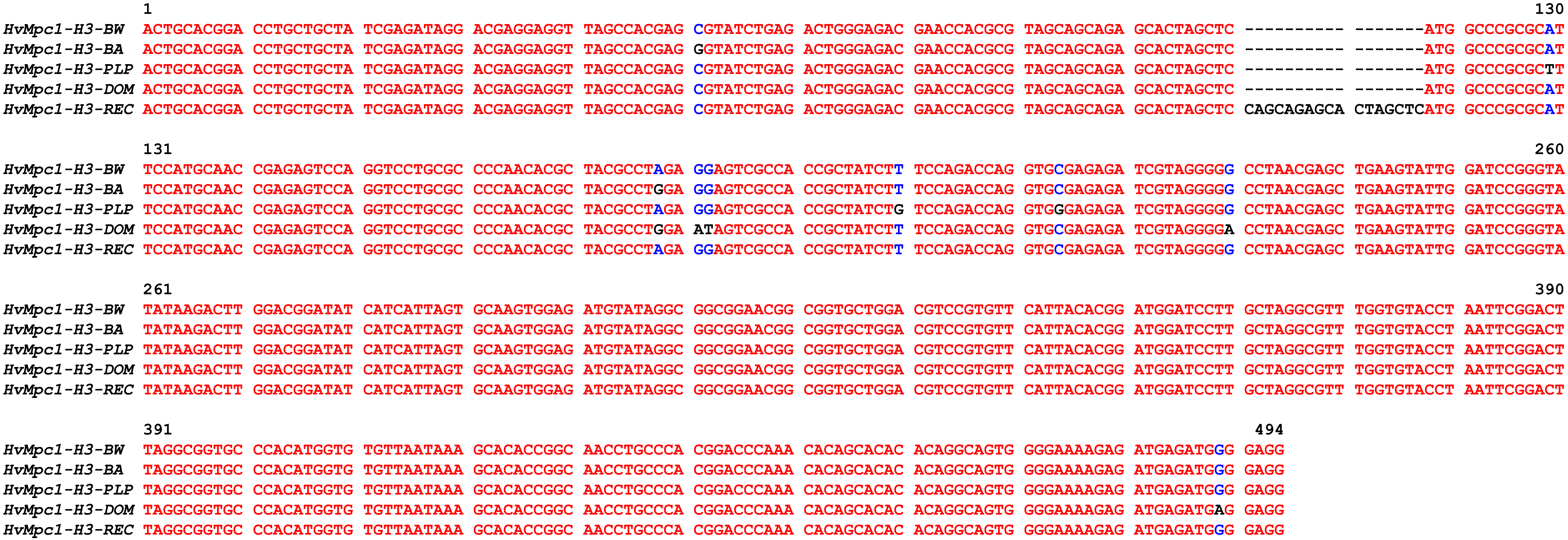
Additional file 1.

A. The exon-intronic structure for *Mpc1* genes of Triticeae tribe.

B. The multiple sequence alignment of promotor sequences of *HvMpc1-H3*. The alignment was performed using MultAlin program. Red is high consensus colour, blue is low consensus colour, black is neutral colour.

A

B



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                1                                                                                                                            130
HvMpc1-H3-BW  ACTGCACGGA CCTGCTGCTA TCGAGATAGG ACGAGGAGGT TAGCCACGAG CGTATCTGAG ACTGGGAGAC GAACCACGCG TAGCAGCAGA GCACTAGCTC ---------- -------ATG GCCCGCGCAT
HvMpc1-H3-BA  ACTGCACGGA CCTGCTGCTA TCGAGATAGG ACGAGGAGGT TAGCCACGAG GGTATCTGAG ACTGGGAGAC GAACCACGCG TAGCAGCAGA GCACTAGCTC ---------- -------ATG GCCCGCGCAT
HvMpc1-H3-PLP ACTGCACGGA CCTGCTGCTA TCGAGATAGG ACGAGGAGGT TAGCCACGAG CGTATCTGAG ACTGGGAGAC GAACCACGCG TAGCAGCAGA GCACTAGCTC ---------- -------ATG GCCCGCGCTT
HvMpc1-H3-DOM ACTGCACGGA CCTGCTGCTA TCGAGATAGG ACGAGGAGGT TAGCCACGAG CGTATCTGAG ACTGGGAGAC GAACCACGCG TAGCAGCAGA GCACTAGCTC ---------- -------ATG GCCCGCGCAT
HvMpc1-H3-REC ACTGCACGGA CCTGCTGCTA TCGAGATAGG ACGAGGAGGT TAGCCACGAG CGTATCTGAG ACTGGGAGAC GAACCACGCG TAGCAGCAGA GCACTAGCTC CAGCAGAGCA CTAGCTCATG GCCCGCGCAT

