

**Coexpression Network Analysis based
Characterization of the R2R3-MYB Family Genes in
Tolerant Poplar Infected with *Melampsora larici-
populina***

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Table S1 Primers used in this study

Module	Gene	Primer
Yellow	<i>Enhanced disease susceptibility 1 family protein</i> (543)	F: 5'-GGCAACAGCTTGGTTCTTGG-3' R: 5'-GGACAGAGTGAAATCCGAGGG-3'
	<i>Leucine-rich repeat receptor-like protein kinase</i> (380)	F: 5'-CTACCCGCTCAAGGTTGGTG-3' R: 5'-GTTGGTAAGAGGACCGGAGG-3'
	<i>LRR receptor-like serine/threonine-protein kinase</i> (386)	F: 5'-GATCGACCCAGATGGCGTTT-3' R: 5'-TGAGAACCCAATCGCCCAAG-3'
	<i>Receptor-like protein</i> (1208)	F: 5'-ATAACTGGCCTGCTTGGGTT-3' R: 5'-GATCACCCATTGCGACTGGA-3'
	<i>Disease resistance protein</i> (428)	F: 5'-ATTGCTGGAGAAGGCACCAT-3' R: 5'-AATAGACCTCCCATCCCCCA-3'
	<i>Disease resistance protein</i> (506)	F: 5'-CAGCTAGTGACGGAAGGGTC-3' R: 5'-GCAACTGAGAGACGCACCTA-3'
	<i>NBS-LRR type disease resistance protein</i> (516)	F: 5'-GAGTCCAGGGTGAAGCAGAG-3' R: 5'-CCGTGCCCAGTATCACTAGC-3'
	<i>Pathogenesis-related family protein</i> (164)	F: 5'-GGTGGATGAGAGGGCAAAC-3' R: 5'-ATCGTTATAGTTGCCTGGGGG-3'
	<i>Pathogenesis-related family protein</i> (141)	F: 5'-TGTGGGTTGATGAGAAGGCT-3' R: 5'-TGCCGGGTGGATCATAGTTG-3'
	<i>Pathogenesis related family protein</i> (237)	F: 5'-GTGCATTCTGGTGGGCCTTA-3' R: 5'-GCACAACCTAAACGAACCGAG-3'
	<i>Pathogenesis-related family protein</i> (626)	F: 5'-CTAACCTGGGACAACACGGT-3' R: 5'-AGGCACATGAGTTGGAGTTGT-3'
	<i>Calcium-binding family protein</i> (196)	F: 5'-AACAGCGAGGCAGTAGTAGC-3' R: 5'-CCTTGCCAGTCGTCTCATCC-3'
	<i>Calmodulin-like protein</i> (699)	F: 5'-TGGAGATGGGTGCATTACCTTC-3' R: 5'-GCTGCATCGTTTTCCCTCATT-3'
	<i>WRKY transcription factor 72</i> (305)	F: 5'-GACTTTGCCGAATCCAAGCC-3' R: 5'-CCGTCATTTCATCGTTGGGGT-3'
	<i>Calcium-dependent protein kinase</i> (341)	F: 5'-GATGTCTGGAGTGCTGGTGT-3' R: 5'-CTTCGGGTCAGGATCAAGCA-3'
	<i>Pathogenesis-related family protein</i> (179)	F: 5'-GGGACTTGAATGCTGTGAGTG-3' R: 5'-GTCCAGTGTTTGTACCCT-3'
	<i>WRKY transcription factor 47 family protein</i> (509)	F: 5'-AAGCCTAACGAGCAAGTCCC-3' R: 5'-GGAGCACCGATAGTAGGCAC-3'
	<i>Auxin-responsive GH3 family protein</i> (1583)	F: 5'-TCAGTGTATCGACAAGGCCG-3' R: 5'-ATTGACGCACCTTGAACCT-3'
	<i>Aux/IAA family protein</i> (1494)	F: 5'-GTGAGGAAGGTTTCAGGGCA-3' R: 5'-CCACCTTGCGAAGATAGGGT-3'
	<i>Flavonol synthase/flavanone 3-hydroxylase-like</i> (276)	F: 5'-TGCGAGAAGGAGCGTATGTC-3' R: 5'-TCCAGGCGCTTATCAGTTGG-3'
	<i>Flavanone 3-dioxygenase-like</i> (602)	F: 5'-TTGGGTGAACAAGGGCAACA-3' R: 5'-CAGCTACCCATTTCCCGTCT-3'

