGAACTAC : 537

JC072A : TGAACAGCACGCTGGGCCGGAGGCGCCGGCGCTGGCGCCGGCGCCGGCGGCAGCAGGGTC : 595  
Ki68 : TGAACAGCACGCTGGGCCGGAGG-----GCCGGCGGCAGCAGGGTC : 579

JC072A : GTCTTCGCGCCGGACACCGGCTCGCACGCCACCCCGCGGGCGGGGAGCCACGAGATG : 655  
Ki68 : GTCTTCGCGCCGGACACCGGCTCGCACGCCACCCCGCGGGCGGGGAGCCACGAGATG : 639

JC072A : ACCGGCGGCCAGAAAGGCGCCGCTCCTCGCGCGGACCTCGGCTCGCCCGGCTCCGACGCA : 715  
Ki68 : ACCGGCGGCCAGAAAGGCGCCGCTCCTCGCGCGGACCTCGGCTCGCCCGGCTCCGACGCA : 699

JC072A : CAAGTGTGGGCGCCCAAGGCGGCGCGGTGCACGGGCGGGCTCTTCTTCCACCGGCGGGAC : 775  
Ki68 : CAAGTGTGGGCGCCCAAGGCGGCGCGGTGCACGGGCGGGCTCTTCTTCCACCGGCGGGAC : 759

JC072A : ACGCACAGCCGACGCGGGGGGACCGAGACGCCGACGCCAATGATGGCCGGTGGTGG : 835  
Ki68 : ACGCACAGCCGACGCGGGGGGACCGAGACGCCGACGCCAATGATGGCCGGTGGTGG : 819

JC072A : GGAGGAGAAGCACGGTCTCGGACGACTGCAGCTCGGCGGCGTCCGGTATCTCCCTCGTA : 895  
Ki68 : GGAGGAGAAGCACGGTCTCGGACGACTGCAGCTCGGCGGCGTCCGGTATCTCCCTCGTG : 879

JC072A : GGAAGCAGCCAGCACGACCCGCTTCTCCGGCGACGGCGACGGCGACTGGATGGACGAC : 955  
Ki68 : GGAAGCAGCCAGCACGACCCGCTTCTCCGGCGACGGCGACGGCGACTGGATGGACGAC : 939

JC072A : GTGAGGGCCCTGGCATCGTTTCTCGAGTCCGACGAGGAGTGGCTCCGCTGTACACGGCC : 1015  
Ki68 : GTGAGGGCCCTGGCGTCTTTCTCGAGTCCGACGAGGAGTGGCTCCGCTGTACACGGCC : 999

JC072A : GAGCAGCTTGTGTAG : 1030  
Ki68 : GAGCAGCTTGTGTAG : 1014

Supplemental Fig. 2.  
Sequence alignment of the coding regions of *P11* from 'JC072A' and 'Ki68'. Exons are shown by yellow lines.