                131                                                                                                                          260
HvMpc1-H3-BW  TCCATGCAAC CGAGAGTCCA GGTCCTGCGC CCCAACACGC TACGCCTAGA GGAGTCGCCA CCGCTATCTT TCCAGACCAG GTGCGAGAGA TCGTAGGGGG CCTAACGAGC TGAAGTATTG GATCCGGGTA
HvMpc1-H3-BA  TCCATGCAAC CGAGAGTCCA GGTCCTGCGC CCCAACACGC TACGCCTGGA GGAGTCGCCA CCGCTATCTT TCCAGACCAG GTGCGAGAGA TCGTAGGGGG CCTAACGAGC TGAAGTATTG GATCCGGGTA
HvMpc1-H3-PLP TCCATGCAAC CGAGAGTCCA GGTCCTGCGC CCCAACACGC TACGCCTAGA GGAGTCGCCA CCGCTATCTG TCCAGACCAG GTGGGAGAGA TCGTAGGGGG CCTAACGAGC TGAAGTATTG GATCCGGGTA
HvMpc1-H3-DOM TCCATGCAAC CGAGAGTCCA GGTCCTGCGC CCCAACACGC TACGCCTGGA ATAGTCGCCA CCGCTATCTT TCCAGACCAG GTGCGAGAGA TCGTAGGGGA CCTAACGAGC TGAAGTATTG GATCCGGGTA
HvMpc1-H3-REC TCCATGCAAC CGAGAGTCCA GGTCCTGCGC CCCAACACGC TACGCCTAGA GGAGTCGCCA CCGCTATCTT TCCAGACCAG GTGCGAGAGA TCGTAGGGGG CCTAACGAGC TGAAGTATTG GATCCGGGTA

                261                                                                                                                          390
HvMpc1-H3-BW  TATAAGACTT GGACGGATAT CATCATTAGT GCAAGTGGAG ATGTATAGGC GGCGGAACGG CGGTGCTGGA CGTCCGTGTT CATTACACGG ATGGATCCTT GCTAGGCGTT TGGTGTACCT AATTCGGACT
HvMpc1-H3-BA  TATAAGACTT GGACGGATAT CATCATTAGT GCAAGTGGAG ATGTATAGGC GGCGGAACGG CGGTGCTGGA CGTCCGTGTT CATTACACGG ATGGATCCTT GCTAGGCGTT TGGTGTACCT AATTCGGACT
HvMpc1-H3-PLP TATAAGACTT GGACGGATAT CATCATTAGT GCAAGTGGAG ATGTATAGGC GGCGGAACGG CGGTGCTGGA CGTCCGTGTT CATTACACGG ATGGATCCTT GCTAGGCGTT TGGTGTACCT AATTCGGACT
HvMpc1-H3-DOM TATAAGACTT GGACGGATAT CATCATTAGT GCAAGTGGAG ATGTATAGGC GGCGGAACGG CGGTGCTGGA CGTCCGTGTT CATTACACGG ATGGATCCTT GCTAGGCGTT TGGTGTACCT AATTCGGACT
HvMpc1-H3-REC TATAAGACTT GGACGGATAT CATCATTAGT GCAAGTGGAG ATGTATAGGC GGCGGAACGG CGGTGCTGGA CGTCCGTGTT CATTACACGG ATGGATCCTT GCTAGGCGTT TGGTGTACCT AATTCGGACT

                391                                                                                      494
HvMpc1-H3-BW  TAGGCGGTGC CCACATGGTG TGTTAATAAA GCACACCGGC AACCTGCCCA CGGACCCAAA CACAGCACAC ACAGGCAGTG GGGAAAAGAG ATGAGATGGG GAGG
HvMpc1-H3-BA  TAGGCGGTGC CCACATGGTG TGTTAATAAA GCACACCGGC AACCTGCCCA CGGACCCAAA CACAGCACAC ACAGGCAGTG GGGAAAAGAG ATGAGATGGG GAGG
HvMpc1-H3-PLP TAGGCGGTGC CCACATGGTG TGTTAATAAA GCACACCGGC AACCTGCCCA CGGACCCAAA CACAGCACAC ACAGGCAGTG GGGAAAAGAG ATGAGATGGG GAGG
HvMpc1-H3-DOM TAGGCGGTGC CCACATGGTG TGTTAATAAA GCACACCGGC AACCTGCCCA CGGACCCAAA CACAGCACAC ACAGGCAGTG GGGAAAAGAG ATGAGATGAG GAGG
HvMpc1-H3-REC TAGGCGGTGC CCACATGGTG TGTTAATAAA GCACACCGGC AACCTGCCCA CGGACCCAAA CACAGCACAC ACAGGCAGTG GGGAAAAGAG ATGAGATGGG GAGG
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