Light cyan	<i>Cytochrome P450 family protein</i> (207)	F: 5'-GGTCATGGCGGAGCTAATGA-3' R: 5'-GGAGAAGTGGGATTGGTGGG-3'
	<i>Peroxidase family protein</i> (315)	F: 5'-CCCACACCGCTTATGAACCT-3' R: 5'-CCAGTGCGTGGACAGGATAA-3'
	<i>Peroxidase family protein</i> (408)	F: 5'-TCGAAACTCGGCTAGAGGTTTT-3' R: 5'-GGCCCAAGGGTAGAAACCAA-3'
	<i>MYB169</i> (204)	F: 5'-GAAGGCCGATGGAATTTGCT-3' R: 5'-GACCACCTATTGCCCCACTT-3'
	<i>MYB194</i> (371)	F: 5'-ACCACCACCACAGCAAGAAG-3' R: 5'-GTGCTTGCGGCCATGTTATT-3'
	<i>MYB024</i> (653)	F: 5'-AGGTAGCGGAGTCGGATGAT-3' R: 5'-GTGGCTTGGACTTGTTCAC-3'
	<i>MYB129</i> (1040)	F: 5'-TGCAATAGATTCCGGCCGTG-3' R: 5'-GTGTGCCTTTCTTCCGTTCC-3'
	<i>MYB011</i> (1654)	F: 5'-GCCAAGACGGTGGGAAAAGA-3' R: 5'-CAGCACCACCCAAACTCGTA-3'
	<i>Receptor-like protein</i> (97)	F: 5'-CGGGTCCATTCTTGTTGCCA-3' R: 5'-ACCCAACGAGGAAGGAATGC-3'
	<i>LRR receptor-like serine/threonine-protein kinase</i> (30)	F: 5'-GTGGAGAACCCTACCCAAA-3' R: 5'-GTGAAACCAAGCTCGTTGCC-3'
	<i>LRR receptor-like serine/threonine-protein kinase</i> (27)	F: 5'-AGCAGTCGTGGACAAAGTGT-3' R: 5'-GGCAACAAGAATGGACCCGA-3'
	<i>Receptor-like protein</i> (43)	F: 5'-CGCACAACAGTTTGACTGGA-3' R: 5'-GGCAAACGTGCAACTCTCG-3'
	<i>Receptor-like protein</i> (85)	F: 5'-CGCTCTGTTGCACCTCAAAG-3' R: 5'-GCTCCTCATTCCTTACGCCC-3'
	<i>Chitinase</i> (317)	F: 5'-GAGATTCACAGGCCACCTCTAA-3' R: 5'-CAGGTGGAGGATCGTATTGGG-3'
	<i>MYB162</i> (28)	F: 5'-CCGGCACCCACAGAAAGTTA-3' R: 5'-ACAGGTTTAGGGAGGTGGAC-3'
	<i>MYB086</i> (44)	F: 5'-CGTGACCGAAATCCCATTCTG-3' R: 5'-TTGCATCGAGACCAAGCTCA-3'
Black	<i>Cytochrome P450 family protein</i> (258)	F: 5'-GCCGATGATGTTTTGCCAG-3' R: 5'-TGTAAGAATCCGGCACCTCG-3'
	<i>Pathogenesis-related family protein</i> (766)	F: 5'-ATTGCGGGACAAGTGACGAT-3' R: 5'-GCACTCACAGCATTCAGTCC-3'
	<i>MYB146</i> (511)	F: 5'-CCGACTATTCTCCCATCCGTG-3' R: 5'-CTTCCACTTCCGTTGTGCTG-3'
	<i>MYB101</i> (984)	F: 5'-GGAGTTATCTTCCGCAGGCT-3' R: 5'-CTGTACGCCCAAGCAATCTC-3'
	<i>Leucine-rich repeat family protein</i> (1)	F: 5'-CCCTCCTTCTTTCGGGACAC-3' R: 5'-GATTACCCAACGGTGCAGGT-3'
Purple	<i>WRKY transcription factor 42 family protein</i> (206)	F: 5'-AACCTCGCTTCTGATCCTG-3' R: 5'-AGGTGGTTGCTCATCTTGGC-3'

	<i>MYB137</i> (230)	F: 5'-GATAGATGCCAACAGCACAGC-3' R: 5'-TGTTGTGGTGGAGGTAGTGC-3'
	<i>MYB104</i> (681)	F: 5'-GGGATTGAAAAGGGGGCCA-3' R: 5'-TGGCCGCAAGTAGTTTACCC-3'
	<i>Phenylalanine ammonia-lyase family protein</i> (24)	F: 5'-TGGAACGGAAACATGCCACA-3' R: 5'-GTGGCAAGCATGGAGTGATG-3'
	<i>Cinnamyl alcohol dehydrogenase</i> (11)	F: 5'-AACAACTCCAAACCACACGC-3' R: 5'-ATGCCCCAATCGTTCTTTGC-3'
Dark	<i>MYB078</i> (27)	F: 5'-AGCTCTTAGGCAACAGATGGG-3' R: 5'-GTGCCGCCTTATTCAATCCTG-3'
grey	<i>MYB214</i> (28)	F: 5'-CTGCTATCGCTGCCCAGTTA-3' R: 5'-CTCCTGTGTCTTTCTCCTGGC-3'
	<i>MYB195</i> (34)	F: 5'-TCATCAAGCAAGGGGTTGGC-3' R: 5'-ATCGCCGTTTACCTCAATGGT-3'
	<i>MYB156</i> (46)	F: 5'-GCACACAAAATCCTGCCACG-3' R: 5'-GCCTCGTATGCCTCCAAGAA-3'
	<i>Protein phosphatase</i> (16)	F: 5'-GGGTCGGTGTCTGTTATAGGG-3' R: 5'-CTTTACACGCCTCCGCTACA-3'
	<i>Protein phosphatase</i> (18)	F: 5'-CACGGTTGTTCTCATGTGGC-3' R: 5'-CCATCCCTTGATTCCACGCT-3'
	<i>Protein phosphatase</i> (96)	F: 5'-GGGATTTGCTGTGGAGTTGC-3' R: 5'-GCCGTTTGGCAGGGGTAATA-3'
	<i>Protein phosphatase</i> (145)	F: 5'-GATTCTCGTGCCGTGCTTTG-3' R: 5'-CCGGTATGACGTAGGGCTTC-3'
Grey 60	<i>Protein phosphatase</i> (146)	F: 5'-CGGTAGCGATTACCCCTTCA-3' R: 5'-GCTTTTCCACCCCTCCTTGA-3'
	<i>bZIP transcription factor 6 family protein</i> (9)	F: 5'-CTGCGAACCAGCTGTCATCA-3' R: 5'-GAGACCTTGACGCTGACTCT-3'
	<i>Calcium binding family protein</i> (138)	F: 5'-CAATTGACGCAACGGTGA-3' R: 5'-GCGCAAACCTCTGCCAAATCA-3'
	<i>MYB049</i> (95)	F: 5'-CTGCCATTGCTGCTCGATTG-3' R: 5'-GCTCAGGATTGAGGAGAGGTC-3'
	<i>18S ribosomal RNA</i>	F: 5'-CGAAGACGATCAGATACCGTCCTA-3' R: 5'-TTTCTCATAAGGTGCTGGCGGAGT-3'

Table S2 Quality statistics of filtered reads

Sample	Total raw reads (Mb)	Total clean reads (Mb)	Total clean bases (Gb)	Clean reads Q20 (%)	Clean reads Q30 (%)	Clean reads ratio (%)
‘Intolerant’	69.68	65.52	6.55	97.34	89.73	94.03
‘Tolerant 1’	69.65	65.15	6.52	97.22	89.62	93.55
‘Tolerant 2’	69.65	65.52	6.55	97.37	90.07	94.07

