

A

MsYABBY5 Unigene0062650	ATGGATATGGCTGACGAGCTGTGTTACNTTCCTTGCAGCTACTGCAATATTATTCCTTGGGTAAAGTGTTCATCG ATGGATATGGCTGACGAGCTGTGTTACNTTCCTTGCAGCTACTGCAANTTTATTCCTTGGGTAAAGTGTTCATCG	75 75
MsYABBY5 Unigene0062650	AGCAGCTTGTGTTGATGAGTACAGTTAGGTGTGGGCACTGCGCCAACTTTTGGACTGTGAATATGGCTGCTGCC AGCAGCTTGTGTTGATGAGTACAGTTAGGTGTGGGCACTGCGCCAACTTTTGGACTGTGAATATGGCTGCTGCC	150 150
MsYABBY5 Unigene0062650	TTCCCTCTCTGACGAGCTCTCTCTTCCAAGATCTTCATCAACATCACCATCAGGGTCTTAGCTACGCTCCATCG TTCCCTCTCTGACGAGCTCTCTCTTCCAAGATCTTCATCAACATCACCATCAGGGTCTTAGCTACGCTCCATCG	225 225
MsYABBY5 Unigene0062650	GATTACAGAGTCGACCTCGGCTCTCTTCCAAATGGAACCTACAGGATGCCAATCGAGCTCTAGCTTCATCAAC GATTACAGAGTCGACCTCGGCTCTCTTCCAAATGGAACCTACAGGATGCCAATCGAGCTCTAGCTTCATCAAC	300 300
MsYABBY5 Unigene0062650	AAACGAGATCAGAGAATCATCAATCGTCCCTCGAGAAGCGGCGAGTGTTCATCTGCATACAATCAGTTCATT AAACGAGATCAGAGAATCATCAATCGTCCCTCGAGAAGCGGCGAGTGTTCATCTGCATACAATCAGTTCATT	375 375
MsYABBY5 Unigene0062650	AAGGAGGAATTCAGAGAATCAAGGCCAACAACTCTGATATCAGCCATAGGGAAGCTTCAGCACTGCTGCCAAA AAGGAGGAATTCAGAGAATCAAGGCCAACAACTCTGATATCAGCCATAGGGAAGCTTCAGCACTGCTGCCAAA	450 450
MsYABBY5 Unigene0062650	AATTGGGCACACTTTTCTCATATCCATTTTGGGCTCATGCTGGAGAGCAAGAACCAGATAATAAACTTGAGGAG AATTGGGCACACTTTTCTCATATCCATTTTGGGCTCATGCTGGAGAGCAAGAACCAGATAATAAACTTGAGGAG	525 525
MsYABBY5 Unigene0062650	SATTCTGAGAAGCATCAATGAGAAGGCGAGCCGTTCTGAACAAAATG SATTCTGAGAAGCATCAATGAGAAGGCGAGCCGTTCTGAACAAAATG	572 572

B

MsYABBY5 Unigene0062650	MDMAEQLCYIPCSYCNIIILAVSVPCSSLFDDVTVRCHCANLWTVNMAAAPPSSLHASSFQDLHHHHQCFSYAPS MDMAEQLCYIPCSYCNIIILAVSVPCSSLFDDVTVRCHCANLWTVNMAAAPPSSLHASSFQDLHHHHQCFSYAPS	75 75
MsYABBY5 Unigene0062650	DYRVDLGSSSKWNYRMFMPQPPSFINKPDQRIINRPPEKQRQVPQSAYNQFIKEEIQRIKANNPDISHREAFSTAAK DYRVDLGSSSKWNYRMFMPQPPSFINKPDQRIINRPPEKQRQVPQSAYNQFIKEEIQRIKANNPDISHREAFSTAAK	150 150
MsYABBY5 Unigene0062650	NWAHFPPIHFGLMLBSNQDNKLEEDSEKHQMRRAAVLN NWAHFPPIHFGLMLBSNQDNKLEEDSEKHQMRRAAVLN	189 189

