

Table S1. EST components for each BnaMYB gene identified

Gene name	EST list(GB#)	numbers
<i>BnaMYB1</i>	FG562006, EV105180, EV104795, EV104301, EV104487, EV217986, EV218259, EV017370, EV007116, EV171276, EV171275, GT080535, GT080173	13
<i>BnaMYB2</i>	EV108364, EV108088, EV107499, EV107802, EV107824	5
<i>BnaMYB3</i>	EV036085, EV137123, CD829890, EV136892, ES267811, EV217210, EV217001, EE392356, EE447724, EV102195, EV176932, EV102118, EV084554, EV113081,	15
<i>BnaMYB4</i>	FG579280, EE432096, FG569527, EV107955, EE554982, CD824305, FG569361, EV001261, EV107589, EV069542, EV053883, CD820923	12
<i>BnaMYB5</i>	FG557455, FG559446, EV066471, FG573585, DY011724, EV029074, EL628966,	8
<i>BnaMYB6</i>	EE426716	1
<i>BnaMYB7</i>	CD814497, EV068015, EV054074, EV056383, EV045384, EV135986, EV135722, EE455594, EV142432, EV142168, EV015761	11
<i>BnaMYB9</i>	EE444903, CN726972	2
<i>BnaMYB10</i>	EE568790	1
<i>BnaMYB12</i>	EV052963, EV214117, FG559530, EV171434, EV171441, EV171478	6
<i>BnaMYB13</i>	DY000543, GR446781	2
<i>BnaMYB15</i>	CX278128, CD834677, ES909302, CJ999528, EV227400, EV226989	6
<i>BnaMYB16</i>	EE469504, EE474289, EV201981, EV186736, EV186534, EV201893	6
<i>BnaMYB17</i>	EG020679, CD813379, CX187948, CD813183, EV028628, EV033184	6
<i>BnaMYB18</i>	EE432793, EG020345	2
<i>BnaMYB21</i>	CX187597, GR441028, EV131386, EV131621, GR440457, EV225302, GR442541, GR449144, EV224973, EV133221, EV133479	11
<i>BnaMYB27</i>	ES900986,	1
<i>BnaMYB28</i>	EV205917, EV019009, GT084146	3
<i>BnaMYB30</i>	ES967084, ES985544, GH709300, CX192819, CN829495, CN829494, CN830411, CN830410, CN830379, CN830378, DY016733, FG567228, EV039358, EV033495,	16
<i>BnaMYB31</i>	EV052208, EV021453, EV055620, EV030145, EL627642, EE414354	6
<i>BnaMYB32</i>	EE460070, FG567004, EE464782, EV163324, EV058208, CD813645, ES996448, EV169541, EV034892, CD815735, EV136510, EV136143, EV162956, EV169537, ES978442, ES903579, GR441366, EV027493, EE421958, EV022772, EV026639	21
<i>BnaMYB34</i>	ES902202, ES901674, ES907416, GT082302, ES913933, EV217367, EV131951, EV132263, ES902202, EE435715, EV217667	11
<i>BnaMYB37</i>	EV050408	1
<i>BnaMYB38</i>	EV047434, EV043318, EE542063	3
<i>BnaMYB41</i>	FG576099	1
<i>BnaMYB43</i>	ES913743	1
<i>BnaMYB44</i>	EE454244, EE408115, EE460613, DY012865, GR449006, GT083755, EE453513, GR444848, EV029474, EV146101, EV029025, ES966920, EV182779, EV164288, EV185978, EV124448, EV124281, EV124528, EV124361, EV182860, FG564972, EE436724, EV186186, CX279215, DY006419, FG556542, GT079317, EV146335, EV164606, EV226115, EE409588, EE474422, DY010719, CX279103, EE420841, ES928719, FG569627, EE478191, CD815989, FG568454, EE482310, FG570148, EV062607, EE426643, CN730439, EE482375, FG557223, EV047348, EE549228,	50
<i>BnaMYB45</i>	ES910249	1

<i>BnaMYB46</i>	EV127369, EV127154, FG562990	3
<i>BnaMYB47</i>	CX281630, EE558066	2
<i>BnaMYB48</i>	EE557265, EE557253, EV021911, EV219591, EV219351, EV218206	6
<i>BnaMYB51</i>	EE441525, EV221769, EV222159, GT083698, ES900783	5
<i>BnaMYB55</i>	EV053995, EV051174	2
<i>BnaMYB56</i>	EE468140, ES994945, EV072908, EV009610, FG560099, FG575184, EV084645, CN727379, DY000266, EV025748, EV217687, EE514247, EE561644, ES994208	14
<i>BnaMYB57</i>	CN727183	1
<i>BnaMYB58</i>	ES903149, EV127893, EV127723	3
<i>BnaMYB59</i>	CN734145, EE432821, EV041668, EE550309, ES956099, EV134091, EV133852, EV102946, ES900670, EV218708, ES982160	11
<i>BnaMYB60</i>	EV201821, CN726921, EG019425, EV201738, EG019781, FG574548	6
<i>BnaMYB61</i>	EV044996, ES909631, EV122101, EV044013, EV059923, EV122017, EV044304, EV042041, EE464021, EV076842, EV073819, EV088869, EV027982, EV026308,	15
<i>BnaMYB62</i>	DY017568, DY017568	2
<i>BnaMYB63</i>	EV085491, EE472135,	2
<i>BnaMYB65</i>	CX190346, CX191895, CX193810, ES905996, EV087133	5
<i>BnaMYB68</i>	ES909381, CX191605, ES909697, ES911294, EE470630, ES900275, EV070292	7
<i>BnaMYB70</i>	ES988352, EV126496, EV126569	3
<i>BnaMYB71</i>	EE463219, ES912837, EL626888	3
<i>BnaMYB73</i>	EV117185, EV118175, EV124377, EV184889, EV226584, EV117101, EV117019, DY002016, ES959932, EV016569, EV226382, EV057240, EV118093, FG576493, EL588855, EV184806, EL591252, DY002002, EV124296, EV225159, EV068002, EV224965, EV019487, EV040914, ES904772, EV047845, EL626849	27
<i>BnaMYB75</i>	ES976916, ES976894	2
<i>BnaMYB77</i>	CD835413, CD814996, CD835248, FG565094, EE455241, EV041049, EE460766, EV059427, CD828382, EL587880, EL587506, EV066198, CD823048, CD831049, EV021763, GT081972, ES979958, EE562286, EV124030, EE467152, FG578598, EV123952, ES988901, ES267253, EV018619, CN732778, EV163421, EE410941, ES979621, ES979658, ES264989, EL625057, EE565075, CN727364, EV061577,	37
<i>BnaMYB78</i>	EX130477	1
<i>BnaMYB81</i>	CX195622, EE445112	2
<i>BnaMYB85</i>	EV075547	1
<i>BnaMYB86</i>	FG555601, EV039089	2
<i>BnaMYB88</i>	EV215661, ES904057, EV204258, EV204013	4
<i>BnaMYB90</i>	EV194857, ES976894, ES976916, EV194929	4
<i>BnaMYB91</i>	GR444849, CN736467, EV034590, EV014478, CN826196, EE441718, CB686393, EV100193, EV100123, EE515947, EE512329, EE553868, EE551924, ES963899, ES965570, ES964808, ES965020, ES965699, ES963678, ES964885, ES963886, ES963998, EE443576, ES964722, ES965468, ES965296, ES965009, ES964883, ES965836, ES964704, ES964909, ES965408, ES965676, ES965619	34
<i>BnaMYB92</i>	ES903861	1
<i>BnaMYB95</i>	EE473909, ES921824, GR442066, CD841264, DY030638, EV019898, ES968873, GR440287, EV038136, EV030103, EV029563, EV026741, EE565640, EE454667, CD815189, GT084601, EE454192	17

<i>BnaMYB96</i>	EV145404, EE561829, EE474153, EV014976, ES898274, EV173476, EV173463, EV169763, EV169753, EG021274	10
<i>BnaMYB99</i>	EV159202, EV159072, EV159317	3
<i>BnaMYB101</i>	GR453309, EE552862	2
<i>BnaMYB102</i>	EV216621	1
<i>BnaMYB103</i>	CX192517, FK252590, EE392431, EV128652, EV128386, FG561365	6
<i>BnaMYB104</i>	EE477460, EL587234	2
<i>BnaMYB105</i>	EV151423	1
<i>BnaMYB106</i>	EL627196, EE502449, EE492636, EE555080, EE453474, EV060957, EV030094, EV154290, EV154349	9
<i>BnaMYB108</i>	ES911647	1
<i>BnaMYB109</i>	EE435105, EV021934, CX189597	3
<i>BnaMYB110</i>	FG568063, EE472472, EE483738, EV003085, FG569763, EE565229	6
<i>BnaMYB111</i>	ES920481, EV197885, EL630384, EV197794, CD838538, CD839606	6
<i>BnaMYB114</i>	EE489982, EE489704, EE490079	3
<i>BnaMYB116</i>	EV100953	1
<i>BnaMYB117</i>	CD841933, CD841114	2
<i>BnaMYB118</i>	CD827885, CD828164, CD828310, CD819510, CD819263, FG561180, FG565690, EV004266, EE500621, EE500392, EE499150, EV005206, EE472461, CD823403,	15
<i>BnaMYB122</i>	ES903348	1
<i>BnaMYB123</i>	FG562315, EV033254, CD821188, EV060679, EV048548, EV027398, EV044112, CD824329, EV079072	9
<i>BnaMYB124</i>	CX189696, DY011287	2

Table S2. Primers used in this study

gene	forward primer sequence(5->3')	reverse primer sequence(5->3')	purpose
<i>BnaMYB1</i>	TTAGGTCATGATCGAGAGAGAGATGTGGG GACG	CGCGTCGACTGTAGACAGGACATTGGTTCTGC	cDNA cloning
	TTAGGTCATGATCGAGAGAGAGATGTGGG	CGCGTCGACTGTAGACAGGACATTGGTTCTGC	transactivation assay
<i>BnaMYB3</i>	GGAACCCTCTTCCTTCCTTG	GCATTACAAGACATTAAAGGCACA	cDNA cloning
	CGCCATGGGAAGGTCACCATGC	CCCCCGGGCTAAAGAATTTTCGATTCCCA	transactivation assay
	TCCAGCGACGACCAAGAGTTA	AAGTACGACAATTCCGACACGAC	qRT-PCR
<i>BnaMYB4</i>	CGCCATGGGAAGGTCACCATGTTGT	CGCGTCGACTATCATCTCCAAGCTTCGAAAACC TAA	cDNA cloning
	CGCCATGGGAAGGTCACCGTGTTGTGAG	CGCGTCGACTTTCATCTCCAAGCTTCTAAAACC AAAA	cDNA cloning
	CGCCATGGGAAGGTCACCATGTTGT	CGCGTCGACTATCATCTCCAAGCTTCGAAAACC TAA	transactivation assay
	GGACTAGTATGGGAAGGTCACCATGTTG	CGCGTCGACTATCATCTCCAAGCTTCGAAAACC	protoplast assay
<i>BnaMYB7</i>	GGAATTCCATATGGGAAGATCTCCCTGCTG	CGCGTCGACGTTTCATTTCCAAGCTCCGAAAATC	cDNA cloning
	GGAATTCCATATGGGAAGATCTCCCTGCTG	CGCGTCGACGTTTCATTTCCAAGCTCCGAAAATC	transactivation assay
<i>BnaMYB12</i>	TCCATTGCTCGAGTCTTG	TCACATAACAATACGGTGCTCAA	cDNA cloning
	CGCCATGGGAAGAGCGCCGTG	CGCGTCGACAGAGAGAAGCCATGCGAC	transactivation assay
	GAGGCCACGATCGGGAAAAG	AGAGAAGCCATGCGACCAAC	qRT-PCR
<i>BnaMYB13</i>	TTAGGTCATGATCGGGAGAAGACCATGCT GTGA	CGCGTCGACGAAAATGTCGGAATTTTCTCCAGT TG	cDNA cloning
	TTAGGTCATGATCGGGAGAAGACCATGCT GTGA	CGCGTCGACGAAAATGTCGGAATTTTCTCCAGT TG	transactivation assay
	CCCAACAACAATCTAGCAGCAGTA	ACGTCGCAGAGTCTTTGATGTT	qRT-PCR
<i>BnaMYB15</i>	TTAGGTCATGATCGGAAGAGCTCCATGCTG	CGCGTCGACGAGCCCAGCTAGTAGATCTTG	cDNA cloning
	TTAGGTCATGATCGGAAGAGCTCCATGCTG	CGCGTCGACGAGCCCAGCTAGTAGATCTTG	transactivation assay
<i>BnaMYB16</i>	GCCAAAAACACCATTCCTTTG	TCATTTTCGTGGAACATTCATCC	cDNA cloning
	GGAATTCATGGGTAGATCACCGTGC	CGCGTCGACGAACATAGGCGTTGAATCG	transactivation assay
	AGGGCTCACGGGTCTCTTG	GCCGGCCGTCTCGTTTTTAT	qRT-PCR