Table S3 Basic information of *R2R3-MYB* genes

<i>R2R3-MYB</i> gene	<i>Populus trichocarpa</i> gene ID for <i>R2R3-MYB</i>	Location on chromosome	GO ID	KOG ID	Arabidopsis homologous genes ID	Arabidopsis homologous genes
<i>MYB001</i>	Potri.001G005100	Chr01	GO:0003677	KOG0048	AT3G13540.1	<i>AtMYB5</i>
<i>MYB002</i>	Potri.001G035800	Chr01	GO:0003677	KOG0724		
<i>MYB003</i>	Potri.001G036000	Chr01	GO:0003677		AT5G06100.2	<i>AtMYB33</i>
<i>MYB003</i>	Potri.001G075400	Chr01	GO:0003677		AT3G11440.1	<i>AtMYB65</i>
<i>MYB004</i>	Potri.001G086700	Chr01	GO:0003677	KOG0048	AT3G12720.1	<i>AtMYB67</i>
<i>MYB005</i>	Potri.001G099800	Chr01	GO:0003677	KOG0048	AT5G49330.1	<i>AtMYB111</i>
<i>MYB006</i>	Potri.001G118800	Chr01	GO:0003677	KOG0048	AT1G63910.1	<i>AtMYB103</i>
<i>MYB007</i>	Potri.001G139900	Chr01	GO:0003677	KOG0048	AT4G12350.1	<i>AtMYB42</i>
<i>MYB008</i>	Potri.001G169600	Chr01	GO:0003677	KOG0048	AT5G16770.1	<i>AtMYB9</i>
<i>MYB009</i>	Potri.001G197000	Chr01	GO:0003677		AT5G40330.1	<i>AtMYB23</i>
<i>MYB010</i>	Potri.001G219100	Chr01	GO:0003677	KOG0048	AT3G13890.2	<i>AtMYB26</i>
<i>MYB011</i>	Potri.001G224500	Chr01	GO:0003677			
<i>MYB012</i>	Potri.001G235500	Chr01	GO:0003677		AT3G11440.1	<i>AtMYB65</i>
<i>MYB013</i>	Potri.001G248800	Chr01	GO:0003677		AT3G46130.1	<i>AtMYB48</i>
<i>MYB014</i>	Potri.001G250000	Chr01	GO:0003677	KOG0724		
<i>MYB015</i>	Potri.001G258700	Chr01	GO:0003677	KOG0048	AT5G58850.1	<i>AtMYB119</i>
<i>MYB016</i>	Potri.001G267300	Chr01	GO:0003677	KOG0048	AT5G12870.1	<i>AtMYB46</i>
<i>MYB017</i>	Potri.001G300200	Chr01	GO:0003677		AT3G08500.1	<i>AtMYB83</i>
<i>MYB018</i>	Potri.001G336700	Chr01	GO:0003677	KOG0048	AT4G37260.1	<i>AtMYB73</i>
<i>MYB019</i>	Potri.001G346600	Chr01	GO:0003677	KOG0048	AT5G14340.1	<i>AtMYB40</i>
<i>MYB020</i>	Potri.001G347200	Chr01	GO:0003677		AT3G27810.1	<i>AtMYB21</i>
<i>MYB021</i>	Potri.001G408700	Chr01	GO:0003677	KOG0048	AT3G27785.1	<i>AtMYB118</i>
<i>MYB022</i>	Potri.001G470500	Chr01	GO:0003677	KOG0048	AT4G21440.1	<i>AtMYB102</i>
<i>MYB023</i>	Potri.002G038500	Chr01	GO:0003677		AT5G56110.1	<i>AtMYB103</i>
<i>MYB024</i>	Potri.002G073500	Chr02	GO:0003677	KOG0048	AT2G31180.1	<i>AtMYB14</i>
<i>MYB025</i>	Potri.002G096800	Chr02	GO:0003677	KOG0048	AT1G17950.1	<i>AtMYB52</i>
<i>MYB026</i>	Potri.002G113700	Chr02	GO:0003677	KOG0048	AT1G34670.1	<i>AtMYB93</i>
<i>MYB027</i>	Potri.002G122600	Chr02	GO:0003677	KOG0048	AT5G65790.1	<i>AtMYB68</i>
<i>MYB028</i>	Potri.002G128900	Chr02	GO:0003677	KOG0048	AT4G37260.1	<i>AtMYB73</i>
<i>MYB029</i>	Potri.002G140900	Chr02	GO:0003677		AT4G37260.1	<i>AtMYB73</i>
<i>MYB030</i>	Potri.002G157600	Chr02	GO:0003677	KOG0048	AT3G60460.1	<i>DUO1</i>
<i>MYB031</i>	Potri.002G173900	Chr02	GO:0003677		AT3G61250.1	<i>AtMYB17</i>
<i>MYB032</i>	Potri.002G185900	Chr02	GO:0003677	KOG0048	AT1G22640.1	<i>AtMYB3</i>
<i>MYB033</i>	Potri.002G191800	Chr02	GO:0003677	KOG0048	AT4G01680.1	<i>AtMYB55</i>
<i>MYB034</i>	Potri.002G198100	Chr02	GO:0003677	KOG0048	AT2G47190.1	<i>AtMYB2</i>
<i>MYB035</i>	Potri.002G228700	Chr02	GO:0003677	KOG0048	AT5G49330.1	<i>AtMYB111</i>
<i>MYB036</i>	Potri.003G064600	Chr02	GO:0003677	KOG0048	AT2G32460.1	<i>AtMYB101</i>
<i>MYB037</i>	Potri.003G079100	Chr03	GO:0003677		AT5G14750.1	<i>AtMYB66</i>
<i>MYB038</i>	Potri.003G094200	Chr03	GO:0003677		AT3G13540.1	<i>AtMYB5</i>
<i>MYB039</i>	Potri.003G114100	Chr03	GO:0003677	KOG0048	AT5G16770.1	<i>AtMYB9</i>
<i>MYB040</i>	Potri.003G123800	Chr03	GO:0003677	KOG0048	AT4G12350.1	<i>AtMYB42</i>
<i>MYB041</i>	Potri.003G132000	Chr03	GO:0003677	KOG0048	AT4G32730.2	<i>AtMYB3R-1</i>
<i>MYB042</i>	Potri.003G144200	Chr03	GO:0003677	KOG0048	AT1G63910.1	<i>AtMYB103</i>
<i>MYB043</i>	Potri.003G144300	Chr03	GO:0003677		AT5G49330.1	<i>AtMYB111</i>

