

A

MsYABBY5 Unigene0062650	ATGGATATGGCTGACGACGCTGTGTTACNTTCCTTGGAGCTACTGCAATATATATCTTGGCGTAAGTGTTCACATG ATGGATATGGCTGACGACGCTGTGTTACNTTCCTTGGAGCTACTGCAATATATATCTTGGCGTAAGTGTTCACATG	75 75
MsYABBY5 Unigene0062650	AGCAGCTTGTTTGATGTAGTGACAGTTAGGTGTGGGCACTGGCCCAATCTTTGGACTGTGAATATGGCTGTCTGCC AGCAGCTTGTTTGATGTAGTGACAGTTAGGTGTGGGCACTGGCCCAATCTTTGGACTGTGAATATGGCTGTCTGCC	150 150
MsYABBY5 Unigene0062650	TTCCCTCTCTGACGCTCCTCCTTCCAAGATCTTCATCACCATCACCATCAGGGTCTTTAGCTACGCTCCATCG TTCCCTCTCTGACGCTCCTCCTTCCAAGATCTTCATCACCATCACCATCAGGGTCTTTAGCTACGCTCCATCG	225 225
MsYABBY5 Unigene0062650	GATTACAGAGTCGACCTTGGCTCCTCTCCAAATGGAACCTACAGGATGCCAATGCAGCTCCTAGCTTCATCAAC GATTACAGAGTCGACCTTGGCTCCTCTCCAAATGGAACCTACAGGATGCCAATGCAGCTCCTAGCTTCATCAAC	300 300
MsYABBY5 Unigene0062650	AAACGAGATCAGAGAATCATCAATCGTCCCTGAGAAGCGGCAAGCTGTTCCATCTGCATACAATCAGTTCATT AAACGAGATCAGAGAATCATCAATCGTCCCTGAGAAGCGGCAAGCTGTTCCATCTGCATACAATCAGTTCATT	375 375
MsYABBY5 Unigene0062650	AAGGAGGAATTCAAAGAATCAAGGCCAACAAATCTGATATCAGCCATAGGGAAGCTTTCAGCACTGCTGCCAAA AAGGAGGAATTCAAAGAATCAAGGCCAACAAATCTGATATCAGCCATAGGGAAGCTTTCAGCACTGCTGCCAAA	450 450
MsYABBY5 Unigene0062650	AATTGGGCACACTTTCCTCATATCCATTTTGGGCTCATGCTGGAGAGCAAGAACCAGATAATAAATTTGAGGAG AATTGGGCACACTTTCCTCATATCCATTTTGGGCTCATGCTGGAGAGCAAGAACCAGATAATAAATTTGAGGAG	525 525
MsYABBY5 Unigene0062650	GATTCTGAGAAGCATCAAAATGAGAAGGGCAGCCGTTCTGAAACAATG GATTCTGAGAAGCATCAAAATGAGAAGGGCAGCCGTTCTGAAACAATG	572 572

B

MsYABBY5 Unigene0062650	MDMAEQLYICPSYCNILAVSVPCSSLDVVTVRCGHCANLWVNMMAAPPSLHASSFQDLHHHHQGF ^{SYAPS} MDMAEQLYICPSYCNILAVSVPCSSLDVVTVRCGHCANLWVNMMAAPPSLHASSFQDLHHHHQGF ^{SYAPS}	75 75
MsYABBY5 Unigene0062650	DYRVDLGSSSKWNYRMPQPPSFINKPDQRIINRPPEKRQRPVSAVNOF ^{IKKEIQRIKANNPDISHREAFSTAAK} DYRVDLGSSSKWNYRMPQPPSFINKPDQRIINRPPEKRQRPVSAVNOF ^{IKKEIQRIKANNPDISHREAFSTAAK}	150 150
MsYABBY5 Unigene0062650	NWAHFFPHIHFLMLBSKNQDNKLEEDSEKHQMRRAVLN NWAHFFPHIHFLMLBSKNQDNKLEEDSEKHQMRRAVLN	189 189