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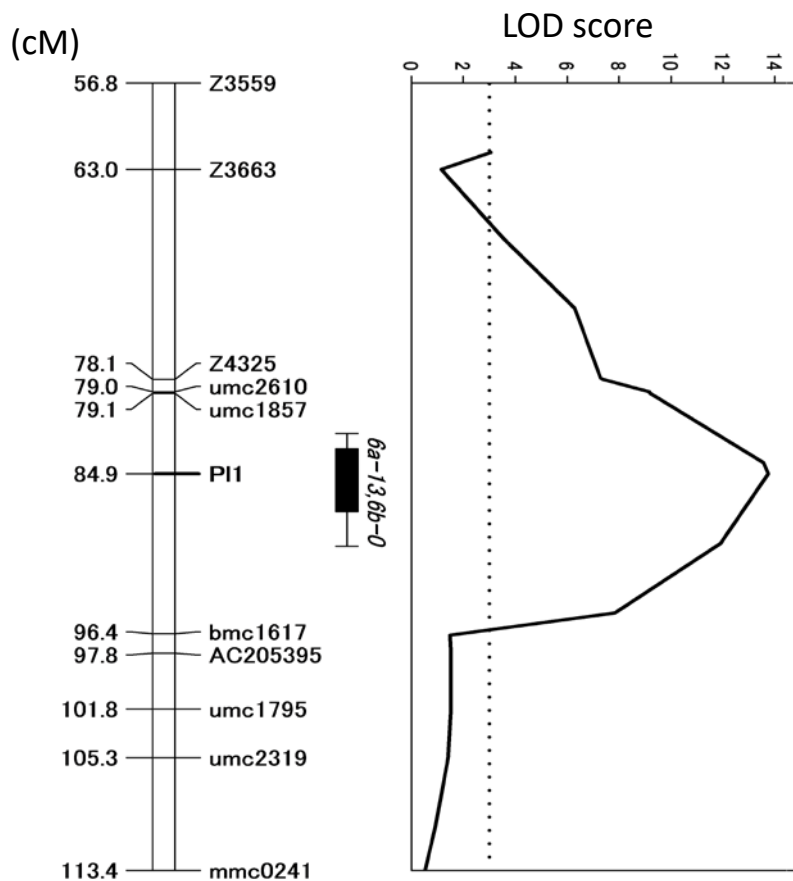
*          20          *          40          *          60          *          80          *          100
PI-Rh : MGRRACCAKEGVKRGAWTAKEDDTLAAYVKAHGEGKWREVPQKAGLRRCCGKSCRLRWLNYLRPNIKRGNISYDEEDLIVRLHKLL---WSLIAGRLPGRT : 97
PI-Bh : MGRRACCAKEGVKRGAWTAKEDDTLAAYVKAHGEGKWREVPQKAGLRRCCGKSCRLRWLNYLRPNIKRGNISYDEEDLIVRLHKLLGNRWSLIAGRLPGRT : 100
PI-Tx303 : MGRRACCAKEGVKRGAWTAKEDDTLAAYVKAHGEGKWREVPQKAGLRRCCGKSCRLRWLNYLRPNIKRGNISYDEEDLIVRLHKLLGNRWSLIAGRLPGRT : 100
PI-Ki68 : MGRRACCAKEGVKRGAWTAKEDDTLAAYVKAHGEGKWREVPQKAGLRRCCGKSCRLRWLNYLRPNIKRGNISYDEEDLIVRLHKLLGNRWSLIAGRLPGRT : 100
PI-bol3 : MGRRACCAKEGVKRGAWTAKEDDTLAAYVKAHGEGKWREVPQKAGLRRCCGKSCRLRWLNYLRPNIKRGNISYDEEDLIVRLHKLLGNRWSLIAGRLPGRT : 100
PI-JC072A : MGRRACCAKEGVKRGAWTAKEDDTLAAYVKAHGEGKWREVPQKAGLRRCCGKSCRLRWLNYLRPNIKRGNISYDEEDLIVRLHKLLGNRWSLIAGRLPGRT : 100
PI-McC : MGRRACCAKEGVKRGAWTAKEDDTLAAYVKAHGEGKWREVPQKAGLRRCCGKSCRLRWLNYLRPNIKRGNISYDEEDLIVRLHKLLGNRWSLIAGRLPGRT : 100
PI-W22 : MGRRACCAKEGVKRGAWTAKEDDTLAAYVKAHGEGKWREVPQKAGLRRCCGKSCRLRWLNYLRPNIKRGNISYDEEDLIVRLHKLLGNRWSLIAGRLPGRT : 100