<i>R2R3-MYB</i> gene	<i>Populus trichocarpa</i> gene ID for <i>R2R3-MYB</i>	Location on chromosome	GO ID	KOG ID	Arabidopsis homologous genes ID	Arabidopsis homologous genes
<i>MYB044</i>	Potri.003G155700	Chr03	GO:0003677	KOG0048	AT2G47460.1	<i>AtMYB12</i>
<i>MYB045</i>	Potri.003G189700	Chr03	GO:0003677	KOG0048	AT3G12720.1	<i>AtMYB67</i>
<i>MYB046</i>	Potri.003G219900	Chr03	GO:0003677	KOG0048	AT5G06100.2	<i>AtMYB33</i>
<i>MYB047</i>	Potri.004G026600	Chr03	GO:0003677	KOG0048	AT3G13540.1	<i>AtMYB5</i>
<i>MYB048</i>	Potri.004G033100	Chr04	GO:0003677		AT4G21440.1	<i>AtMYB102</i>
<i>MYB049</i>	Potri.004G086300	Chr04	GO:0003677	KOG0048	AT4G21440.1	<i>AtMYB102</i>
<i>MYB050</i>	Potri.004G088100	Chr04	GO:0003677	KOG0048	AT5G16600.1	<i>AtMYB43</i>
<i>MYB051</i>	Potri.004G102600	Chr04	GO:0003677	KOG0048	AT4G09460.1	<i>AtMYB6</i>
<i>MYB052</i>	Potri.004G115600	Chr04	GO:0003677	KOG0048	AT2G37630.1	<i>AtMYB91</i>
<i>MYB053</i>	Potri.004G118000	Chr04	GO:0003677	KOG0048	AT3G30210.1	<i>AtMYB121</i>
<i>MYB054</i>	Potri.004G126700	Chr04	GO:0003677		AT3G30210.1	<i>AtMYB121</i>
<i>MYB055</i>	Potri.004G138000	Chr04	GO:0003677	KOG0048	AT5G62470.2	<i>AtMYB96</i>
<i>MYB056</i>	Potri.004G174400	Chr04	GO:0003677	KOG0048	AT4G38620.1	<i>AtMYB4</i>
<i>MYB057</i>	Potri.004G215100	Chr04	GO:0003677	KOG0048	AT4G38620.1	<i>AtMYB4</i>
<i>MYB058</i>	Potri.005G001600	Chr04	GO:0003677	KOG0048	AT5G57620.1	<i>AtMYB36</i>
<i>MYB059</i>	Potri.005G063200	Chr05	GO:0003677	KOG0048	AT1G09540.1	<i>AtMYB61</i>
<i>MYB060</i>	Potri.005G074500	Chr05	GO:0003677	KOG0048	AT4G33450.1	<i>AtMYB69</i>
<i>MYB061</i>	Potri.005G087700	Chr05	GO:0003677	KOG0048	AT1G34670.1	<i>AtMYB93</i>
<i>MYB062</i>	Potri.005G096600	Chr05	GO:0003677			
<i>MYB062</i>	Potri.005G112000	Chr05	GO:0003677			
<i>MYB063</i>	Potri.005G118500	Chr05	GO:0003677	KOG0048	AT1G79180.1	<i>AtMYB63</i>
<i>MYB064</i>	Potri.005G142600	Chr05	GO:0003677	KOG0048	AT4G38620.1	<i>AtMYB4</i>
<i>MYB065</i>	Potri.005G164900	Chr05	GO:0003677	KOG0048	AT4G18770.1	<i>AtMYB98</i>
<i>MYB066</i>	Potri.005G186400	Chr05	GO:0003677	KOG0048	AT4G37260.1	<i>AtMYB73</i>
<i>MYB067</i>	Potri.005G224100	Chr05	GO:0003677	KOG0048	AT1G34670.1	<i>AtMYB93</i>
<i>MYB068</i>	Potri.006G066400	Chr05	GO:0003677	KOG0048	AT1G17950.1	<i>AtMYB52</i>
<i>MYB069</i>	Potri.006G085600	Chr05	GO:0003677	KOG0048	AT3G23250.1	<i>AtMYB15</i>
<i>MYB070</i>	Potri.006G085900	Chr06	GO:0003677	KOG0048	AT5G52600.1	<i>AtMYB82</i>
<i>MYB071</i>	Potri.006G097300	Chr06	GO:0003677	KOG0048	AT5G02320.1	<i>AtMYB3R-5</i>
<i>MYB072</i>	Potri.006G122100	Chr06	GO:0003677	KOG0048	AT2G37630.1	<i>AtMYB91</i>
<i>MYB073</i>	Potri.006G123400	Chr06	GO:0003677	KOG0724		
<i>MYB074</i>	Potri.006G170800	Chr06	GO:0003677	KOG0048	AT3G53200.1	<i>AtMYB27</i>
<i>MYB075</i>	Potri.006G221200	Chr06	GO:0003677	KOG0048	AT5G57620.1	<i>AtMYB36</i>
<i>MYB076</i>	Potri.006G221500	Chr06	GO:0003677	KOG0048	AT5G57620.1	<i>AtMYB36</i>
<i>MYB077</i>	Potri.006G221800	Chr06	GO:0003677		AT3G13540.1	<i>AtMYB5</i>
<i>MYB078</i>	Potri.006G234200	Chr06	GO:0003677	KOG0048	AT5G35550.1	<i>AtMYB123</i>
<i>MYB079</i>	Potri.006G241700	Chr06	GO:0003677	KOG0048	AT4G38620.1	<i>AtMYB4</i>
<i>MYB080</i>	Potri.006G275900	Chr06	GO:0003677	KOG0048	AT5G65790.1	<i>AtMYB68</i>
<i>MYB081</i>	Potri.007G007900	Chr06	GO:0003677	KOG0048	AT4G32730.2	<i>AtMYB3R-1</i>
<i>MYB082</i>	Potri.007G048900	Chr06	GO:0003677	KOG0048	AT1G22640.1	<i>AtMYB3</i>
<i>MYB083</i>	Potri.007G064600	Chr07	GO:0003677	KOG0048	AT3G49690.1	<i>AtMYB84</i>
<i>MYB084</i>	Potri.007G067600	Chr07	GO:0003677	KOG0048	AT4G37260.1	<i>AtMYB73</i>
<i>MYB085</i>	Potri.007G076200	Chr07	GO:0003677			
<i>MYB086</i>	Potri.007G093900	Chr07	GO:0003677	KOG0048	AT1G79180.1	<i>AtMYB63</i>
<i>MYB087</i>	Potri.007G106100	Chr07	GO:0003677	KOG0724		