C

MsMYB Unigene0030793	ATGGGAAGAGCGCCGTGCTGTGAGAAAGTTGGGTTGAAGAGAGGGAGATGGACTGCAGAAGAAGATGAAAGCTTC ATGGGAAGAGCGCCGTGCTGTGAGAAAGTTGGGTTGAAGAGAGGGAGATGGACTGCAGAAGAAGATGAAAGCTTC	75 75
MsMYB Unigene0030793	AGAAAAATATATTACGAAAAATGGTGAAGGCTGCTGGCGATCATTCGCCAAGAATCGAGGTTTACTTAGATGTGGA AGAAAAATATATTACGAAAAATGGTGAAGGCTGCTGGCGATCATTCGCCAAGAATCGAGGTTTACTTAGATGTGGA	150 150
MsMYB Unigene0030793	AAGAGTTCGAGACTGAGATGGATTAAATTTTGGAGATCATGATGTGAAGAGAGGGAATATTTCTCTCAAGAAGAA AAGAGTTCGAGACTGAGATGGATTAAATTTTGGAGATCATGATGTGAAGAGAGGGAATATTTCTCTCAAGAAGAA	225 225
MsMYB Unigene0030793	GAAATCATCATTAATCTCCATGCATCTATGGGCAACAGGTGGTCCCTGATCGCCGCGCACTTGCCGGGTAGAACAA GAAATCATCATTAATCTCCATGCATCTATGGGCAACAGGTGGTCCCTGATCGCCGCGCACTTGCCGGGTAGAACAA	300 300
MsMYB Unigene0030793	GACAAATGAAATCAAAAATTAAGGAACTCCCATTTGAGAGAGAAATTCACGGTTTCCGCC...CTAATCCACAG GACAAATGAAATCAAAAATTAAGGAACTCCCATTTGAGAGAGAAATTCACGGTTTCCGCCSCCTAATCCACAG	372 375
MsMYB Unigene0030793	TTTCATTCGCGCGCGCGCTCCGCTCCGCTCTCTCCAGCCCAAGAGCAAGAACAGCAATAAAGAGGCAAG TTTCATTCGCGCGCGCGCTCCGCTCCGCTCTCTCCAGCCCAAGAGCAAGAACAGCAATAAAGAGGCAAG	447 450
MsMYB Unigene0030793	SCGGCAGCTAAAACGCCACTGCGCGCTGCTCATGCGGACTACCCCACTCCGGAGAAAGATCCTCGTGGGC SCGGCAGCTAAAACGCCACTGCGCGCTGCTCATGCGGACTACCCCACTCCGGAGAAAGATCCTCGTGGGC	522 525
MsMYB Unigene0030793	AGACCTGGGAAGGAGAGCAAGAGTGAAGCGAGAGAGCGGAGCTCCATGGTGGGAGAGTGGACGATTTAAC AGACCTGGGAAGGAGAGCAAGAGTGAAGCGAGAGAGCGGAGCTCCATGGTGGGAGAGTGGACGATTTAAC	597 600
MsMYB Unigene0030793	ATGACGAGAGACTTGACGCGCTCTGCGGCCCCACACTGGACTTCGAGACCGGAAGTCAAAATTTCCGATCCGCGT ATGACGAGAGACTTGACGCGCTCTGCGGCCCCACACTGGACTTCGAGACCGGAAGTCAAAATTTCCGATCCGCGT	672 675
MsMYB Unigene0030793	CTGGGCAGCTAGATAACTCGTCTGCAAAATTAAGAGAACGCTTTCTGGATTGTGACGACGAGGACGAC CTGGGCAGCTAGATAACTCGTCTGCAAAATTAAGAGAACGCTTTCTGGATTGTGACGACGAGGACGAC	747 750
MsMYB Unigene0030793	AAGTGAATTCACACGTGGCAACGGAGAAATGGATGGTGCATGCTTCTTGGTGTGTGTCATG AAGTGAATTCACACGTGGCAACGGAGAAATGGATGGTGCATGCTTCTTGGTGTGTGTCATG	812 815
MsMYB Unigene0030793	MGRAPCCEKVLKGRWTAEEDEKLKRYIQENGEGCWRSLPKNAGLLRCGSKRLRWINYLRSDVKRGNISSQBE MGRAPCCEKVLKGRWTAEEDEKLKRYIQENGEGCWRSLPKNAGLLRCGSKRLRWINYLRSDVKRGNISSQBE	75 75
MsMYB Unigene0030793	EIIINLHASMGNRWSLIAHLPGRTDNEIKNYWNSHLRSKFHGF...FNPQFI PPPPPPP...PSSKPKTKNSNKKAK EIIINLHASMGNRWSLIAHLPGRTDNEIKNYWNSHLRSKFHGF...FNPQFI PPPPPPP...PSSKPKTKNSNKKAK	149 150
MsMYB Unigene0030793	AAAKTATAAVVMPTTPTPEKESSVGRPGKRESEARESGSSMVGELDDLNTEDLSGLWGPTLDFGTGSEISDPG AAAKTATAAVVMPTTPTPEKESSVGRPGKRESEARESGSSMVGELDDLNTEDLSGLWGPTLDFGTGSEISDPG	224 225
MsMYB Unigene0030793	LGQLNSSLQIYETLSWINDEDDKWNNSVANGEMDGAMLSWLI LGQLNSSLQIYETLSWINDEDDKWNNSVANGEMDGAMLSWLI	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.