<i>BnaMYB28</i>	GGACTAGTGGTAGATCACCGTGCTGT GGAATTCATGTCAAGAAAGCCATGTTGTGT GGAATTCATGTCAAGAAAGCCATGTTGTGT	CGCGTCGACGAACATAGGCGTTGAATCG CGCGTCGACTTCAGAGGGAATCATAATCCATG CGCGTCGACTTCAGAGGGAATCATAATCCATG	GFP fusion cDNA cloning transactivation assay
<i>BnaMYB30</i>	GCAAAAAGAGAAAAGGGAGTGA	TTTCAGGCCCTAGTGATTTT	cDNA cloning
<i>BnaMYB31</i>	GGAATTCATGGTGAGACCCCCTTGT GGAATTCCATATGGGTAGACCACCTTGTTG GGAATTCCATATGGGTAGACCACCTTGTTG	CGCGTCGACGAAGAAATTAGGGTTTTTCATC CGCGTCGACGGACAAATCTTGACCGTTGTTGC CGCGTCGACGGACAAATCTTGACCGTTGTTGC	transactivation assay cDNA cloning transactivation assay
<i>BnaMYB32</i>	TTAGGTCATGATCGGGAGGTCTCCATGCTG C TTAGGTCATGATCGGGAGGTCTCCATGCTG C AAGGAGGAAAGTTCTAGGGAGGAG CGGGATCCATGGGGAGGTCTCCATGCTG	CGCGTCGACGTTTCATTTCCAAGCTAGTATAATC CAAG CGCGTCGACGTTTCATTTCCAAGCTAGTATAATC CAAG CCATGGCGGGCTGATTCT CGCGTCGACGTTTCATTTCCAAGCTAGTATAATC	cDNA cloning transactivation assay transactivation assay qRT-PCR protoplast assay
<i>BnaMYB34</i>	CGCCATGGTGAGAACACCATGCTGC CGCCATGGTGAGAACACCATGCTGC	CCCTCGAGGACAAAGACACCAATCTTGGAATC CCCTCGAGGACAAAGACACCAATCTTGGAATC	cDNA cloning
<i>BnaMYB38</i>	CGGAATTCATGGGAAGGGCTCCATGTTGTG CGGAATTCATGGGAAGGGCTCCATGTTGTG GGACTAGTGGGAAGGGCTCCATGTTGTG	CGCGTCGACATAGTACAACATGAACGTATCAT CGCGTCGACATAGTACAACATGAACGTATCAT CGCGTCGACATAGTACAACATGAACGTATCAT	transactivation assay GFP fusion cDNA cloning transactivation assay
<i>BnaMYB41</i>	TTAGGTCATGATCGGAAGATTACCTTGTTG	CGCGTCGACAAGCAACCCCATAAAGTCATCAA	GFP fusion cDNA cloning
<i>BnaMYB43</i>	GGAATTCCATATGGGGAGGCAGCCATGTT GT GGAATTCCATATGGGGAGGCAGCCATGTT GT	CGCGTCGACATCTAAAACCATTCTTGAACATCC GC CGCGTCGACATCTAAAACCATTCTTGAACATCC GC	cDNA cloning transactivation assay
<i>BnaMYB44</i>	TCACAACAAAACAGAGCTTCTCA TTAGGTCATGATCGCGGATCGTATTAAAGG	CGAGATCGCTCACTCGATTT CCCTCGAGCTACTCGATTCTTCCAACTCC	cDNA cloning transactivation assay
<i>BnaMYB46</i>	CAGCGAGGAGTCAAACCGTAGTCA CGCCATGGTAAGGAAACCAGAGGTAGGAA CGCCATGGTAAGGAAACCAGAGGTAGGAA	TCACCTCCGCCTTAATCATCTCCT CGCGTCGACTGTGCTTTGTTTGAAGTTGAAGTG CGCGTCGACTGTGCTTTGTTTGAAGTTGAAGTG	qRT-PCR cDNA cloning transactivation assay

<i>BnaMYB47</i>	CAGGGCTACAAGGGGAACTCTACT CGCCATGGGGAGGAAGACGTGG CGCCATGGGGAGGAAGACGTGG	GGTCCCAATATTCTTCCACTCTCA CGCGTCGACGAAGAGATAATCAAGTATCTGAG CGCGTCGACGAAGAGATAATCAAGTATCTGAG	qRT-PCR cDNA cloning transactivation assay
<i>BnaMYB48</i>	GAAGAAAGAGGATGAATATGATGCAAGAG	TTTTCAACGAATGAATGGAATCCT	cDNA cloning
<i>BnaMYB51</i>	CGCCATGGTGC GGACACCGTGTTGC CGCCATGGTGC GGACACCGTGTTGC	CGCGTCGACTGCAAATAGTTATCAATATCTTC CGCGTCGACTGCAAATAGTTATCAATATCTTC	cDNA cloning transactivation assay
<i>BnaMYB56</i>	GAAAGAAAATGAATCCAAATCTCCTTGAG TTAGGTCATGAATCCAAATCTCCTTGA GTGGCCATTACTTCTTTGATTTTC	TCCTACCCCGGCTAACTTCT CGCGTCGACAGAAGCTCCA ACTCCAAG CCTACCCCGGCTAACTTCTACC	cDNA cloning transactivation assay qRT-PCR
<i>BnaMYB58</i>	GGAATTCATATGGGCAAAGGGAGAGCTC CA	CGCGTCGACATGATTTATCAGGACCTCATAACT CTC	cDNA cloning
<i>BnaMYB59</i>	TGAGATGAAAAATGTGCAAGAAGA	TTTTGAGAAAAAGGGAGATGGA	cDNA cloning
<i>BnaMYB61</i>	TCCCTCCTTAGCACAGCATT	ACCCCATGAATACCACTTGAA	cDNA cloning
<i>BnaMYB62</i>	TTAGGTCATGATCGGTAGACATTCTTGCTG GAGCCAAAGCCAGAACGAGAAT	CGCGTCGACAAGAGACTGACCAAAGAGAC ACCCCATGAATACCACTTGAAACC	transactivation assay qRT-PCR
	CGCCATGGAAAATTCAATGAAGAACAAGA CGCCATGGAAAATTCAATGAAGAACAAGA CGCCATGGAAAATTCAATGAAGAACAAGA	CGCGTCGACCTCCCTAAACTGCCAAATGTCATC CGCGTCGACCTCCCTAAACTGCCAAATGTCATC CGCGTCGACCTCCCTAAACTGCCAAATGTCATC	cDNA cloning transactivation assay GFP fusion
	CAGAAGACGTGTTGAGAAGAAAAA GGAATTCATATGTCAGGTCCGTCTAGAAA AGTTACATGGCGGATTTACAGAGA GGACTAGTTCAGGTCCGTCTAGAAAGAA	TTTGCTTCCTTGTTCTGTCTCTC CGCGTCGACCTCCATCTTCCCAATACCGA TTGCCCGAGAAACAGAGTGAAAAA CGCGTCGACCTCCATCTTCCCAATACCGA	cDNA cloning transactivation assay qRT-PCR GFP fusion
<i>BnaMYB77</i>	GTGACCTCACTCCTGTCATTCG TTAGGTCATGATCGCGGATCGCGTGAAAG GGCGCGTAGAGCTGAGTTTATGAC TTAGGTCATGATCGCGGATCGCGTGAAAG GGACTAGTATGGCGGATCGCGTGAAAGGT	CATTTGACCACAACCCAAATCTG CGCGTCGACCTCAACCTTAGGTGTGATTC ATCCACCACCGTTGTTTCTCTGC CGCGTCGACCTCAACCTTAGGTGTGATTC CGCGTCGACCTCAACCTTAGGTGTGATTC	cDNA cloning transactivation assay qRT-PCR GFP fusion
<i>BnaMYB78</i>	TTAGGTCATGATCGACGGCAAAGAAGCT TAGAGATC GGACTAGTATGGACGGCAAAGAAGCTTA	CGCGTCGACGAAGCTTCCATTGTTGAGGAGC CGCGTCGACGAAGCTTCCATTGTTGAGGAGC	protoplast assay cDNA cloning overexpression

	GGACTAGTATGGACGGCAAAGAAGCTTA	CGCGTCGACGAAGCTTCCATTGTTGAGGAGC	GFP fusion
	GGAATTCCATATGGACGGCAAAGAAGCT	CGCGTCGACGAAGCTTCCATTGTTGAGGAGC	transactivation assay
	GGACTAGTATGGACGGCAAAGAAGCTTA	CGCGTCGACGAAGCTTCCATTGTTGAGGAGC	protoplast assay
<i>BnaMYB81</i>	TTAGGTCATGATCGGTAAAGTTCGCCATGA	CGCGTCGACCTTGGTGTAGTCCCTATCCTCAC	cDNA cloning
	TTAGGTCATGATCGGTAAAGTTCGCCATGA	CGCGTCGACCTTGGTGTAGTCCCTATCCTCAC	transactivation assay
<i>BnaMYB88</i>	GGAATTCCATATGGAAGAGACAAGGAAGA	CGCGTCGACGTATCCGGGTTTGACCCTAAA	cDNA cloning
	GGAATTCCATATGGAAGAGACAAGGAAGA	CGCGTCGACGTATCCGGGTTTGACCCTAAA	transactivation assay
<i>BnaMYB90</i>	TTAGGTCATGATCGAGGATTCGTCCAAAGG	CGCGTCGACATCAAGTTCTACAGTCTCTCCATC	cDNA cloning
	TTAGGTCATGATCGAGGATTCGTCCAAAGG	CGCGTCGACATCAAGTTCTACAGTCTCTCCATC	transactivation assay
	GGTGGGAGAGTTTGCTAGAGGAGAG	AAGGTTGCCCCCATTTTTGTTG	qRT-PCR
<i>BnaMYB91</i>	TTAGGTCATGAAGGAGAGGCAACGTTGGA	CGCGTCGACTGGCCGGTCTAATAGCCTCTG	cDNA cloning
	TTAGGTCATGAAGGAGAGGCAACGTTGGA	CGCGTCGACTGGCCGGTCTAATAGCCTCTG	transactivation assay
	GGACTAGTATGAAGGAGAGGCAACGTTGG	CGCGTCGACTGGCCGGTCTAATAGCCTCTG	protoplast assay
<i>BnaMYB92</i>	CGCCATGGGAAGATCTCCTTGTAGTGATGA	CGCGTCGACAAGAATGTTGGAAAATATGGAAT	cDNA cloning
	CGCCATGGGAAGATCTCCTTGTAGTGATGA	CGCGTCGACAAGAATGTTGGAAAATATGGAAT	transactivation assay
<i>BnaMYB95</i>	CGGAATTCATGGGGAGGACGACGTG	CGCGTCGACAAGGAGGAACAGGTCAAGTTG	cDNA cloning
	CGGAATTCATGGGGAGGACGACGTG	CGCGTCGACAAGGAGGAACAGGTCAAGTTG	transactivation assay
	TAGGCAAGGAAGATGAGGAAGTGA	CAGCGACGAAGCCAGGTGTAT	qRT-PCR
<i>BnaMYB96</i>	GGAATTCCATATGGGAAGACCACCTTGTTG	CGCGTCGACGAAAATTGCTTCTTGTCTTCTAA	cDNA cloning
	GGAATTCCATATGGGAAGACCACCTTGTTG	CGCGTCGACGAAAATTGCTTCTTGTCTTCTAA	transactivation assay
<i>BnaMYB106</i>	GGTGGACCATCATGATCATCTAATG	TTGGGAAGCTATCGACATTACA	cDNA cloning
	TTAGGTCATGATCGGAAGATCGCCGTGCTG	CCCTCGAGGAACATGGTTGATGAATCG	transactivation assay
	CGGCAGAAGGAATTGAAGAAGG	ATGAATCGGACGGTGTGGAATC	qRT-PCR
<i>BnaMYB108</i>	GGAATTCCATATGGATGAGAAAGGAAGAA	CGCGTCGACGAAGTCGTTATTATTGTTGAACTG	cDNA cloning
	GCTTC	TTG	
	GGAATTCCATATGGATGAGAAAGGAAGAA	CGCGTCGACGAAGTCGTTATTATTGTTGAACTG	transactivation assay
	GCTTC	TTG	
	GCCTCCGCCGCATCATTA	GTTCCGGTTTTGGAGCGTTGTAGTA	qRT-PCR
	GGACTAGTGATGAGAAAGGAAGGAAGCTT	CGCGTCGACGAAGTCGTTATTATTGTTGAACTG	GFP fusion
<i>BnaMYB109</i>	CGCCATGGATCGATCGGAGCCGTTAC	CGCGTCGACGCTTCTTGCACAAAAGAAATGTT	cDNA cloning

	CGCCATGGATCGATCGGAGCCGTTAC	CGCGTCGACGCTTCTTGCACAAAAGAAATGTT G	transactivation assay
<i>BnaMYB111</i>	CGCCATGGGAAGGGCTCCTTGTTGT	CGCGTCGACTATGCTATCCACTTGCTGTATTTTC TC	cDNA cloning
	CGCCATGGGAAGGGCTCCTTGTTGT	CGCGTCGACTATGCTATCCACTTGCTGTATTTTC TC	transactivation assay
<i>BnaMYB116</i>	TTAGGTCATGATCTCAAATATAATGAAGAA	CGCGTCGACAACATCCATTTCAATGGGTTC	cDNA cloning
	TTAGGTCATGATCTCAAATATAATGAAGAA	CGCGTCGACAACATCCATTTCAATGGGTTC	transactivation assay
<i>BnaMYB122</i>	CGCCATGGTACGGACACCGTGTTGC	CGCGTCGACCCAAACCAGTTGTCAATCCC	cDNA cloning
	CGCCATGGTACGGACACCGTGTTGC	CGCGTCGACTCCAAACCAGTTGTCAATCCC	transactivation assay
<i>BnaMYB123</i>	CGCCATGGTAATGAGAAAGAGAGAAAGTA GTAAGGTGA	CGCGTCGACACAATTAAGTCCCAGAGACAAT CTTC	cDNA cloning
<i>BnaMYB124</i>	CGCCATGGAAGATACGAAGAAGAAAAAGA	CGCGTCGACTTAGGGATGATGATGGATCAGAG	cDNA cloning
	CGCCATGGAAGATACGAAGAAGAAAAAGA	CGCGTCGACTTAGGGATGATGATGGATCAGAG	transactivation assay
<i>BnaUP1</i>	AGCCTGAGGAGATATTAGCAGGAA	ATCTCACTGCAGCTCCACCAT	qRT-PCR, reference gene
<i>BnaUBC9</i>	GCATCTGCCTCGACATCTTGA	GACAGCAGCACCTTGGAATG	qRT-PCR, reference gene
<i>GUS</i>	CGCCATGGTAGATCTGAGGGTAAA	CGCGTCGACCACGTGATGGTGATGGTGAT	overexpression
<i>NbRbohA</i>	GGCAAGCAGGAAAGATCAGACACG	CGCAAAAGCAAAGAAGAAGAAAA	qRT-PCR
<i>NbRbohB</i>	CAGTCTCTTACCATGCCAAAAA	CCCACAATAGAAGACCCCAACT	qRT-PCR
<i>NbAOX1a</i>	TGAGACGGCAGTAGAGCACAATG	AAGGGCAATCAATCAATCAAAACA	qRT-PCR
<i>NbAPX1</i>	GGAGTGGTTGCTGTTGAAGTC	GGAGAGCCTTGTCTGATGG	qRT-PCR
<i>NbAPX6</i>	TTCCCGATGCTGGTCCTCCTTCC	TGCCCAACCACTACGCTCTG	qRT-PCR
<i>NbCAT3</i>	TGCGCATCACAATAATCACCAT	TGTCGCGCTTTCCTGTCAA	qRT-PCR
<i>NbGPX2</i>	TTGTTTTGCCACTACCTTGTTTCAG	TTCATTTGGGGGTGTCAGATTAG	qRT-PCR
<i>NbGST</i>	TGAAGGAAAGCGAAGCACAAT	ACGACGGCGGAATCAAACA	qRT-PCR
<i>NbSOD</i>	GCCGTCCTTAGCAGCAGTGAA	CCGGGTTTTAGGCCAGAGACAT	qRT-PCR
<i>NbMC4</i>	TGGTAACGGGGAGGGTGAAAGTGG	TCCTGAACCGGCATAAACCTCCTG	qRT-PCR
<i>NbMC8</i>	CTGCAGGCGGAGACTCTTATGGTG	GCCTGGGCGTTGCGTGTAGC	qRT-PCR
<i>NbVPE1a</i>	ACAGGGTAGAAGCGCATCATTAT	AGCTTACATTCCCTTCCAAACTG	qRT-PCR