C

MsMYB Unigene0030793	ATGGGAAGACGCCCGTCTGTGAGAAAGTTGGTTGAGAGAGAGGAGATGGACTGCAGAAGAATGAAAGCTC ATGGGAAGACGCCCGTCTGTGAGAAAGTTGGTTGAGAGAGAGGAGATGGACTGCAGAAGAATGAAAGCTC	75 75
MsMYB Unigene0030793	AGAAAAATATATTCAGGAAAATGGTGAAGGCTGCTGGCGATCATTGCCCAAGAATCAGGTTTACTTAGATGTGGA AGAAAAATATATTCAGGAAAATGGTGAAGGCTGCTGGCGATCATTGCCCAAGAATCAGGTTTACTTAGATGTGGA	150 150
MsMYB Unigene0030793	AAGAGTGCAGACTGAGATGGATTAATTTTGGAGATCGATGTGAAGAGAGGGAATATTTCTTCAAGAAGAA AAGAGTGCAGACTGAGATGGATTAATTTTGGAGATCGATGTGAAGAGAGGGAATATTTCTTCAAGAAGAA	225 225
MsMYB Unigene0030793	GAAATCATTAATTAATCTCCATGCATCTATGGCAACAGTGGTCCCTGATCGCCGCACTTGCCTGGTAGAACA GAAATCATTAATTAATCTCCATGCATCTATGGCAACAGTGGTCCCTGATCGCCGCACTTGCCTGGTAGAACA	300 300
MsMYB Unigene0030793	GACAAATGAAATCAAAAATTAAGGAACTCCCATTTGAGAGAAAATTCACGGTTTCCGCC...CTAATCCACAG GACAAATGAAATCAAAAATTAAGGAACTCCCATTTGAGAGAAAATTCACGGTTTCCGCC...CTAATCCACAG	372 375
MsMYB Unigene0030793	TTTCATTCGCGCCGCCCTCCGCCTCCGCTCCTCTCCAGCCCAAGAAGCAAGAACAAGTAATAAGAAGCAAAAG TTTCATTCGCGCCGCCCTCCGCCTCCGCTCCTCTCCAGCCCAAGAAGCAAGAACAAGTAATAAGAAGCAAAAG	447 450
MsMYB Unigene0030793	SCGGCAGCTAAAAGTCCCACTGCGCCGTCGTGATGCGGACTACCCCACTCCGGAGAAAGATCCTCGTGGGC SCGGCAGCTAAAAGTCCCACTGCGCCGTCGTGATGCGGACTACCCCACTCCGGAGAAAGATCCTCGTGGGC	522 525
MsMYB Unigene0030793	AGACTGGGAAGGAGAGCAAAAGTGAAGCGAGAGAGAGCGCAGCTCCATGTTGGGAGAGTGTGACGATTTAAAT AGACTGGGAAGGAGAGCAAAAGTGAAGCGAGAGAGAGCGCAGCTCCATGTTGGGAGAGTGTGACGATTTAAAT	597 600
MsMYB Unigene0030793	ATGACGGAGGACTTACGCGCTCTGGGCCCCACACTGACTTCGGACCCGGAAGTGAATTTCCGATCCGGT ATGACGGAGGACTTACGCGCTCTGGGCCCCACACTGACTTCGGACCCGGAAGTGAATTTCCGATCCGGT	672 675
MsMYB Unigene0030793	CTGGCCAGCTAGATAACTCGTCTGCAAAATTAAGGAAACGCTTTTCGGATTGTGGACGACGAGGACGAC CTGGCCAGCTAGATAACTCGTCTGCAAAATTAAGGAAACGCTTTTCGGATTGTGGACGACGAGGACGAC	747 750
MsMYB Unigene0030793	AAGTGAATTCACACGTGGCAACGGAGAAATGGATGGTGAATGCTTCTTGGTGTGTGTCATG AAGTGAATTCACACGTGGCAACGGAGAAATGGATGGTGAATGCTTCTTGGTGTGTGTCATG	812 815
MsMYB Unigene0030793	MGRAPCCEKVGKRGRTABEEDKLRKYIQENGEQWRSLPKNAGLLRCGKSCRLRWINYLRSVDRKRNISSQBE MGRAPCCEKVGKRGRTABEEDKLRKYIQENGEQWRSLPKNAGLLRCGKSCRLRWINYLRSVDRKRNISSQBE	75 75
MsMYB Unigene0030793	EIIINLHASMGNRWSLAAHLPGRTDNEIKNYWNSHLRKFHGF ^{FPNQFIPPPPPP} PSKPKKTKNSNKKAK EIIINLHASMGNRWSLAAHLPGRTDNEIKNYWNSHLRKFHGF ^{FPNQFIPPPPPP} PSKPKKTKNSNKKAK	149 150
MsMYB Unigene0030793	AAKTATAAVVMPTTPEKESSVGRPKB ^{RESEARESGSSMVGELDDL} NMTEDLSGLWPTLDFGTGSEISDRG AAKTATAAVVMPTTPEKESSVGRPKB ^{RESEARESGSSMVGELDDL} NMTEDLSGLWPTLDFGTGSEISDRG	224 225
MsMYB Unigene0030793	LGQLDNSSLQIYEP ^{TLNWINDEDDKWSNVD} NGEMDGAMLSWLI LGQLDNSSLQIYEP ^{TLNWINDEDDKWSNVD} NGEMDGAMLSWLI	269 270

D

Supplementary Figure 7 Alignment of nucleotide and amino acid sequences of MsYABBY5 and MsMYB with their homologs in *M. canadensis*. A, B: nucleotides and amino acid sequences of MsYABBY5 and Unigene0062650; C, D: nucleotides and amino acid sequences of MsMYB and Unigene0030793.