<i>R2R3-MYB</i> gene	<i>Populus trichocarpa</i> gene ID for <i>R2R3-MYB</i>	Location on chromosome	GO ID	KOG ID	Arabidopsis homologous genes ID	Arabidopsis homologous genes
<i>MYB088</i>	Potri.007G134500	Chr07	GO:0003677	KOG0048	AT5G10280.1	<i>AtMYB92</i>
<i>MYB089</i>	Potri.008G041900	Chr07	GO:0003677	KOG0048	AT4G33450.1	<i>AtMYB69</i>
<i>MYB090</i>	Potri.008G062700	Chr07	GO:0003677		AT1G17950.1	<i>AtMYB52</i>
<i>MYB091</i>	Potri.008G064200	Chr08	GO:0003677	KOG1878		
<i>MYB092</i>	Potri.008G070900	Chr08	GO:0003677	KOG0048	AT3G55730.1	<i>AtMYB109</i>
<i>MYB093</i>	Potri.008G081600	Chr08	GO:0003677	KOG0724		
<i>MYB094</i>	Potri.008G088000	Chr08	GO:0003677		AT4G37260.1	<i>AtMYB73</i>
<i>MYB095</i>	Potri.008G089200	Chr08	GO:0003677	KOG0048	AT3G12720.1	<i>AtMYB67</i>
<i>MYB096</i>	Potri.008G089700	Chr08	GO:0003677	KOG0048	AT1G69560.1	<i>AtMYB105</i>
<i>MYB097</i>	Potri.008G101400	Chr08	GO:0003677	KOG0048	AT3G01140.1	<i>AtMYB106</i>
<i>MYB098</i>	Potri.008G122100	Chr08	GO:0003677	KOG0048	AT3G01140.1	<i>AtMYB106</i>
<i>MYB099</i>	Potri.008G128500	Chr08	GO:0003677	KOG0048	AT3G06490.1	<i>AtMYB108</i>
<i>MYB100</i>	Potri.008G148400	Chr08	GO:0003677	KOG0048	AT1G68320.1	<i>AtMYB62</i>
<i>MYB101</i>	Potri.008G148500	Chr08	GO:0003677	KOG0048	AT4G38620.1	<i>AtMYB4</i>
<i>MYB102</i>	Potri.008G166700	Chr08	GO:0003677	KOG0048	AT1G14350.1	<i>AtMYB124</i>
<i>MYB103</i>	Potri.008G173400	Chr08				
<i>MYB104</i>	Potri.008G180800	Chr08	GO:0003677	KOG0048	AT3G23250.1	<i>AtMYB15</i>
<i>MYB105</i>	Potri.009G007100	Chr08	GO:0003677	KOG0048	AT4G13480.1	<i>AtMYB79</i>
<i>MYB106</i>	Potri.009G018700	Chr08	GO:0003677	KOG0048	AT5G14340.1	<i>AtMYB40</i>
<i>MYB107</i>	Potri.009G027300	Chr09	GO:0003677	KOG0048	AT5G57620.1	<i>AtMYB36</i>
<i>MYB108</i>	Potri.009G042600	Chr09	GO:0003677	KOG0048	AT5G06100.2	<i>AtMYB33</i>
<i>MYB109</i>	Potri.009G044100	Chr09	GO:0003677		AT3G46130.1	<i>AtMYB48</i>
<i>MYB110</i>	Potri.009G053900	Chr09	GO:0003677	KOG0724		
<i>MYB111</i>	Potri.009G061500	Chr09	GO:0003677	KOG0048	AT5G58850.1	<i>AtMYB119</i>
<i>MYB112</i>	Potri.009G096000	Chr09	GO:0003677	KOG0048	AT5G12870.1	<i>AtMYB46</i>
<i>MYB113</i>	Potri.009G134000	Chr09	GO:0003677	KOG0048	AT3G08500.1	<i>AtMYB83</i>
<i>MYB114</i>	Potri.010G004300	Chr09	GO:0003677		AT4G37260.1	<i>AtMYB73</i>
<i>MYB115</i>	Potri.010G064000	Chr09	GO:0003677	KOG0048	AT4G38620.1	<i>AtMYB4</i>
<i>MYB116</i>	Potri.010G093000	Chr10	GO:0003677	KOG0048	AT1G57560.1	<i>AtMYB50</i>
<i>MYB117</i>	Potri.010G093100	Chr10	GO:0003677	KOG0048	AT4G13480.1	<i>AtMYB79</i>
<i>MYB118</i>	Potri.010G114000	Chr10	GO:0003677	KOG0048	AT2G02820.2	<i>AtMYB88</i>
<i>MYB119</i>	Potri.010G123000	Chr10				
<i>MYB120</i>	Potri.010G141000	Chr10	GO:0003677	KOG0048	AT4G38620.1	<i>AtMYB4</i>
<i>MYB121</i>	Potri.010G149900	Chr10	GO:0003677	KOG0048	AT1G68320.1	<i>AtMYB62</i>
<i>MYB122</i>	Potri.010G165700	Chr10	GO:0003677	KOG0048	AT5G49330.1	<i>AtMYB111</i>
<i>MYB123</i>	Potri.010G167500	Chr10	GO:0003677	KOG0048	AT3G06490.1	<i>AtMYB108</i>
<i>MYB124</i>	Potri.010G174500	Chr10	GO:0003677	KOG0048	AT3G01140.1	<i>AtMYB106</i>
<i>MYB125</i>	Potri.010G195000	Chr10	GO:0003677		AT1G69560.1	<i>AtMYB105</i>
<i>MYB126</i>	Potri.010G220000	Chr10	GO:0003677	KOG0048	AT3G12720.1	<i>AtMYB67</i>
<i>MYB127</i>	Potri.010G240800	Chr10	GO:0003677	KOG0048	AT3G55730.1	<i>AtMYB109</i>
<i>MYB128</i>	Potri.011G040200	Chr10	GO:0003677	KOG1878		
<i>MYB129</i>	Potri.011G040300	Chr10	GO:0003677			
<i>MYB130</i>	Potri.011G040400	Chr11	GO:0003677	KOG0048	AT4G38620.1	<i>AtMYB4</i>
<i>MYB131</i>	Potri.011G041600	Chr11	GO:0003677	KOG0048	AT4G38620.1	<i>AtMYB4</i>
<i>MYB132</i>	Potri.011G125900	Chr11	GO:0003677	KOG0048	AT2G31180.1	<i>AtMYB14</i>