<i>NbVPE1b</i>	TCCCAGCGTCCCATCCAATACTT	CAATAATGATGCGCTTCTAACCTGT	qRT-PCR
<i>NbVPE3</i>	CTCTGTTGGCATAATGGCTTCTCT	CTGCATACCTTCTTTCTCCCTCTG	qRT-PCR
<i>NbACRE31</i>	AAGGTCCCCTCTTCGTCGGATCTTCG	AAGAATTCGGCCATCGTGATCTTGGTC	qRT-PCR
<i>NbACRE132</i>	AAGGTCCAGCGAAGTCTCTGAGGGTGA	AAGAATTCCAATCCTAGCTCTGGCTCCTG	qRT-PCR
<i>NbCYP71D20</i>	AAGGTCCACCGCACCATGTCCTTAGAG	AAGAATTCCTTGCCCTTGAGTACTTGC	qRT-PCR
<i>NbCP23</i>	GCTGTGGGTTACGGTGTGAAAATGGT	AAACTCAGGCAACGACAGGGTAGGATG	qRT-PCR
<i>NbHIN1</i>	CTTCCATACCGCCACCAGCAAATCC	GCAAAGGCAGCCGAAGAGACAGC	qRT-PCR
<i>NbPR2</i>	AAGCCTGGACCTATTGAAACCTAT	AACCGAACTGTCCCAAACCTCCAC	qRT-PCR
<i>NbPR5</i>	CCCGGCGCAACTATCCAACCTCTCC	GCCGCCACCGATGCACTTCAAT	qRT-PCR
<i>NbSAG12</i>	ATATGGGATGTGAGGGAGGTCTTA	TCAATGGCAACGGATACAGGT	qRT-PCR
<i>NbSAG101</i>	TGGAAGAGGCTGGGTATTATGACA	GCCAACGCTTTTCGGAGATTTC	qRT-PCR
<i>NbZAT12</i>	CGGTTCGTCGGAAAGAAGATGATA	TCGCAAAACCGGAGATGAAAC	qRT-PCR
<i>NbPP2A</i>	GACCCTGATGTTGATGTTTCGCT	GAGGGATTTGAAGAGAGATTTC	qRT-PCR, reference gene
<i>NbL23</i>	AAGGATGCCGTGAAGAAGATGT	GCATCGTAGTCAGGAGTCAACC	qRT-PCR, reference gene
<i>NbF-box</i>	GGCACTCACAAACGTCTATTTC	ACCTGGGAGGCATCCTGCTTAT	qRT-PCR, reference gene
<i>ProNbRbohB</i>	GGGGTACCCTGCTAAAAATAAAGATTTCT TGAAATTTC	CGCCATGGCTATAGTTTTTTCTTTGAGAAATAA TA	fLUC fusion
<i>ProNbHIN1</i>	GGGGTACCAACCACGTACACAAGATTTCA ACA	CGCCATGGCTCAAGAAAAATAAAGTACAGATT ATATTGCTT	fLUC fusion
<i>ProNbGST</i>	GGGGTACCACCCCCCTTTTTTTTTTTTAA A	CGCCATGGTTTCTGGATATACAGCTAAAGATA AAGAAT	fLUC fusion
<i>ProBnaRbohA</i>	GGGGTACCCTATTTGTCTAACCAAAAATTT AACATAAAGCT	CGCCATGGGAAGATCCAGCGAACACTAGGGAT	fLUC fusion
<i>ProBnaRbohB</i>	GGGGTACCGCAAACCTTTTAATATACCTTTT CAACGGTT	CGCCATGGTGTTTCAAAGGATGAAAAAAGAG ATAATCAC	fLUC fusion
<i>ProBnaGST1</i>	GGGGTACCGGTGGTTGATTATTTCTCTGAT TTTAATGT	CGCCATGGACTAATGCTTGTTTTGTTTTGTTTT TCTT	fLUC fusion

ProBnaHINI GGGTACCAATCCCAACTTGGGTCCACATT CGCCATGGTTCAGGTTGTGGAGGTTAGAATTA fLUC fusion
ATG

Restriction sites were underlined.

Table S3: R2R3 type MYB genes identified from lower species

species	Gene model	Description	Type	code
<i>Ostreococcus tauri</i>	17156	e_gw1.05.00.32.1	R2R3	OtMYB1
	23487	estExt_fgenesh1_pg.C_Chr_0	R2R3	OtMYB2
	36773	1500010069	R2R3	OtMYB3
<i>Chlamydomonas reinhardtii</i>	205725	OVA_Chltre2_kg.scaffold_500	R2R3	CrMYB1
	376761	estExt_fgenesh1_pm.C_chrom	R2R3	CrMYB2
	377858	estExt_fgenesh1_pm.C_chrom	R2R3	CrMYB3
	100734	e_gw1.23.519.1	R2R3	SmMYB1
<i>Selaginella moellendorffii</i>	113921	e_gw1.47.324.1	R2R3	SmMYB2
	140962	estExt_Genewise1.C_11907	R2R3	SmMYB3
	179572	estExt_Genewise1Plus.C_540	R2R3	SmMYB4
	233652	fgenesh1_pm.C_scaffold_470	R2R3	SmMYB5
	437219	estExt_fgenesh2_pg.C_00034	R2R3	SmMYB6

Note: The respective sequences were identified from Phytozome database and subjected to domain analysis in the SMART program.

BnaMYB1	1	-----MEREMWGRSGIG-----EIEEAVAG-GRRDEHDGGV
AtMYB1	1	-----MEAEIVRRSEVTGLRREVEESSIGRGDCDGDGGDV
BnaMYB109	1	-----MDRSEPLPFPSADSVKV
BnaMYB44	1	-----
BnaMYB77	1	-----
BnaMYB73	1	-----
BnaMYB96-1	1	-----
BnaMYB96-2	1	-----
BnaMYB30	1	-----
BnaMYB31	1	-----
AtMYB0_GL1	1	-----
BnaMYB4-1	1	-----
BnaMYB4-2	1	-----
BnaMYB4-3	1	-----
BnaMYB32-1	1	-----
BnaMYB32-2	1	-----
BnaMYB7	1	-----
BnaMYB3	1	-----
BnaMYB51	1	-----
BnaMYB122	1	-----
BnaMYB34	1	-----
BnaMYB16	1	-----
BnaMYB106	1	-----
BnaMYB47	1	-----
BnaMYB95	1	-----
BnaMYB41	1	-----
BnaMYB92	1	-----
BnaMYB43-1	1	-----
BnaMYB43-2	1	-----
BnaMYB12	1	-----
BnaMYB111	1	-----
BnaMYB13	1	-----
BnaMYB15	1	-----
BnaMYB58	1	-----
BnaMYB123-1	1	-----
BnaMYB123-2	1	-----
BnaMYB81-1	1	-----MIG
BnaMYB81-2	1	-----MIG
BnaMYB48	1	-----
BnaMYB59	1	-----
BnaMYB62	1	-----MEN
BnaMYB116	1	-----MSN
BnaMYB78-1	1	-----MDGKRSLEM
BnaMYB78-2	1	-----MDGKRSLEI
BnaMYB108-1	1	-----M
BnaMYB108-2	1	-----M
OsMYB2	1	-----MDM
BnaMYB91-1	1	-----
BnaMYB91-2	1	-----
BnaMYB88	1	-----MEE
BnaMYB124	1	-----MED
BnaMYB28	1	-----
ZmC1	1	-----
BnaMYB38	1	-----
BnaMYB61	1	-----
BnaMYB46	1	-----
BnaMYB90	1	-----
BnaMYB56	1	MNPNLLEKDQTSNETIHGSRRFKEANNFRSSPKSHTNFSLARNHPLNKTFPVLKSEDEHE
consensus	1	