*          120         *          140         *          160         *          180         *          200
PI-Rh : DNEIKNYWNSTLGRRAGAGAGGGSRVVFAPDTGSHATFPAAGSREMTGGQKGAAPRADLGSPE---SAAVVWAPKAARCTGGLFFPHRRDTHTPHAGT : 193
PI-Bh : DNEIKNYWNSTLGRRAGAGAGGGSRVVFAPDTGSHATFPAAGSREMTGGQKGAAPRADLGSPE---SAAVVWAPKAARCTGGLFFPHRRDTHTPHAGT : 196
PI-Tx303 : DNEIKNYWNSTLGRRAGAGAGGGSRVVFAPDTGSHATFPAAGSREMTGGQKGAAPRADLGSPE---SAAVVWAPKAARCTGGLFFPHRRDTHTPHAGT : 189
PI-Ki68 : DNEIKNYWNSTLGRRAGAGAGGGSRVVFAPDTGSHATFPAAGSREMTGGQKGAAPRADLGSPE---SAAVVWAPKAARCTGGLFFPHRRDTHTPHAGT : 190
PI-bol3 : DNEIKNYWNSTLGRRAGAGAGGGSRVVFAPDTGSHATFPAAGSREMTGGQKGAAPRADLGSPE---SAAVVWAPKAARCTGGLFFPHRRDTHTPHAGT : 196
PI-JC072A : DNEIKNYWNSTLGRRAGAGAGGGSRVVFAPDTGSHATFPAAGSREMTGGQKGAAPRADLGSPE---SAAVVWAPKAARCTGGLFFPHRRDTHTPHAGT : 196
PI-McC : DNEIKNYWNSTLGRRAGAGAGGGSRVVFAPDTGSHATFPAAGSREMTGGQKGAAPRADLGSPE---SAAVVWAPKAARCTGGLFFPHRRDTHTPHAGT : 190
PI-W22 : DNEIKNYWNSTLGRRAGAGAGGGSRVVFAPDTGSHATFPAAGSREMTGGQKGAAPRADLGSPE---SAAVVWAPKAARCTGGLFFPHRRDTHTPHAGT : 191

*          220         *          240         *          260         *
PI-Rh : ETPTE---MMAGGGGGEARSSDCSSAASVSPLVGSSQHDPCFSGDGDGDWMDDVRALASFLESDEEWLRCHTABQLV : 268
PI-Bh : ETPTE---MMAGGGGGEARSSDCSSAASVSPLVGSSQHDPCFSGDGDGDWMDDVRALASFLESDEEWLRCHTABQLV : 271
PI-Tx303 : ETPTE---MMAGGGGGEARSSDCSSAASVSPLVGSSQHDPCFSGDGDGDWMDDVRALASFLESDEEWLRCHTABQLV : 264
PI-Ki68 : ETPTE---MMAGGGGGEARSSDCSSAASVSPLVGSSQHDPCFSGDGDGDWMDDVRALASFLESDEEWLRCHTABQLV : 265
PI-bol3 : ETPTE---MMAGGGGGEARSSDCSSAASVSPLVGSSQHDPCFSGDGDGDWMDDVRALASFLESDEEWLRCHTABQLV : 271
PI-JC072A : ETPTE---MMAGGGGGEARSSDCSSAASVSPLVGSSQHDPCFSGDGDGDWMDDVRALASFLESDEEWLRCHTABQLV : 271
PI-McC : ETPTE---MMAGGGGGEARSSDCSSAASVSPLVGSSQHDPCFSGDGDGDWMDDVRALASFLESDEEWLRCHTABQLV : 266
PI-W22 : ETPTE---MMAGGGGGEARSSDCSSAASVSPLVGSSQHDPCFSGDGDGDWMDDVRALASFLESDEEWLRCHTABQLV : 267

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Supplemental Fig. 3. Alignment of amino acid sequences of *P1* alleles.



Supplemental Fig. 4. Linkage map of the *PI1* region on chromosome 6.

Mapping and QTL analysis showed that *PI1* is located on chromosome 6 as previously reported (Hollick et al. 1995), and detected a large-effect QTL at the *PI1* locus. The LOD score was obtained using  $F_3$  populations.