<i>R2R3-MYB</i> gene	<i>Populus trichocarpa</i> gene ID for <i>R2R3-MYB</i>	Location on chromosome	GO ID	KOG ID	Arabidopsis homologous genes ID	Arabidopsis homologous genes
<i>MYB133</i>	Potri.011G167600	Chr11	GO:0003677	KOG0048	AT4G21440.1	<i>AtMYB102</i>
<i>MYB134</i>	Potri.012G039400	Chr11	GO:0003677	KOG0048	AT4G21440.1	<i>AtMYB102</i>
<i>MYB135</i>	Potri.012G055600	Chr11	GO:0003677	KOG0048	AT5G56110.1	<i>AtMYB103</i>
<i>MYB136</i>	Potri.012G060300	Chr12	GO:0003677	KOG0048	AT1G17950.1	<i>AtMYB52</i>
<i>MYB137</i>	Potri.012G072500	Chr12	GO:0003677	KOG0048	AT1G68320.1	<i>AtMYB62</i>
<i>MYB138</i>	Potri.012G080400	Chr12	GO:0003677			
<i>MYB139</i>	Potri.012G082000	Chr12	GO:0003677	KOG0048	AT3G28470.1	<i>AtMYB35</i>
<i>MYB140</i>	Potri.012G084100	Chr12	GO:0003677	KOG0048	AT5G14750.1	<i>AtMYB66</i>
<i>MYB141</i>	Potri.012G127700	Chr12	GO:0003677		AT4G18770.1	<i>AtMYB98</i>
<i>MYB142</i>	Potri.012G140500	Chr12	GO:0003677	KOG0048	AT5G26660.1	<i>AtMYB86</i>
<i>MYB143</i>	Potri.012G140700	Chr12	GO:0003677	KOG0048	AT4G12350.1	<i>AtMYB42</i>
<i>MYB144</i>	Potri.013G001000	Chr12	GO:0003677	KOG0048	AT5G52260.1	<i>AtMYB19</i>
<i>MYB145</i>	Potri.013G046300	Chr12	GO:0003677	KOG0048	AT3G61250.1	<i>AtMYB17</i>
<i>MYB146</i>	Potri.013G056400	Chr13	GO:0003677	KOG0048	AT1G09540.1	<i>AtMYB61</i>
<i>MYB147</i>	Potri.013G056500	Chr13	GO:0003677	KOG0050	AT1G09770.1	<i>AtMYBCDC5</i>
<i>MYB148</i>	Potri.013G067000	Chr13	GO:0003677	KOG0048	AT3G13540.1	<i>AtMYB5</i>
<i>MYB149</i>	Potri.013G067500	Chr13	GO:0003677	KOG0048	AT3G13540.1	<i>AtMYB5</i>
<i>MYB150</i>	Potri.013G109300	Chr13	GO:0003677	KOG0048	AT5G17800.1	<i>AtMYB56</i>
<i>MYB151</i>	Potri.013G130900	Chr13	GO:0003677	KOG0048	AT1G08810.1	<i>AtMYB60</i>
<i>MYB152</i>	Potri.013G148600	Chr13	GO:0003677	KOG0048	AT1G22640.1	<i>AtMYB3</i>
<i>MYB153</i>	Potri.013G149100	Chr13	GO:0003677	KOG0048	AT4G26930.1	<i>AtMYB97</i>
<i>MYB154</i>	Potri.013G149200	Chr13	GO:0003677	KOG0048	AT4G21440.1	<i>AtMYB102</i>
<i>MYB155</i>	Potri.014G022500	Chr13	GO:0003677	KOG0048	AT3G23250.1	<i>AtMYB15</i>
<i>MYB156</i>	Potri.014G035100	Chr13	GO:0003677	KOG0048	AT2G31180.1	<i>AtMYB14</i>
<i>MYB157</i>	Potri.014G054700	Chr14	GO:0003677	KOG0048	AT4G37260.1	<i>AtMYB73</i>
<i>MYB158</i>	Potri.014G079300	Chr14	GO:0003677		AT4G37260.1	<i>AtMYB73</i>
<i>MYB159</i>	Potri.014G081200	Chr14	GO:0003677	KOG0048	AT3G60460.1	<i>DUO1</i>
<i>MYB160</i>	Potri.014G100800	Chr14	GO:0003677	KOG0048	AT4G32730.2	<i>AtMYB3R-1</i>
<i>MYB161</i>	Potri.014G111200	Chr14	GO:0003677		AT3G61250.1	<i>AtMYB17</i>
<i>MYB162</i>	Potri.014G117000	Chr14	GO:0003677	KOG0048	AT2G16720.1	<i>AtMYB7</i>
<i>MYB163</i>	Potri.014G122700	Chr14	GO:0003677	KOG0048	AT4G01680.1	<i>AtMYB55</i>
<i>MYB164</i>	Potri.015G033600	Chr14	GO:0003677	KOG0048	AT2G47190.1	<i>AtMYB2</i>
<i>MYB165</i>	Potri.015G041100	Chr14	GO:0003677		AT5G49330.1	<i>AtMYB111</i>
<i>MYB166</i>	Potri.015G041500	Chr15	GO:0003677		AT1G17950.1	<i>AtMYB52</i>
<i>MYB167</i>	Potri.015G046200	Chr15	GO:0003677	KOG0048	AT1G22640.1	<i>AtMYB3</i>
<i>MYB168</i>	Potri.015G067700	Chr15	GO:0003677	KOG0048	AT3G18100.1	<i>AtMYB4R-1</i>
<i>MYB169</i>	Potri.015G075600	Chr15	GO:0003677	KOG0048	AT1G25340.1	<i>AtMYB116</i>
<i>MYB170</i>	Potri.015G075800	Chr15	GO:0003677	KOG0048	AT3G28470.1	<i>AtMYB35</i>
<i>MYB171</i>	Potri.015G077700	Chr15	GO:0003677	KOG0048	AT5G14750.1	<i>AtMYB66</i>
<i>MYB172</i>	Potri.015G082700	Chr15	GO:0003677	KOG0048	AT5G14750.1	<i>AtMYB66</i>
<i>MYB173</i>	Potri.015G129100	Chr15	GO:0003677		AT4G18770.1	<i>AtMYB98</i>
<i>MYB174</i>	Potri.015G143400	Chr15	GO:0003677	KOG0048	AT1G57560.1	<i>AtMYB50</i>
<i>MYB175</i>	Potri.015G143500	Chr15	GO:0003677	KOG0048	AT4G22680.1	<i>AtMYB85</i>
<i>MYB176</i>	Potri.016G099200	Chr15	GO:0003677		AT5G52260.1	<i>AtMYB19</i>
<i>MYB177</i>	Potri.016G112300	Chr15	GO:0003677		AT3G61250.1	<i>AtMYB17</i>