BnaMYB1 31 AMFVVG--EGTSCR**RRKKR**IKGTWSREEDVMSSELVEKFGPR-NWSLWARSIP---GRSGK
 AtMYB1 36 GEDAAGFVGTSGRGRDRVKGPWSKEEDVLSSELVKRLGAR-NWSFIARSIP---GRSGK
 BnaMYB109 19 TTAAAGDSSGGYBIKSKVKGPWSTEEDAVLTKLVSKLGPR-NWSLARGIP---GRSGK
 BnaMYB44 1 -----MADRKIGPWSPEEDEQLRKLIVKYGPR-NWTVLSKSIIP---GRSGK
 BnaMYB77 1 -----MADRVKGPWSQEEDEQLRLMVEKYGPR-NWSATLSKSIIP---GRSGK
 BnaMYB73 1 -----MSGPSRKNMERIKGPWSPEEDDLLQSLVQKHGPR-NWSLISKSIIP---GRSGK
 BnaMYB96-1 1 -----MGRPP**CC**CKTG-VKKGAWTPEEDIILVSYIQEHGPG-NWRSVPTNT--GLRRCCK
 BnaMYB96-2 1 -----MGRPP**CC**CKTG-VKKGAWTPEEDIILVSYIQEHGPG-NWRAVPTNT--GLRRCCK
 BnaMYB30 1 -----MVRPP**CC**CKEG-VKKGAWTPEEDIILVSYIQEHGPG-NWRAVPTNT--GLRRCCK
 BnaMYB31 1 -----MGRPP**CC**CKME-VKKGAWTPEEDIILVSYIQEHGPG-SWRCVPTNT--GLRRCCK
 AtMYB0_GL1 1 ---MRIRRRDEKENQE-YKKGLWTVEDNILMDYVLNHGTG-QWNRVLPKRT--GLKRCCK
 BnaMYB4-1 1 -----MGRSP**CC**CKAH-TNKGAWTKEEDARLTAYIKAHGEG-CWRSPLPKAA--GLRRCCK
 BnaMYB4-2 1 -----MGRSP**CC**CKAH-TNKGAWTKEEDARLTAYIKAHGEG-CWRSPLPKAA--GLRRCCK
 BnaMYB4-3 1 -----MGRSP**CC**CKAH-TNKGAWTKEEDERLTAYIKAHGEG-CWRSPLPKAA--GLRRCCK
 BnaMYB32-1 1 -----MGRSP**CC**CKDH-TNKGAWTKEEDQKLSYIKSHGEG-CWRSPLPASA--GLRRCCK
 BnaMYB32-2 1 -----MGRSP**CC**CKDH-TNKGAWTKEEDQKLSYIKSHGEG-CWRSPLPASA--GLRRCCK
 BnaMYB7 1 -----MGRSP**CC**CKEH-MNKGAWTKEEDERLVSYIKSHGEG-CWRSPLPAAA--GLRRCCK
 BnaMYB3 1 -----MGRSP**CC**CKAH-MNKGAWTKEEDQLLVDIRKHGEG-CWRSPLPAAA--GLRRCCK
 BnaMYB51 1 -----MVRT**PC**CKAELGLKKGAWTPEEDQKLVSYVNHGEG-GWRILPEKA--GLKRCCK
 BnaMYB122 1 -----MVRT**PC**CRAELGLKKGAWTPEEDQKLVSYVNHGEG-GWRILPEKA--GLKRCCK
 BnaMYB34 1 -----MVRT**PC**CKEEGLKKGAWTPEEDQKLVSYVNHGEG-GWRILPEKA--GLKRCCK
 BnaMYB16 1 -----MGRSP**CC**CKMG-LKKGAWTSEEDQKLVSYVNHGEG-SWRSLEPKA--GLRRCCK
 BnaMYB106 1 -----MGRSP**CC**CKAG-LKKGAWTPEEDQKLVSYVNHGEG-SWRSLEPKA--GLRRCCK
 BnaMYB47 1 -----MGR**KTW**FD**DDG**MKKGAWTAEEDQKLVSYVNHGEG-SWRSLEPKA--GLRRCCK
 BnaMYB95 1 -----MGR**TTW**FD**DDG**VRKGAWTAEEDQKLVSYVNHGEG-SWRSLEPKA--GLRRCCK
 BnaMYB41 1 -----MIG**RLP**CC**CK**NG-VKKGAWTPEEDQKLVSYVNHGEG-SWRSLEPKA--GLRRCCK
 BnaMYB92 1 -----MGRSP**CC**SDSG-LKKGAWTPEEDQKLVSYVNHGEG-SWRSLEPKA--GLRRCCK
 BnaMYB43-1 1 -----MGR**QP**CC**CK**VGLKKGAWTAEEDQKLVSYVNHGEG-SWRSLEPKA--GLRRCCK
 BnaMYB43-2 1 -----MGR**QP**CC**CK**VGLKKGAWTAEEDQKLVSYVNHGEG-SWRSLEPKA--GLRRCCK
 BnaMYB12 1 -----MGRAP**CC**CKVGLKGRWTAEEEDQKLVSYVNHGEG-SWRSLEPKA--GLRRCCK
 BnaMYB111 1 -----MGRAP**CC**CKIG-LKGRWTAEEEDQKLVSYVNHGEG-SWRSLEPKA--GLRRCCK
 BnaMYB13 1 -----MGR**RP**CC**CK**MG-LKKGAWTAEEDQKLVSYVNHGEG-SWRSLEPKA--GLRRCCK
 BnaMYB15 1 -----MGRAP**CC**CKMG-LNKGAWTPEEDQKLVSYVNHGEG-SWRSLEPKA--GLRRCCK
 BnaMYB58 1 ---MG**KGR**AP**CC**CKTK-VKRGWTSQEDDKLVSFIHKYGE-NWRSLEPKA--GLRRCCK
 BnaMYB123-1 1 ---MM**KR**RESSKVKKEELNRGAWTQEDDKLVSFIHKYGE-NWRSLEPKA--GLRRCCK
 BnaMYB123-2 1 ---MM**KR**RESSKVKKEELNRGAWTQEDDKLVSFIHKYGE-NWRSLEPKA--GLRRCCK
 BnaMYB81-1 4 KVRHDSGSGKDFAIKTFHKGAWTSAEDQLLIGYVDKHGEG-NWNTVQKHS--GLRRCCK
 BnaMYB81-2 4 KVRHDSGSGKDFAIKTFHKGAWTSAEDQLLIGYVDKHGEG-NWNTVQKHS--GLRRCCK
 BnaMYB48 1 -----MN**MQ**EE-----NRKGAWTQEDIILVNFVHLFGDR-RWDFIAKVS--GLNRTGK
 BnaMYB59 1 ---MKNVQEE-----YRKGAWTQEDIILVNFVHLFGDR-RWDFIAKVS--GLNRTGK
 BnaMYB62 4 SMKNK**SF**KES---EEAKLRRGPWTL**EE**DTLLTTYILHNGEG-RWNLAACA--GLKRTGK
 BnaMYB116 4 IM**KK**CNENE---ESAEQRKGAWT**LE**EDTLLTNYIAHNGEG-RWNLAACA--GL**KK**GK
 BnaMYB78-1 10 NKNIGDFENN-VDEMDLRRGPWTL**EE**DFKLTNYIATHGEG-RWNSLSRCA--GLKRTGK
 BnaMYB78-2 10 NKNMGDFENN-VDEMDLRRGPWTL**EE**DFKLTNYIATHGEG-RWNSLSRCA--GLKRTGK
 BnaMYB108-1 2 DEKGRSFKNN-MDEMDLRRGPWTL**EE**DFKLTNYIATHGEG-RWNSLSRCA--GLQRTGK
 BnaMYB108-2 2 DEKGRSFKNNMDEIDLRRGPWTL**EE**DFKLTNYIATHGEG-RWNSLSRCA--GLQRTGK
 OsMYB2 4 AHERDASSEE-EVMGGDLRRGPWTL**EE**DLNLYIAAHGEG-RWNSLSRCA--GLKRTGK
 BnaMYB91-1 1 -----MKERQRWSGEEDALLRAYVRQFGPR-EWHLVSERMKNKPLNRDAK
 BnaMYB91-2 1 -----MKERQRWSGEEDALLRAYVRQFGPR-EWHLVSERMKNKPLNRDAK
 BnaMYB88 4 **TR**KKKK-----D**S**KKKERHIVTWSQ**Q**EDDILRKQITLHGTD-NWAIIASNFS---DKSTR
 BnaMYB124 4 **TK**KKKKNINNED**S**KKKERHIVT**W**APEEDVILRDQITLHGTE-NWAIIASKFK---DKSTR
 BnaMYB28 1 -----MSR**KP**CC**V**GEG-LKKGAWT**TE**EDDKLVSFIHKYGE-GWRDIPQKAG--LKRRCCK
 ZmC1 1 -----MGR**RAC**CA**K**EG-VKRGAWT**SK**EDDALAAYVKAHGE-KWREVPQKAG--LKRRCCK
 BnaMYB38 1 -----MGRAP**CC**CKAN-VKRGWTSPEEDAKLVDYIEKQGTGGNWI**AL**PHKAG--LKRRCCK
 BnaMYB61 1 -----MGR**HS**CC**Y**KQK-LRKGAWT**PE**EDDKLVSFIHKYGE-CWSSVPLKAG--LKRRCCK
 BnaMYB46 1 -MRKPEVGSATHQVKKMKGLWSP**EE**DSRLM**Q**YMISSGQG-CWSDVAKNAG--LKRRCCK
 BnaMYB90 1 -----ME**S**SKGLTKGAWT**AE**EDSLLRCDIKYGE-KWHPVPLRAG--LKRRCCK
 BnaMYB56 61 SENGW**KRR**QSGIKAKVCSRGHW**R**PT**ED**AKL**KEL**V**AE**FC**PQ**-N**W**N**V**L**AN**HL---LGRSGK
 consensus 61 * . * . . . * . *

R2 repeat

BnaMYB1	85	SCRLRWCNQLDPSLKRNPFFTEVEDEAIIITAHATHGNKWSIIAKLLPGRTDNAIKNHNWAT
AtMYB1	92	SCRLRWCNQLNPNLIRNSFTEVEDEQAIIAAHATHGNKWAVIAKLLPGRTDNAIKNHNWNSA
BnaMYB109	75	SCRLRWCNQLDPCLEHRKPFSAEEDETIIRAHAAQFGNKWATIAARLLNGRGTDAVKNHNWNS
BnaMYB44	43	SCRLRWCNQLSPQVEHRPFSAEEDETIIRAHAAQFGNKWATIAARLLNGRGTDAVKNHNWNS
BnaMYB77	43	SCRLRWCNQLSPEVEHRPFSPEEDETIVSARAKFGNKWATIAARLLNGRGTDAVKNHNWNS
BnaMYB73	50	SCRLRWCNQLSPEVEHRAFTAEEDETIIRAHARFGNKWATISRLNGRGTDAVKNHNWNS
BnaMYB96-1	52	SCRLRWYNLRLPGIKRGNFTEHEEKMIVHLQALLGNRWAAIASYLPERTDNDIKNYWNTH
BnaMYB96-2	52	SCRLRWYNLRLPGIKRGNFTEHEEKMIVHLQALLGNRWAAIASYLPERTDNDIKNYWNTH
BnaMYB30	52	SCRLRWYNLRLPGIKRGNFTEHEEKMIVHLQALLGNRWAAIASYLPERTDNDIKNYWNTH
BnaMYB31	52	SCRLRWYNLRLPGIKRGNFTEHEEKMIVHLQALLGNRWAAIASYLPERTDNDIKNYWNTH
AtMYB0_GL1	54	SCRLRWYNLSPNVNKGNFTEQEEDELIIRLHKLGNRWSLIAKRVPGRTDNOVKNYWNTH
BnaMYB4-1	52	SCRLRWYNLRLPDLKRCNFTEDEDELI IKLHSLGNKWSLIAARLPGRTDNEIKNYWNTH
BnaMYB4-2	52	SCRLRWYNLRLPDLKRCNFTEDEDELI IKLHSLGNKWSLIAARLPGRTDNEIKNYWNTH
BnaMYB4-3	52	SCRLRWYNLRLPDLKRCNFTEDEDELI IKLHSLGNKWSLIAARLPGRTDNEIKNYWNTH
BnaMYB32-1	52	SCRLRWYNLRLPDLKRCNFTLEEDDLI IKLHSLGNKWSLIAARLPGRTDNEIKNYWNTH
BnaMYB32-2	52	SCRLRWYNLRLPDLKRCNFTLEEDDLI IKLHSLGNKWSLIAARLPGRTDNEIKNYWNTH
BnaMYB7	52	SCRLRWYNLRLPDLKRCNFTREDEDEVI INLHSLGNKWSLIAARLPGRTDNEIKNYWNTH
BnaMYB3	52	SCRLRWYNLRLPDLKRCNFTTEEEDELI IKLHSLGNKWSLIAARLPGRTDNEIKNYWNTH
BnaMYB51	53	SCRLRWANYLRPDIKRGEFTEDEERSI ISLHATHGNKWAIIARLPGRTDNEIKNHNWTH
BnaMYB122	52	SCRLRWANYLRPDIKRGEFSQEEEDSIIRLHATHGNKWSIAIARLPGRTDNEIKNHNWTH
BnaMYB34	52	SCRLRWANYLRPDIKRGEFTPEEDDTI IKLHAKGNKWAIIATCLAGRTDNEIKNYWNTN
BnaMYB16	52	SCRLRWYNLRLPDIKRCKFNLQEEQTI IQLHALLGNRWSAIATHLPKRTDNEIKNYWNTH
BnaMYB106	52	SCRLRWYNLRLPDIKRCKFTVQEEQTI IQLHALLGNRWSAIATHLPKRTDNEIKNYWNTH
BnaMYB47	52	SCRLRWLNYLRPGIKRCKFTPQEEEAIIKLVAVLGNRWAAIAKEMENRTDNDIKNHNWSC
BnaMYB95	52	SCRLRWLNYLRPGIKRCKFTPQEEEDI IKLVAVLGNRWAAIAKQMPNRSDNDIKNHNWSC
BnaMYB41	53	SCRLRWYNLRLPDIKRGRFSFEEETI IQLHSLGNKWSIAIARLPGRTDNEIKNHNWTH
BnaMYB92	52	SCRLRWYNLRLPDIKRCKFSPDEEQTI INLHAVLGNKWSIIANHLPGRTDNEIKNFWNTH
BnaMYB43-1	52	SCRLRWYNLRLPDLKRGLLSECEEQMVIDLHAQLGNRWSKIIASHLPGRTDNEIKNHNWTH
BnaMYB43-2	52	SCRLRWYNLRLPDLKRGLLSECEEQMVIDLHAQLGNRWSKIIASHLPGRTDNEIKNHNWTH
BnaMYB12	52	SCRLRWYNLRSDLKRCNITLEEEELVVKLHSTLGNRWSLIAASHLPGRTDNEIKNYWNTH
BnaMYB111	52	SCRLRWYNLRLPDLKRCNITAEETI IKLHSLGNRWSIIATHLPGRTDNEIKNYWNTH
BnaMYB13	52	SCRLRWYNLRLPDIKRCNFTPQEEETI INLHQLGNRWSIAIAKLPGRTDNEIKNFWNTH
BnaMYB15	52	SCRLRWYNLRLPDIKRCNFTQAEEDAIIISLHQLGNRWSIAIAKLPGRTDNEIKNFWNTH
BnaMYB58	54	SCRLRWYNLRLPDIKRCNFTLEEEETI IKLHQSFGNKWSKIIASKLPGRTDNEIKNFWNTH
BnaMYB123-1	55	SCRLRWKNYLRLPGIKRCNISSDEEELIIRLHNLGNRWSLIAARLPGRTDNEIKNHNWNSN
BnaMYB123-2	55	SCRLRWKNYLRLPGIKRCNISSDEEELIIRLHNLGNRWSLIAARLPGRTDNEIKNHNWNSN
BnaMYB81-1	61	SCRLRWVNLRLPDLKKGSTFDKKEQRVVELHASMGNKWARMMAAQLPGRTDNEIKNFWNTR
BnaMYB81-2	61	SCRLRWVNLRLPDLKKGSTFDKKEQRVVELHASMGNKWARMATELPGRTDNEIKNFWNTR
BnaMYB48	48	SCRLRWVNYLHPGLKRCMTPQEEERLVTELHAKWGNRWSKIIARLPGRTDNEIKNYWRTH
BnaMYB59	48	SCRLRWVNYLHPGLKRCMTHQEEERLVTELHAKWGNRWSKIIARLPGRTDNEIKNYWRTH
BnaMYB62	58	SCRLRWLNYLKPDIRRGNLTPQEQLLIELHLSKGNRWSKIIAQYLPGRTDNEIKNYWRTR
BnaMYB116	58	SCRLRWLNYLKPDIRRGNLTPQEQLLIELHLSKGNRWSKIIAQYLPGRTDNEIKNYWRTR
BnaMYB78-1	66	SCRLRWLNYLRLPDRRCNITLLEEQLLIELHSRWGNRWSKIIAQYLPGRTDNEIKNYWRTR
BnaMYB78-2	66	SCRLRWLNYLRLPDRRCNITLLEEQLLIELHSRWGNRWSKIIAQYLPGRTDNEIKNYWRTR
BnaMYB108-1	58	SCRLRWLNYLRLPDRRCNITLLEEQLLIELHSRWGNRWSKIIAQYLPGRTDNEIKNYWRTR
BnaMYB108-2	59	SCRLRWLNYLRLPDRRCNITLLEEQLLIELHSRWGNRWSKIIAQYLPGRTDNEIKNYWRTR
OsMYB2	60	SCRLRWLNYLRLPDLRRCNITPQEQLLIELHSRWGNRWSKIIAQYLPGRTDNEIKNYWRTR
BnaMYB91-1	44	SCLERWKNYLKPGLKKGSLTEEEQRLVIRLQEKHGKWKKIAAEVPGRTAKRLGKWWEVF
BnaMYB91-2	44	SCLERWKNYLKPGLKKGSLTEEEQRLVIRLQEKHGKWKKIAAEVPGRTAKRLGKWWEVF
BnaMYB88	56	QCRRRWYTYLNSDFKTCGWSPEEDTLICEAQRVFGNRWTEIAKVVSGRTDNAVKNRFTTTL
BnaMYB124	60	QCRRRWYTYLNSDFKTCGWSPEEDTLICEAQRVFGNRWTEIAKVVSGRTDNAVKNRFTTTL
BnaMYB28	52	SCRLRWLNYLKPDIKRGEFSSEEEQIIIMLHASRGNKWSVIARLPGRTDNEIKNYWNTH
ZmC1	52	SCRLRWLNYLRLPDIRRGNISYDEEDLIIRLHRLGNRWSLIAARLPGRTDNEIKNYWNTH
BnaMYB38	53	SCRLRWLNYLRLPDIRRGNISYDEEDLIIRLHRLGNRWSLIAARLPGRTDNEIKNYWNTH
BnaMYB61	52	SCRLRWLNYLRLPDLKRCGAFSPEEENLIVEIHSVLGNRWSQIAARLPGRTDNEIKNHNWNS
BnaMYB46	57	SCRLRWLNYLRLPDLKRCGAFSPEEENLIVEIHSVLGNRWSQIAARLPGRTDNEIKNHNWNS
BnaMYB90	48	SCRLRWLNYLKPDIKRCKLSSDEEVLRLHKLGN-----RLPGRTDNDIKNYWNTH
BnaMYB56	117	SCRLRWLNYLRLPDIRRGNISYDEEDLIIRLHRLGNRWSLIAARLPGRTDNEIKNYWNTH
consensus	121	.*.*.*.*.*.....*.....*.....*.....*.....*.....*.....*.....*.....*

R2 repeat(continued)

R3 repeat

BnaMYB1	145	LRRR	CTDFETPTN-----	TATGNLVLHDSRLDRMTNTIASSEETLSS
AtMYB1	152	LRRRF	FIDFEK-AKN-----	IGTGSLVVDDSGFDRIT-TVASSEETLSS
BnaMYB109	135	LRRK	YADLWKNSNQ-----	VTTAYIKNENVEQQVPQEEIVSPP-----
BnaMYB44	103	LKRK	CG-GFYASA-----	EDQRPVKRS---VSDGY-----
BnaMYB77	103	LKRK	CSDGNPTAE-----	EDQDPAKKRRSMSSESV-----
BnaMYB73	110	LKRK	CSAFTSEGQS-----	CDFGGNGGYDGNLGEEQPLKRTASG-----
BnaMYB96-1	112	LKKKL	KKKINESGEE-----	DNDDFFSSKTIISQK-----
BnaMYB96-2	112	LKKKL	KKKINESGEE-----	DNDGFTSSHTIISQK-----
BnaMYB30	112	LKKKL	LNKANQVSHQ-----	EHDQSRDRSSLSS-----
BnaMYB31	112	LKKKL	NLQRQNGS-----	NDDDTNMTMTEMSSCD-----
AtMYB0_GL1	114	LSKKL	LVGDYSSAVK-----	TTGEDDD-----
BnaMYB4-1	112	IRRKL	INRGIDPT-----	HRPVQESSASQDS-----
BnaMYB4-2	112	IRRKL	INRGIDPT-----	HRPVQESSASQDS-----
BnaMYB4-3	112	IRRKL	INRGIDPT-----	HRPIQESS-ASQDS-----
BnaMYB32-1	112	VKRKL	LRGGIDPAT-----	HRPIKARRDASEAR-----
BnaMYB32-2	112	MKRKL	LRGGIDPAT-----	HRPIKARRDASEAR-----
BnaMYB7	112	IKRKL	LSKGIDPNT-----	HRSINAG-KVSDSK-----
BnaMYB3	112	IKRKL	LSRGIDPNT-----	HRSINGSATPPSKT-----
BnaMYB51	113	IKKRL	IKKGVDPV-----	HKSLISDKSENLEIPEKQNVIIQTIIT--
BnaMYB122	112	IKKRL	IKKGIDPL-----	HKSLNGKSSDHPETPPDKSSVHQ-----
BnaMYB34	112	IKKRL	KQFGIDPT-----	HKPINSTDQGTGSEP-----
BnaMYB16	112	IKKRL	VKMGIDPVT-----	HKPKNETPLSTLGG-----
BnaMYB106	112	IKKRL	VKMGIDPVT-----	HKHKNETLMSSTGQ-----
BnaMYB47	112	IKKRL	SKNGIDPMT-----	HEPIINNLTVTITT-----
BnaMYB95	112	IKKRL	VRSRIDPMT-----	HKPVVTVAKATSS-----
BnaMYB41	113	IKRKL	VRSRIDPVT-----	HSPRLDLLD-----
BnaMYB92	112	LKKKL	IQMGIDPMT-----	HLPRTDIFSSLSQL-----
BnaMYB43-1	112	IKKRL	LRKMIDPMT-----	HKPLPEQDGSQQAQ-----
BnaMYB43-2	112	IKKRL	LRKMIDPMT-----	HKPLPEQDGSQQAQ-----
BnaMYB12	112	LRK	LHNFIIRK-P-----	SISHNVPDVVINAP-----
BnaMYB111	112	LSRK	IYAFTTVTGD-----	EHSLKVVDDLVLNKS-----
BnaMYB13	112	LKKRL	IQ---HNQ-----	DQNISETICDNDEQ-----
BnaMYB15	112	LKKRL	LE---DNQPA-----	KPKTSNKKKSTKPK-----
BnaMYB58	114	LKKRL	NSYINHNAS-----	DEAASKGSLNKEET-----
BnaMYB123-1	115	IKRKL	PKSQTNQK-----	SRKHSNNNNMNKVC-----
BnaMYB123-2	115	IKRKL	PKSQTNQK-----	SRKHSNNNNMNKVS-----
BnaMYB81-1	121	VKKL	QRLGLPIYPD-----	EVREQAMNAAAQNGQNSD---HSQESL
BnaMYB81-2	121	VKRL	QRLGLPIYPD-----	EVREQAMNAAAQNGHNSDLSLGDGHSQESL
BnaMYB48	108	MRKKA	QAEKKRHVSP-----	SSSCSKCCSSSMTTNT-----
BnaMYB59	108	MRKQA	QAEKKRPMSP-----	TSSSSNCCSSSMTQD-----
BnaMYB62	118	VQKQA	RQLNIESNS-----	DKFFDAVRSFWVPRLI-----
BnaMYB116	118	VQKQA	RQLNIDSS-----	HQFLEVRSFWVPRLI-----
BnaMYB78-1	126	VQKHAK	QLRCDVNS-----	QQFKDTMRYLWMPRLV-----
BnaMYB78-2	126	VQKHAK	QLRCDVNS-----	QQFKDTMRYLWMPRLV-----
BnaMYB108-1	118	VQKHAK	QLKCDVNS-----	QQFKDTMKYMWMPRLV-----
BnaMYB108-2	119	VQKHAK	QLKCDVNS-----	QQFKDTMKYMWMPRLV-----
OsMYB2	120	VQKHAK	QLKCDVNS-----	QQFKDVMRYLWMPRLV-----
BnaMYB91-1	104	KEKQ	QREEKESNKR-----	VEPIDESKYDRILESFAEKLVK-----
BnaMYB91-2	104	KEKO	OREEKESNKR-----	VEPIDESKYDRILESFAEKLVK-----
BnaMYB88	116	CKKRA	KYEEAMAKDNTLASCNKRMLLPDCGISTPPKAESVSPLAKKIRRSDIPGPTVFGG	
BnaMYB124	120	CKKRA	KHEAMANSN-----NKRMLFLDG-ISTPQKADNEAPISKRTRRSHILELTEMNN	
BnaMYB28	112	LKKRL	IEQDASSD-----	KQYSRSSSMPSMCTPS-----
ZmC1	112	LGRR	AGAGAGAGGS-----	WVVVAPDTGSHATP-----
BnaMYB38	113	LKKKL	IATMAPPPP-----	HLLAIASSSSSPS-----
BnaMYB61	112	IKKKL	RQRGIDPNT-----	HKPISEVDKDKTTATS-----
BnaMYB46	117	IKKRL	KKMSDTSNLVN-----	NSSSSPDTSDLN-----
BnaMYB90	101	LSKK	HEPCCCKTKMK-----	-----
BnaMYB56	177	MA	RRTRKSQRQRHQ-----	-----
consensus	181	-----

R3 repeat (continued)

BnaMYB1	188	GGG-----GGGGGHITTPLVSSDGKEATS-MEISEEQPSDKANEE
AtMYB1	193	GG-----GCHVTTPIVSPEGKEATSMEMSEEQCVEKTNGE
BnaMYB109	173	-----QVVDVPMYDEPTQVLDDVTMDDASPNEPQEQQA
BnaMYB44	129	-----PPVANGLLMSPGSPGSDVSDSSTLPVLTSVEVF
BnaMYB77	133	-----PPVDTGLYMSPESPT-DVGSDS SAVPPQR----F
BnaMYB73	149	-----GGVSTGLYMSPGSPGSDVSEQSCGVPHV----F
BnaMYB96-1	140	-----QHQSSN-----KGQWERRLQT
BnaMYB96-2	140	-----QHHSSN-----KGQWERRLQT
BnaMYB30	140	-----PSSSSANSNSNINIARGQWERRLQT
BnaMYB31	140	-----NNNNTNRRSVN----KGQWEKKLQT
AtMYB0_GL1	135	-----
BnaMYB4-1	140	-----KPTQLAEAITSNNTINISFTN---TPKMES---T
BnaMYB4-2	140	-----KPTQLIEAITSNNTINISFTS---TPKMES---T
BnaMYB4-3	139	-----KPTHL-EAITSN-TINISFASSSSTPKMEIFQES
BnaMYB32-1	140	-----ETEDSLVKVLSFGPQLEKEES----SREEG----
BnaMYB32-2	140	-----ETEDSLVKVISFGPQLEKEES----SREEG----
BnaMYB7	139	-----KTEDQVVKDVSFGYLFDKTEK----SEEQK----
BnaMYB3	140	-----TTPSLQNDPVRFDVDFSGPDQQ--RTVKPEPMLLD
BnaMYB51	154	-----SDDDL DNEKVKNNNEK PGLSSAKFLNRVANRFGKRINQSVLSEIIGSGGPLTT
BnaMYB122	149	-----DDDDQKSNKNNALGSL SARFLNRVANRFGKRINQSVLSDIIGSGDPTT
BnaMYB34	140	-----KHKHKL GSSG SARLLNRVASKYSVDSNRDLLTGI I IGNSTNIA
BnaMYB16	140	-----LSKNAATLSHMAQWESARLEAEAR-LARESKLLHY
BnaMYB106	140	-----SKSAAATLSHMAQWESARLEAEAR-LARESKLLHY
BnaMYB47	140	-----EEECGSSPTNTSLTTEGHFSSSPGLARLLNKLA
BnaMYB95	140	-----TTSSPTTPSSSSSSSS--FSSTSS--ARLLNKLA
BnaMYB41	136	-----LSSLAAIFNQPKFSSVATNASSLLNPDVRLA
BnaMYB92	140	-----MSLSSNLRGFVDMQQQFPNGQDQITILKLQTEMAKL
BnaMYB43-1	140	-----GSKSLVPHDDKNNKQDQEDKQTKKEQEHHLGIDL
BnaMYB43-2	140	-----GSKSLVPHDDKNNKQDQEDKQTKKEQEHHLGIDL
BnaMYB12	139	-----PRSPR-----PPTKRRPGRTSRSTMKPKTHANI
BnaMYB111	140	-----SSSLGAKNTNKTKKKKGRFSRSSMKKHKQMVTA
BnaMYB13	135	-----LVSVM-----DEKRPSPPQQSSSSTNISAV
BnaMYB15	137	-----SQSVP-----AKSKSTKTESELASSSNPSFE
BnaMYB58	142	-----SQESS-----PNASRSFGGSNIVSKEEEDDV
BnaMYB123-1	143	-----VIRPKAIRFPKALTFQNKSSIGST
BnaMYB123-2	143	-----VIRPKAIRCPKALTFQKQSSIGST
BnaMYB81-1	159	EPDCLEIPEFDKYLQLN--NYQSVLLRNVP MGNMMKHCS--FQPNMYNLIGSPYMSP-
BnaMYB81-2	164	ELDCLEIPELNFKHLQLNGGSSFLQSM LSSVPTGNQMRQNPGLFQPN IYVNIASPYHQP
BnaMYB48	138	-----TQDVSE-----SRMSSGKVSFYDTGGNREMNO
BnaMYB59	137	-----TGGSNKMNQ
BnaMYB62	148	-----EKMEQNSSTTYACPQNNNNNNNNSSLLPSPQTFE
BnaMYB116	148	-----HKMKDYS-----NTNSKAPPTDSLGP
BnaMYB78-1	156	-----ERIQASA-----STSTGSATTSSCVTTPSDQFLM
BnaMYB78-2	156	-----ERIQAAS-----ASSTGSAKSCVTTTTDQFVI
BnaMYB108-1	148	-----ERIQSASASASALISTTGSATTSSCITTSNNEFMT
BnaMYB108-2	149	-----ERIQSA--AASLTSTTGSATTSSCITTSNNEFMT
OsMYB2	150	-----ERIQAAAAGQQQ-QQEGGTDTPPLSWQHGGSDGLY
BnaMYB91-1	140	-----ERSSVPSAVMASSNGGFQQAPPNNNNNNNNNNHVI PP
BnaMYB91-2	140	-----ERSSVP-AVMASSNGGFQQAPPPN-----NNHVI PP
BnaMYB88	176	YGDRSHIKVNSGVNQHSSYGDRSHIKVVNQIRPPFWVIAHNEEKIQKDSAKESEGEDKE
BnaMYB124	173	YGN----VEPCLNQA----RSPFVLAHNATG----IDSL EEQYQTSNVKESDGE--
BnaMYB28	143	-----SGFNTVFENTSKDGTVPVREDDSLSRKKRLKKSST
ZmC1	140	-----AATSGACETGQNSAAHRADPDSA
BnaMYB38	141	-----SSHYNMTNSLPPYNPSISTNELLTPHQEMMT
BnaMYB61	142	-----NNNNHKSPSSSSPTNQDFFLERPSDFSDYFGL
BnaMYB46	147	-----TTSSLELKDIIGSFMSLQEQGF INI
BnaMYB90	115	-----KRNVTFSSTTQAQKI
BnaMYB56	191	-----PPQAPSGNAEMA VSSSYNHGDEFFG
consensus	241	