<i>R2R3-MYB</i> gene	<i>Populus trichocarpa</i> gene ID for <i>R2R3-MYB</i>	Location on chromosome	GO ID	KOG ID	Arabidopsis homologous genes ID	Arabidopsis homologous genes
<i>MYB178</i>	Potri.017G017600	Chr16	GO:0003677	KOG0048	AT5G57620.1	<i>AtMYB36</i>
<i>MYB179</i>	Potri.017G071500	Chr16	GO:0003677	KOG0724		
<i>MYB180</i>	Potri.017G075000	Chr17	GO:0003677		AT1G17950.1	<i>AtMYB52</i>
<i>MYB181</i>	Potri.017G082500	Chr17	GO:0003677	KOG0048	AT3G27810.1	<i>AtMYB21</i>
<i>MYB182</i>	Potri.017G085200	Chr17	GO:0003677	KOG0048	AT3G28470.1	<i>AtMYB35</i>
<i>MYB183</i>	Potri.017G086300	Chr17	GO:0003677	KOG0048	AT3G47600.1	<i>AtMYB94</i>
<i>MYB184</i>	Potri.017G099500	Chr17	GO:0003677	KOG0048	AT1G69560.1	<i>AtMYB105</i>
<i>MYB185</i>	Potri.017G112300	Chr17	GO:0003677	KOG0048	AT3G01140.1	<i>AtMYB106</i>
<i>MYB186</i>	Potri.017G125600	Chr17	GO:0003677		AT3G30210.1	<i>AtMYB121</i>
<i>MYB187</i>	Potri.017G125700	Chr17	GO:0003677	KOG0048	AT2G37630.1	<i>AtMYB91</i>
<i>MYB188</i>	Potri.017G125800	Chr17	GO:0003677	KOG0048	AT1G66370.1	<i>AtMYB113</i>
<i>MYB189</i>	Potri.017G125900	Chr17	GO:0003677	KOG0048	AT1G66370.1	<i>AtMYB113</i>
<i>MYB190</i>	Potri.017G126000	Chr17	GO:0003677	KOG0048	AT1G66370.1	<i>AtMYB113</i>
<i>MYB191</i>	Potri.017G128900	Chr17	GO:0003677	KOG0048	AT1G66370.1	<i>AtMYB113</i>
<i>MYB192</i>	Potri.017G130300	Chr17	GO:0003677		AT1G66370.1	<i>AtMYB113</i>
<i>MYB193</i>	Potri.018G005300	Chr17	GO:0003677	KOG0048	AT4G09460.1	<i>AtMYB6</i>
<i>MYB194</i>	Potri.018G038000	Chr17	GO:0003677	KOG0048	AT5G16600.1	<i>AtMYB43</i>
<i>MYB195</i>	Potri.018G049000	Chr18	GO:0003677	KOG0048	AT5G14750.1	<i>AtMYB66</i>
<i>MYB195</i>	Potri.018G049200	Chr18	GO:0003677	KOG0048	AT1G22640.1	<i>AtMYB3</i>
<i>MYB196</i>	Potri.018G049600	Chr18	GO:0003677	KOG0048	AT4G32730.2	<i>AtMYB3R-1</i>
<i>MYB197</i>	Potri.018G058800	Chr18	GO:0003677		AT5G14750.1	<i>AtMYB66</i>
<i>MYB199</i>	Potri.018G095900	Chr18	GO:0003677	KOG0048	AT2G16720.1	<i>AtMYB7</i>
<i>MYB200</i>	Potri.018G127700	Chr18	GO:0003677	KOG0048	AT3G49690.1	<i>AtMYB84</i>
<i>MYB200</i>	Potri.019G018200	Chr18	GO:0003677	KOG0048	AT5G57620.1	<i>AtMYB36</i>
<i>MYB201</i>	Potri.019G018400	Chr18	GO:0003677	KOG0048	AT5G57620.1	<i>AtMYB36</i>
<i>MYB202</i>	Potri.019G036300	Chr18	GO:0003677	KOG0048	AT5G52600.1	<i>AtMYB82</i>
<i>MYB203</i>	Potri.019G036400	Chr19	GO:0003677	KOG0048	AT3G23250.1	<i>AtMYB15</i>
<i>MYB204</i>	Potri.019G040900	Chr19	GO:0003677	KOG0050	AT1G09770.1	<i>AtMYBCDC5</i>
<i>MYB205</i>	Potri.019G045900	Chr19	GO:0003677	KOG0048	AT3G13540.1	<i>AtMYB5</i>
<i>MYB206</i>	Potri.019G050900	Chr19	GO:0003677	KOG0048	AT3G13540.1	<i>AtMYB5</i>
<i>MYB207</i>	Potri.019G081500	Chr19	GO:0003677	KOG0048	AT1G69560.1	<i>AtMYB105</i>
<i>MYB208</i>	Potri.019G118200	Chr19	GO:0003677	KOG0048	AT1G08810.1	<i>AtMYB60</i>
<i>MYB209</i>	Potri.019G118700	Chr19	GO:0003677	KOG0048	AT5G16770.1	<i>AtMYB9</i>
<i>MYB210</i>	Potri.019G118800	Chr19	GO:0003677	KOG0048	AT1G22640.1	<i>AtMYB3</i>
<i>MYB211</i>	Potri.019G118900	Chr19	GO:0003677	KOG0048	AT4G21440.1	<i>AtMYB102</i>
<i>MYB212</i>	Potri.T011400	Chr19	GO:0003677	KOG0048	AT5G16770.1	<i>AtMYB9</i>
<i>MYB213</i>	Potri.T125000	Chr19	GO:0003677	KOG0048	AT5G16770.1	<i>AtMYB9</i>
<i>MYB214</i>	Potri.T144800	Chr19	GO:0003677	KOG0048	AT1G79180.1	<i>AtMYB63</i>
<i>MYB215</i>	Potri.001G005100	scaffold_25	GO:0003677	KOG0048	AT4G38620.1	<i>AtMYB4</i>
<i>MYB216</i>	Potri.001G035800	scaffold_221	GO:0003677	KOG0048	AT3G30210.1	<i>AtMYB121</i>
<i>MYB217</i>	Potri.001G036000	scaffold_408	GO:0003677	KOG0048	AT4G38620.1	<i>AtMYB4</i>

Table S4. Number of *R2R3-MYB* genes in each module.