BnaMYB1 227 DISRQECNNDPPTLFRPVAKLSSFN-----PYNHMEGSSPTHTLNQNK-
 AtMYB1 229 GISRQD-DKDPPTLFRPVPRLSSFN-----ACNHMEGSPSPHIQDQNQ-
 BnaMYB109 205 PIEKSSIPVFRPVARAGAFRVYNPT-----SQRNGYRDHNVPCEGPL-
 BnaMYB44 163 KPVPRAGGVMLPLPIETSTFCDDPA-----TSLSLSLPGADVSEESNR-
 BnaMYB77 162 KPMTSSS-----EEDPA-----TTLSSLSL-VPVQSERN-
 BnaMYB73 179 KPTARSG---AVTEVTASTSGEDPP-----TCLSSLSL-PWNNRCETETV-
 BnaMYB96-1 156 DINMAKQALSEALSLDKKPPSSSVIIPQNI PSFSSVLLDNCHDPSSSSSSTTTTTTTS-
 BnaMYB96-2 156 DINMAKQALCEALSLDKKPS-----KFSPSSSSLSIIPQNI PSFSSSSTTTTTITT--
 BnaMYB30 165 DIHLAKKALSEALSP-----AVAPINTATSSSAESRLTTSSASG-
 BnaMYB31 161 DINMAKQALFQALS LD-----QASSITPDPDSPK-
 AtMYB0_GL1 135 -----SPPSLFITAAP-
 BnaMYB4-1 168 SCFQVKPEKISMLTFKEEKDE-----FLIEEKLPD LNLELRISLDPD-
 BnaMYB4-2 168 SCFQVKPEKISMLTFKEEKDE-----FLTEEKLPD LNLELRISLDPD-
 BnaMYB4-3 171 TSFPGKQEKISMVTFKEEKDE-----CPVEENFPD LNLELRISLDPD-
 BnaMYB32-1 166 RFKKS-----LTCKTK-----SLD LNLELRISPPW-
 BnaMYB32-2 166 RFKKS-----LTCKTK-----SLD LNLELRISPPW-
 BnaMYB7 165 QNKKQKQNLINGLVCKEERVEHHP-----AVVVQEIFCPN LNLELRISPPW-
 BnaMYB3 172 REETNNNNINNTSSGTTSEK-----DIQTDDDW LNLELRISPPW-
 BnaMYB51 207 TTTSHATTTSTVTNSESDKSTSS-----SFTPTSDLLCQMTVNGNATSSP-
 BnaMYB122 198 FTTPTTSASECEKSSSSFSKNSS-----DLLINENMILDATSLSSSTFS--
 BnaMYB34 182 DISQNTGDVDSPTKNSTLLN-----QMAAASSGFIILTNTSTSPG-
 BnaMYB16 174 QTKVSSSHHDHLNI ISSDQ-----QKQQQLESPTSTVTFSEAKT
 BnaMYB106 174 QNNKAAAPNCLSHKASSTNWTKP-----NQKGDQQLSPTSTVTFSEN LH
 BnaMYB47 175 GIASRQHDLDR IKNILLDR-----
 BnaMYB95 171 GISSRKHELDRIK NIMSE-----
 BnaMYB41 169 SLLLPPQQPLQNPNTLYAS-----NLDQNLQTPNTSVSSQDS--
 BnaMYB92 175 QLFQYLLQPPTMSNNIRNP-----NDFDILSLLNSIASFKEI--
 BnaMYB43-1 175 DKSNTISTDDGFCIDEVP-----LLDPHEILLDIS----
 BnaMYB43-2 175 DKSNTISTDDGFCIDEVP-----LLDPHEILLDIS----
 BnaMYB12 168 RKMKKTSEPPEPEASAAVKAGEETLMMELNGAEALGPCNYVYVTCHEGGNNNNNNNS-
 BnaMYB111 174 SQCLPQPKELESEISEGWNS-----GNYEGKSLGAYE WL DGEIERL-
 BnaMYB13 161 TTSSNNNDVSNNNIKDSATS-----PED-----
 BnaMYB15 163 SLFSASLSASDEVSE TLTS-----HEDHSKEAQMDNKLREMI-
 BnaMYB58 168 QIGETF EYFQDYSELAGLLQ-----EVDKPELLEIP-----
 BnaMYB123-1 167 SLLTVKENVIDHQAGSP SLLG-----
 BnaMYB123-2 167 SLLTVKENVIDQQASSP SLLG-----
 BnaMYB81-1 213 NRKRVREQETDFLDTGDYATNEQSAQLWNQ-----KQFHVVPESHLLGNATTYSSP--
 BnaMYB81-2 224 NRKRFREPETA FPYTGGYATDEHSAQLWNSPFVESTPGQFN VAPDSHFLGNATTYSSPSE
 BnaMYB48 166 EETKDGYSMDDIWKEIDHSAVNI IQ-----PVKDIYL-EQSYCLSYPNL--
 BnaMYB59 147 ECDDGNYSMDDIWREIDQSGANI IK-----PVKDIYYSEQSCYFNFPPLP-
 BnaMYB62 183 SMSTQTYQDLSGLSNMDGSSSSS-----AFMPDLMTVPHFMDPN-TI-
 BnaMYB116 169 VVQDNNF SHNSGLNIDCSTSMSQD-----LAKISQLMDLSDLETTNSMC-
 BnaMYB78-1 185 TSYDAGLNNNNNTNMDHLSFMSNP-----NGYVTQETSSVSVSPTSGL-
 BnaMYB78-2 185 TSYDDGANNNN-TSIDHLGLTNNP-----NGYVTS GTSSVTVSPASGL-
 BnaMYB108-1 183 YDY-----NNNNSIGERLGMNN-----NNYITL ENSSVAVSPVSDL-
 BnaMYB108-2 181 YDY-----NNN NF IGERLGMNN-----NDYITPENSSVAVSPVSDL-
 OsMYB2 184 ESPELPAPDASCWPAEYCAAAGGAQ-----SGGTPAPELSSTTAGSSSLS-
 BnaMYB91-1 179 WLATSNNGNNVVARPPSVTLT LSPSVAATPPQQQPIPWLQQQPEASPGGLV LGSMI PSC
 BnaMYB91-2 171 WLATSNNGNNVVARPPSVTLT LSPSVAATPPQQ-PIPWLQQQPEASPGGLV LGSMI PSC
 BnaMYB88 236 MFLKKDDPKVTS LMQQAELLSLAQKVN---TEQSMENAWKVLQDFFNKSKENDIFRYG-
 BnaMYB124 218 MFLKKDDPKVTALMQQAELLSLAQKVNADNTEQSMENAWKVLQDFLNK GKENDLLRYG-
 BnaMYB28 178 SRLLNKVAAKATSMKEALSASMEGS-----LNANTSFSNGYSEQILNEDD-
 ZmC1 163 GTTTTSAAVWAPKAVRCTGG-----LFFFHRD TTPAHAG-
 BnaMYB38 173 MMDQQQQQLLYQEAVDSL VNS-----PNSNKLIMSHQEDS-
 BnaMYB61 175 QKLNFN SNLGLSVTADSSPLCSMIP-----SQFSTGNMVGSVFQTP-
 BnaMYB46 171 PSFTNTPITNNNPFAPHMIS-----
 BnaMYB90 130 DVFKPRPRLFTVNNGC SHLHG-----LPEVDVVPCLGLNNIN-
 BnaMYB56 216 TVVNGTFVNEEDEAGDDDG S-----TVSTCTTELSLTPPS-
 consensus 301

BnaMYB1	270	-----FQCKQDTAMLRLLEGAYSERFVPQKCGSGCCSVS
AtMYB1	271	-----LQSSKQDAAMLRLLEGAYSERFVPQTCGGGCCSN
BnaMYB109	248	-----IQAAKPDLAGKFLQSLCGEPNIPSKCGHGCSHP
BnaMYB44	206	-----SHESTNNNTSRSHNTNTMSLMQFSGGFRGAIEEMG
BnaMYB77	191	-----TGSSDN-----SLPFRFRQMKINVEERG
BnaMYB73	219	-----RVNEPTQVNENTVTDGGYTAELFFVRKEEVEEEKG
BnaMYB96-1	215	-----NTTNIYPSGVYASSAENIARLLQDFMKDTPKPLTL
BnaMYB96-2	208	-----TTQCLSGVYASSAENIARLLQDFMKDTPKSLTL
BnaMYB30	205	-----FLRTQETSTTYASSIENIAKLLKGWVKKSPTQNSA
BnaMYB31	191	-----PHDHHSTAIYASSTDNISKLLQNWTSSTSS--SLMP
AtMYB0_GL1	147	-----SSCHHQENIYENIAKSFNGVVSASYEDKPKQELA
BnaMYB4-1	209	-----VVE-----GKSTRER-CFKCSLGMINGMEC
BnaMYB4-2	209	-----VVE-----GKSTRAR-CFRCSLGMINGMEC
BnaMYB4-3	212	-----VVDHHHQGFVGEKTTTPRRCFKCSLGTINGMEC
BnaMYB32-1	191	-----QDQQQ-RDERKLLFGREKYLCSACRFLGNGKEY
BnaMYB32-2	191	-----QDQHR-RDERKLLFRKEKYLCSACRFLGNGKEC
BnaMYB7	211	-----HNKNH-DDN----TREKSTTYTTSRLYVQNGMES
BnaMYB3	213	-----TKSYR-YELTRKANPDLAESTRRWSFELLGAQAE
BnaMYB51	253	-----STFSEASVNDSLMYCDNEDNLGFSN-FLN-----
BnaMYB122	243	-----SDTSDPSVYD-HIFDDLEDMTAFSSRFLNDVVSH
BnaMYB34	226	-----FSDNCSFSDGFTEFFSNEEISGMYTNVDNVGLME
BnaMYB16	213	EFVGS-----STCLNMIKETENDWISSTIHEFERVEEGLTGLLLG
BnaMYB106	221	LMIMPGENNNESEIQNMTEFALSSSTSSDVKDSQDWMRQINCPAEGIEEGFTSLLLL
BnaMYB47	194	-----KITINDQDEEGGLRRDQKIG---EEDDFLIW
BnaMYB95	190	-----PRQAVEEDKMMIGKEDEEVTGCSMEIDENLIS
BnaMYB41	206	-----QPQAECTAPTQDETSYFEPIMNARLEVGPSDVLP
BnaMYB92	212	-----TSNNLDLGSNLQDFNSLPSLKTLSNIGPSSVLPQ
BnaMYB43-1	206	-----FADHHTSDENAHINISNSTSPSSSSTSSCISS
BnaMYB43-2	206	-----FAQHHTSDENAHINISNSTSPSSSSTSSCISS
BnaMYB12	227	-----IDGDKGVSSFDEDIIDLLLDESAPSHVLTSCGGNA
BnaMYB111	215	-----MSSFVWECASEEAVISMNDDDPDQNKVCESGDNIS
BnaMYB13	184	-----VLPLIDESFWSEVVS---MDYNI
BnaMYB15	201	-----TTTDQDSFSFINFGEDIDESFWNETLYSQDEENHT
BnaMYB58	199	-----FDIDPDVWNFLEGFQQPENSLTPKDHQE
BnaMYB123-1	188	-----DLKIDFDKIQSEYLFSDLMD
BnaMYB123-2	188	-----DLKIDFDKIQSEYLFSDLMD
BnaMYB81-1	264	PSEPE-----AEKLELPSFQCFDP---PGDWETQHSNMPAVESDRTL
BnaMYB81-2	284	PLIHG-----AEKLELPSFQCFDTQEEPQDWEAQHSNMPQAIESDNTLV
BnaMYB48	209	-----ASPSWESS-----LDSIWKMEEDKSKMSSFAN
BnaMYB59	192	-----QASPTWESS-----LESTWNMDAYESKMSSF
BnaMYB62	224	-----IDGSMCYHE-----DNAQELSGYILGTEEY
BnaMYB116	214	-----LEGSRGSSN-----QYVNEHRCLHEEYIVTT
BnaMYB78-1	228	-----TEYHIGSEVEKVEN--NQDQSLVGPQIMSPPENYLD
BnaMYB78-2	227	-----TEYHIGSEVGIETSFDPDQSLVGPQILLPSQNYLD
BnaMYB108-1	220	-----TDYYNAPKP-----NPDQNLVGPQMLP--DNYFD
BnaMYB108-2	218	-----TDYYNAPKP-----NPDQNLVGPQMLP--DNYFD
OsMYB2	229	-----TDSGAGAPSWPTQADGAEWFTTACDASSATGGVAM
BnaMYB91-1	239	S-----GSNESVFMSELVECCRELEEGHRAWAEHKKEAAWRL
BnaMYB91-2	230	S-----GSNESVFMSELVECCRELEEGHRAWAEHKKEAAWRL
BnaMYB88	292	-----LPDIDFQLEEFKDLVEDLRSSNEDSQASWRQPDLDHSPASSDYSSGSTTMPH
BnaMYB124	277	-----FPDIDFQLEEFKDLIGDLRSSYEDNDPSWRQPDLDHSPASSDYSSGSTILLD
BnaMYB28	223	-----SSNASLINTLAEFDPFLQTTTFYPENEMNTTSDLD
ZmC1	198	-----ETATPMAGGGGGGGGEGAG
BnaMYB38	208	-----REQSTNKGIMLLSDVRS
BnaMYB61	216	-----VCVKPSVTLAPDNTSNFFDNGGFSWSGPNSSSSSSSLVK
BnaMYB46	192	-----HPCIDDFTPYVDGLYGVNTGLQGLYFPPLEC
BnaMYB90	168	-----NVCENSMTYCNKAGEKYEYELFS
BnaMYB56	252	-----STHQLRFFNYDSTLAP
consensus	361	

BnaMYB1 305 -----QKDSLLGPEFVDYLDPPPTFPSYELAAIATDISSSLAWLRSGLLESSVRTMEEAAGR
 AtMYB1 306 PDGSFQQESLLGPEFVDYLDSPPTFPSSELAIAIATEIGSLAWLRSGLLESSVRVMEAVGR
 BnaMYB109 283 AE---PGKSVLGAEFVDYEEPCPVFNQELISIAIDLNNIAWIKSGLDNAIVREAEQNLKM
 BnaMYB44 241 RSF-----GGNGGEFMAVVQEMIK-----AEVRSYMAEMQRNHSGGGFVGGGFRDNG---
 BnaMYB77 216 G-----EARRAEFMTVVHEMVK-----AEVRSYMAEMQRNN-GGGFVGGGFYDSG---
 BnaMYB73 254 IS-----GFGGEFMTVVQEMIR-----TEVRSYMAEDLQRGVGGGGSIGSGGGGGGS
 BnaMYB96-1 250 TSSS-PISETGPLASAAEEGGEGFEQSFSSFNMSMEETQNLQTETNFHFDQESKPAITMD
 BnaMYB96-2 241 TSSSSPVSETGPLVSAATEEGGEGFEQSFSSFNMSMEETHNLTQETSFFHFDQESKPVITME
 BnaMYB30 240 DQMVSPDSEAKEVIKSNVEKDCAGAFQSFSGFDHLKDRD----SAGVSPDHETKPDITG-
 BnaMYB31 224 NTSSLSNNRSSSTGEGGVLDHQCSLFSNPSESGSVDERLNNIMTETNIFKG-ESKSNVDRE
 AtMYB0_GL1 182 QKDVLMTATNDPSHYYG--NNALVWHDDDFELSSLVMMNFASGDVEYCL-----
 BnaMYB4-1 233 RCGSMRCDVVGSSSGSTGKGGDIS---HGFDLGLATKETTTS-LLGFRSLEMI-----
 BnaMYB4-2 233 RCGSIRCDVVGSSSGSTGNGGDIS---HGFDLGLATKETTTSLLGFRSLEMI-----
 BnaMYB4-3 246 RCGMRCDVVGSSKGS-GKGSMS---NGFDLGLAKKETNTC-LGFRSLEMK-----
 BnaMYB32-1 224 SCENVRCHIDSSSSSYSSSDISS-SVVGFDLGLNTSS-----VLDYTSLEMN-----
 BnaMYB32-2 224 SCENVRCHIDSSSSSYSSSDISS-SVVGFDLGLNTSS-----VLDYTSLEMN-----
 BnaMYB7 240 SSDTAKCQTEDSSSISHSSLDISSISSVGYDFLGLNTR-----FMDFRSLEMN-----
 BnaMYB3 246 VCLCCRIGSHNESCRNCRSDVLT-----TWESKIL-----
 BnaMYB51 281 -DEDFMMLEESSVDNTEFMKELSRFLEED----VNDDVEVMPVYEHQDNIEDIDNYFA-
 BnaMYB122 276 DDEDFLMLDESCLEKTSFMRELTRILQDDKIETTMCSDSRVTPISEVDVSSFEGIDNWF-
 BnaMYB34 260 ELEDILSYDGDVGDIKDSPEVDVTDMDMDFLDSWNKEDD--LDLEKFVSSLDKIGVFFV-
 BnaMYB16 254 G-GGSLGLSFSADKNETAGESSGGGGGECNDYEDNKNYLESIFSVDPSDSTPMF--
 BnaMYB106 281 GDSGDRSLSIGKKDEETVAGAVEVNESDY-SYEDNKNYWNSILNLVDSTPDSSTMF--
 BnaMYB47 222 DD-----GEVRRYMDIDPMEYETTPY-----DSVLYESTQILDYLF--
 BnaMYB95 222 TTSSYEYLTCDFTPTPTYPGFVAADFDDYSLVEPYDLYR-----SDFYHETSDDQLDLFLL
 BnaMYB41 241 LS-----ESFDLDSLSTPYYSPPQNNIEAEANSSSLFDFRFPDNFTFDDFMGL
 BnaMYB92 247 IPEDNHFKFCNERENLPVSPPIWLSDPNTSNQHMLPSLDPSSAVSDDMIRNQYVIEHVNSN
 BnaMYB43-1 238 VPGEFESKFLDEMDTIDLKWLSSDHSSSDNI IYKDDKFHNNVDTMNLWDINYLSSLELFM
 BnaMYB43-2 238 VPGEFESKFLDEMDTIDLKWLSSDHSSSDNI IYKDDKFHNNVDTMNLWDINYLSSLELFM
 BnaMYB12 262 ELNHLGDSEEAKRSEILNQESIDCLQSCPSMESFLNYEHQVNNNAFTDEFIDWDCVWQQ
 BnaMYB111 250 CCVDLFEEEQKGLGSLHVDQDMNIEKEREESILSSNSNESGDKD-WWVGLCDSSEVGFGI
 BnaMYB13 204 SGDEEIKIEDWESSLDSNIKGYNHDMESWFDNLLTSNLTGTGENSDIF-----
 BnaMYB15 236 SNLDEMQQEFQHLRSVGNEMIFDSEMDFWFDVLPVRSRGGEQDLLAGL-----
 BnaMYB58 227 SEEDEVDKWFKNLESELGLEEDDSQQQQEQNNEAKEDSPSPSLESYEVLINH-----
 BnaMYB123-1 208 FDGLGCGNVMSLVSSDEVLDGYVSADTSCLGNDLNRPFSTCLQEDCLWDFNC-----
 BnaMYB123-2 208 FDGLGCGNVMSLVSSDEVLDGYVSADTSCLGNDLNRPFSTCLQEDCLWDFNC-----
 BnaMYB81-1 305 QS-PLTD----CPS---SGLLESVYVYSSGGEKQATNSTDPDPSPLLLQSSSLFGHIELTPA
 BnaMYB81-2 328 LSSPLTDPTPSECPSSFCGLLESVYVYSSGGEKQTT-TTDPDSP-LLQSSLLGHIDITPA
 BnaMYB48 236 DQFPFCFQHSRSPWSSG-----
 BnaMYB59 220 DQFPLSVLNMVDHHRGL-----
 BnaMYB62 251 MENS DIS--TECQVAEAY---ENVTQDPMWN-----MDDIWQFRE-----
 BnaMYB116 241 MGNSDILPLQDCHVGVAYSTYEEDVTQDPMWN-----MDDIWQFEYAPFN--
 BnaMYB78-1 262 VNGGLLS----EDLTQSYHNWFENDN-GMIPPYSDFSFWNIG-SDED-FWLLLQQQQQLVN
 BnaMYB78-2 263 DKSGLLNGGLRDMQEQQSYHNLFENIN-GMIPSYSDSFWNIG-SDED-FWLLLQQQQQLLN
 BnaMYB108-1 247 YS-GLLDEDLTATHEQSNLDWFENID-EVVSSSESSELWNIGESDED-FWFCQQQQQ-FNN
 BnaMYB108-2 245 YS-GLLDEDLTATHEQSNLHWFENID-EVVSSSESSELWNIGESDED-FWFCQQQQQ-FNN
 OsMYB2 265 RDTELELAQPPCQGGQTWTTSESSLPLGLTFPDLAADFEIGGFVDVDFWTSMEDDQLWCP
 BnaMYB91-1 276 RRLELQLESEKTSRQREKTEEIEAKMKALREEQKMAMEKIEGEYREQLVGLRRDAEAKDQ
 BnaMYB91-2 267 RRLELQLESEKTSRQREKTEEIEAKMKALREEQKMAMEKIEGEYREQLVGLRRDAEAKDQ
 BnaMYB88 344 SSGDQTQQPMLLP-----DNEQVDLLSTCHEIVP-----MSVEEFPNSPVQVTPFLRS
 BnaMYB124 329 QSGDKTQPSLPDPPTQTEHKESGEDFLSTCDVLPKNPDENKPISGDEENFSSPIQVTPFLRS
 BnaMYB28 257 IDQDYFSHFLENFGRDDDHNEEHYMNHNHGHDLMSDVSQEVSSTSVDDQDNTNEGWSNY
 ZmC1 216 SSDDCSSAASVSLRVGSHDEPCFSGDGDGDMDDVRLASFLSEDEDLRCQTAGQLA--
 BnaMYB38 228 TTSTVTRVKMEQHDHHEERSMEDYGMEEINHLINSSCTSSSSNSLWFDENKTDDTFMLY
 BnaMYB61 254 PNHNLEEMKWEYSMNTPFNRRSTLNSQPIYIKSEAEYLADVSNITDPWSQSQENLNTP
 BnaMYB46 224 QEGDWYKADINSHVAEMKTNAGNVPAESMRVEEYWDLDQLMSTVPSFHFNFKQST---
 BnaMYB90 189 NLMDGENMWWESLLEESKQKPLVPGGTATKMGATFAFDVEQLWNMLDGETVELD-----
 BnaMYB56 268 GKAGQCQVRAEVSQKSKLDHQNHHTITVSRKVEVKMKS GHYFFDFLGVGAS-----
 consensus 421

BnaMYB1	360	LRPQGTRGHRDHCLVSEQGKSRTNVLST-----
AtMYB1	366	LRPQGSRGHRDHYLVSSEQGTNITNVLST-----
BnaMYB109	340	DQITFNDPRIRFSGMMPRQHFFCARS-----
BnaMYB44	288	-----MIPMSQVGVGRIE-----
BnaMYB77	260	-----ITPKVE-----
BnaMYB73	302	CMPQSVNSRRVGFREFIVNQIGIGKME-----
BnaMYB96-1	309	HDFGLISQG---SLSLLEKWLFDEN-----MVGMSLEGQEAI-----
BnaMYB96-2	301	QDPGLISQG---SLSLFEKWLFDEN-----MVAMSLEGQEAI-----
BnaMYB30	295	----YSNQS---QWSLFEKWLFDEN-----GQVGDILLDENPNFF-----
BnaMYB31	283	ATNNVTTDDPAGSLSLIEQWLYDDQGLVDQCDDVQEDLIDVSLEGKNNGNNGDLS
AtMYB0_GL1		-----
BnaMYB4-1		-----
BnaMYB4-2		-----
BnaMYB4-3		-----
BnaMYB32-1		-----
BnaMYB32-2		-----
BnaMYB7		-----
BnaMYB3		-----
BnaMYB51		-----
BnaMYB122		-----
BnaMYB34		-----
BnaMYB16		-----
BnaMYB106		-----
BnaMYB47		-----
BnaMYB95	276	-----
BnaMYB41	290	L-----
BnaMYB92	307	LTSSSQESGASASAAWPDHLLDDSI-----
BnaMYB43-1	298	NDHDDGFVSGGCSRMLD-----
BnaMYB43-2	298	NDHDDGFVSGGCSRMLD-----
BnaMYB12	322	GDDNNIFDEKEGSDSMVSWLLDGEDEATIGKSNCESEPLDHDEENALVAWLLS-
BnaMYB111	309	NDELLGWEFQGLTCTDLDLWDLDFGEIQVDSI-----
BnaMYB13		-----
BnaMYB15		-----
BnaMYB58		-----
BnaMYB123-1		-----
BnaMYB123-2		-----
BnaMYB81-1	356	FEN-----NTETDMFPFGPTSSSERGTSLESGDWIRQLLGEDRDYTK-----
BnaMYB81-2	386	TANTAGHNSSAETDLVHFGPTFSNERRTSFEGGDWIRQLLGEDRDYTK-----
BnaMYB48		-----
BnaMYB59		-----
BnaMYB62		-----
BnaMYB116		-----
BnaMYB78-1	315	NGSF-----
BnaMYB78-2	320	NGSF-----
BnaMYB108-1	303	NNDF-----
BnaMYB108-2	301	NNDF-----
OsMYB2	325	TQAAV-----
BnaMYB91-1	336	KLADQWTSKHIRLTKFLEQHIGCRQLLDRP-----
BnaMYB91-2	327	KLADQWTSKHIRLTKFLEQHIGCRQLLDRP-----
BnaMYB88	392	LAAGIPSPQFSESERNFVLKTLGVESPCPS-ATNLSQPPPCRVLLDSL-----
BnaMYB124	389	LADGIPSPQFSESERSFLKTLGISSPCPSANPSQPPPCRVLLHSL-----
BnaMYB28	317	LLDHADFIHMDYDSL-----
ZmC1		-----
BnaMYB38	288	Y-----
BnaMYB61	314	EDSDVFSKDLQRMAVSFGQSL-----
BnaMYB46		-----
BnaMYB90		-----
BnaMYB56		-----
consensus	481	

Figure S1. Multiple sequence alignment and comparison of R2R3-MYB proteins from canola. Identical amino acids are shaded in black, and similar amino acids are shaded in gray. The amino-terminal R2 and R3 repeats of MYB domains for DNA-binding are shown below the alignment. The conserved repression motif LxLxL in BnaMYB3, -4, -7, -32, -44, -73, -77 and -91 is highlighted in blue. The nuclear localization sequence (NLS) predicted by NucPred (<http://www.sbc.su.se/~maccallr/nucpred/cgi-bin/multi.cgi>) and PredictNLS (<https://www.predictprotein.org/home>) are shown in red boxes. The carboxy-terminal region is highly variable and no conserved motif could be detected.

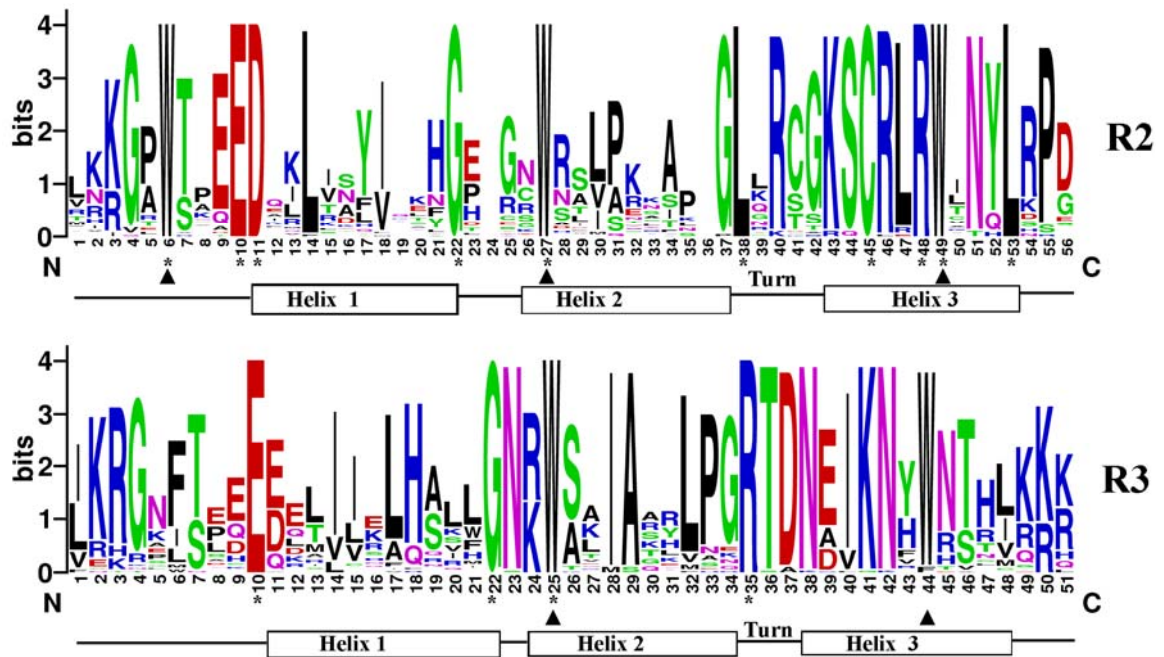


Figure S2. Sequence conservation of the R2R3-MYB domain.

The R2 and R3 MYB repeats are highly conserved across all R2R3-MYB proteins. The sequence logos of the R2 (Top) and R3 (Bottom) MYB repeats are based on full-length alignments of all canola R2R3-MYB proteins. The overall height of each stack indicates the conservation of the sequence at that position, whereas the height of letters within each stack represents the relative frequency of the corresponding amino acid. The asterisks indicate the position of the conserved amino acids that are identical among all the 53 canola R2R3-MYB proteins. Arrowheads show the typical, conserved tryptophan (W) residues in the MYB domain. The positions of the three α -helices that form each of the two MYB repeat are marked as Helix 1 to Helix 3. The sequence logos were generated by Weblogo (<http://weblogo.berkeley.edu/>).

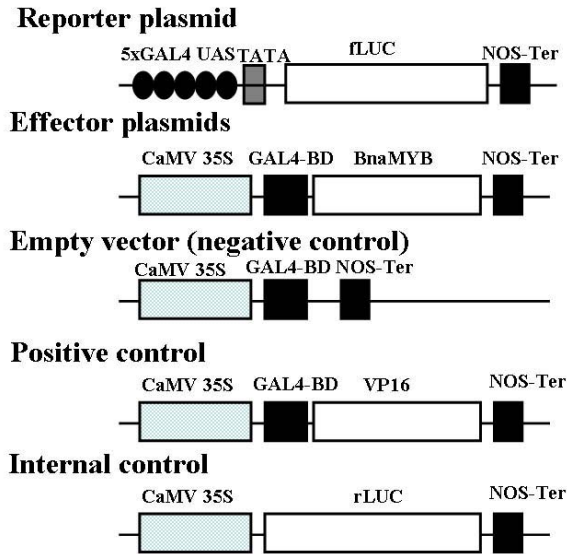
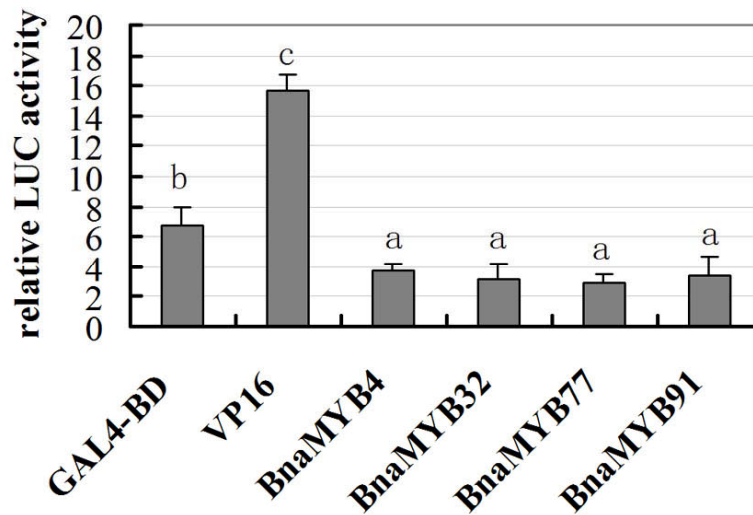
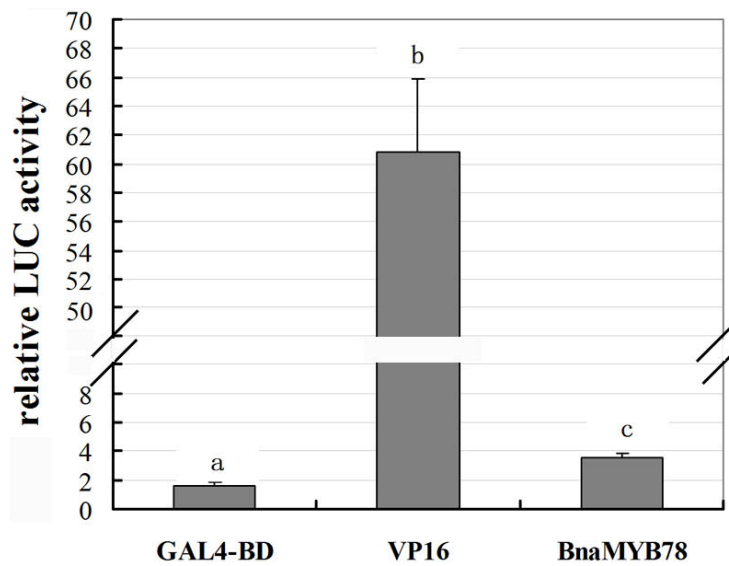
A**B****C**

Figure S3. Transcriptional regulation activity of BnaMYBs in protoplast assay.

(A) Schematic representation of constructs used in Arabidopsis protoplast transient

expression assay. The reporter plasmid contains five copies of the GAL4 responsive element, minimal TATA box region (starting at position -46) of CaMV 35S promoter, the firefly luciferase (fLUC) gene, and a nopaline synthase (NOS) terminator. Each of the effectors contains a GAL4 DNA-binding domain (GAL4-BD). The vector GAL4-BD was also used as a negative control. The GAL4-BD fused with viral protein VP16 was used as a positive control. All the effector constructs or internal control were driven by CaMV 35S promoter and ended by NOS terminator sequence.

(B) Effects of the BnaMYBs on reporter gene expression as revealed by relative LUC activity. The GAL4-BD and VP16 were used as negative and positive controls respectively. Identical and different letters indicate non- and significant differences.

(C) Effect of the BnaMYB78 on reporter gene expression as revealed by relative LUC activity. The GAL4-BD and VP16 were used as negative and positive controls respectively. Identical and different letters indicate non- and significant differences.

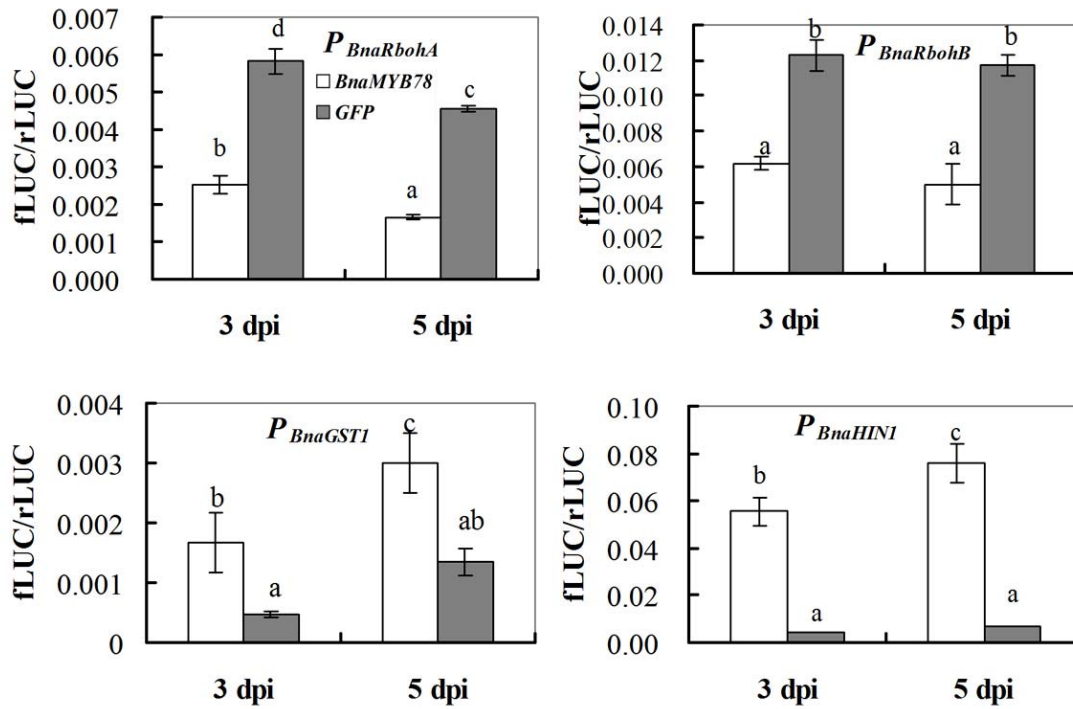


Figure S4. Dual LUC assay of downstream genes of BnaMYB78.

Promoter regions of genes were cloned and fused to upstream of firefly luciferase (fLUC) in the pGreenII0800-LUC vector, in which renilla luciferase (rLUC) under the control of the 35S promoter was used as the endogenous control. The effector plasmid is pYJHA-BnaMYB78 and the control plasmid is pYJGFP. Agrobacterial suspensions harboring the respective plasmids were coinfiltrated into *N.benthamiana* leaves, with enzymatic activity assayed 3 and 5 days post-infiltration (dpi). The ability of BnaMYB78 transcription factor to activate the reporter *fLUC* gene was indicated by the ratio of fLUC to rLUC. Error bars indicate the S.E. of three biological replicates. Identical and different letters represent non- and significant differences.

Supplemental methods:

1. Protoplast transactivation assay in Arabidopsis

The coding regions of BnaMYB genes were amplified by high-fidelity PCR with primers included in Table S2. The PCR products were digested and then cloned into pRT107-BD plasmid ¹ to yield 35S::GAL4BD-BnaMYBs. Reporter plasmid GAL4UAS::LUC contains five copies of GAL4 binding element and minimal TATA region of 35S promoter of cauliflower mosaic virus (CaMV), which are located upstream of the firefly luciferase (fLUC) gene. Internal control pPTRL contains *Renilla* Luciferase (rLUC) driven by 35S promoter was described previously ². All plasmids were isolated and purified through an Endofree Plasmid Maxi Kit (CWBiotech, Beijing).

The isolation and transfection of Arabidopsis mesophyll protoplast were based on the protocol described previously ³. For co-transfection assays, 6 µg of fLUC reporter and 6 µg of effector plasmids were used for each PEG transfection. For normalization values, 1 µg of pPTRL plasmid were used as internal control. After cultured for 16 h, luciferase activities were examined with using a dual-LUC reporter assay system (Promega, E1910) on a GloMaxTM20-20 luminometer. Each transfection was repeated three times.

2. Quantification of hydrogen peroxide in leaf tissues

Hydrogen peroxide was extracted and determined according to ^{4,5} with modifications. Briefly, 0.1 g leaf discs was ground in liquid nitrogen and extracted with 5 ml of 5% (w/v) trichloroacetic acid (TCA), followed by extraction in chloroform and isoamylol (24:1, v/v) and then centrifuged at 16 000 g for 10 min. The supernatant was neutralized to pH 7.5 with 1 M ammonium hydroxide (NH₄OH), and then the supernatant was divided into two aliquots of 100 µl. 0.4 ml of 100 mM Tris-HCl (pH 8.5) was added into both aliquots. Afterwards, 25 units of catalase (CAT, EC 1.11.1.6, Sigma) was added to one aliquot (blank) and equal amount of ddH₂O was added to the other aliquot and then kept at room temperature for 30 min. Finally, 0.5 ml colorimetric reagent (0.3 mM potassium titanium oxalate and 0.3 mM 4-(2-pyridylazo) resorcinol monosodium salt, freshly made and mixed at 1:1, v/v) was added and kept

at room temperature for 10 min. Then the absorbance at 508 nm was monitored and concentration of H₂O₂ was calculated against a standard curve of H₂O₂ (Alfa Aesar, France).

References:

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