Module	<i>R2R3-MYB</i> gene number	<i>R2R3-MYB</i> gene list
Black	7	<i>MYB044; MYB087; MYB101; MYB146; MYB151;</i> <i>MYB185; MYB208</i>
Blue	12	<i>MYB009; MYB012; MYB059; MYB064; MYB072;</i> <i>MYB073; MYB080; MYB108; MYB115; MYB163;</i> <i>MYB171; MYB187</i>
Brown	8	<i>MYB003; MYB074; MYB091; MYB128; MYB147;</i> <i>MYB168; MYB196; MYB204</i>
Cyan	1	<i>MYB079</i>
Dark grey	5	<i>MYB078; MYB082; MYB156; MYB195; MYB214</i>
Dark orange	1	<i>MYB069</i>
Green	7	<i>MYB032; MYB047; MYB092; MYB099; MYB102;</i> <i>MYB142; MYB210</i>
Green yellow	7	<i>MYB016; MYB033; MYB063; MYB112; MYB120;</i> <i>MYB138; MYB143</i>
Grey	14	<i>MYB050; MYB055; MYB066; MYB071; MYB084;</i> <i>MYB110; MYB114; MYB127; MYB133; MYB150;</i> <i>MYB152; MYB157; MYB164; MYB215</i>
Grey60	1	<i>MYB049</i>
Light cyan	3	<i>MYB086; MYB162; MYB202</i>
Magenta	2	<i>MYB014; MYB179</i>
Orange	3	<i>MYB013; MYB109; MYB123</i>
Purple	3	<i>MYB100; MYB104; MYB137</i>
Red	1	<i>MYB002</i>
Saddle brown	1	<i>MYB028</i>
Sienna3	1	<i>MYB149</i>
Sky blue	1	<i>MYB023</i>
Steel blue	1	<i>MYB121</i>
Tan	4	<i>MYB001; MYB051; MYB056; MYB183</i>
Turquoise	5	<i>MYB077; MYB081; MYB118; MYB140; MYB193</i>
White	2	<i>MYB062; MYB093</i>
Yellow	7	<i>MYB011; MYB024; MYB046; MYB057; MYB129;</i> <i>MYB169; MYB194</i>

Table S5. MMs and ICs of *R2R3-MYB* genes in each module.

<i>R2R3-MYB</i> gene	Module	MM	MM <i>p</i> value	IC
<i>MYB044</i>	Black	0.627874724	8.54726×10^{-6}	3.427004152
<i>MYB087</i>	Black	0.671122407	1.14921×10^{-6}	2.763145536
<i>MYB101</i>	Black	0.566304327	9.26032×10^{-5}	1.171477162
<i>MYB146</i>	Black	0.648559262	3.40491×10^{-6}	6.579215683
<i>MYB151</i>	Black	0.865970139	1.31653×10^{-13}	17.73649977
<i>MYB185</i>	Black	0.692285279	3.79954×10^{-7}	8.891348023
<i>MYB208</i>	Black	0.750319452	1.05996×10^{-8}	7.066277215
<i>MYB062</i>	White	0.678540965	7.87712×10^{-7}	0.489775652
<i>MYB093</i>	White	0.745846493	1.44439×10^{-8}	0.783534373
<i>MYB014</i>	Magenta	0.558837968	0.000119795	0.947459378
<i>MYB179</i>	Magenta	0.637881088	5.52247×10^{-6}	2.037364064
<i>MYB069</i>	Dark orange	0.673595342	1.01446×10^{-6}	0.679365906
<i>MYB121</i>	Steel blue	0.904804413	2.03574×10^{-16}	4.389406567
<i>MYB009</i>	Blue	0.613309528	1.57167×10^{-5}	8.497728333
<i>MYB012</i>	Blue	0.626047181	9.24181×10^{-6}	0.829905505
<i>MYB059</i>	Blue	0.756646953	6.76563×10^{-9}	15.2612066
<i>MYB064</i>	Blue	0.43178415	0.004300036	0.959459586
<i>MYB072</i>	Blue	0.782213599	9.51352×10^{-10}	25.14181107
<i>MYB073</i>	Blue	0.763211875	4.1851×10^{-9}	9.472659372
<i>MYB080</i>	Blue	0.52067841	0.000407797	1.052434481
<i>MYB108</i>	Blue	0.647581022	3.56192×10^{-6}	3.363281016
<i>MYB115</i>	Blue	0.75733021	6.44025×10^{-9}	11.96338784
<i>MYB163</i>	Blue	0.569807756	8.18895×10^{-5}	1.690731541
<i>MYB171</i>	Blue	0.848230552	1.33213×10^{-12}	22.47055256
<i>MYB187</i>	Blue	0.904361183	2.22459×10^{-16}	54.19187082
<i>MYB077</i>	Turquoise	0.662704538	1.7419×10^{-6}	4.407770097
<i>MYB081</i>	Turquoise	0.674634488	9.62327×10^{-7}	12.2241848
<i>MYB118</i>	Turquoise	0.781580565	1.00182×10^{-9}	11.84263065
<i>MYB140</i>	Turquoise	0.632968001	6.85661×10^{-6}	6.321588442
<i>MYB193</i>	Turquoise	0.720784153	7.32169×10^{-8}	11.04833153
<i>MYB149</i>	Sienna3	0.727082616	4.95111×10^{-8}	0.783569409
<i>MYB078</i>	Dark grey	0.885749529	6.53023×10^{-15}	9.303088284
<i>MYB082</i>	Dark grey	0.64125458	4.7495×10^{-6}	1.275682224
<i>MYB156</i>	Dark grey	0.818967892	3.40094×10^{-11}	6.00625534
<i>MYB195</i>	Dark grey	0.842065172	2.78202×10^{-12}	7.616312535
<i>MYB214</i>	Dark grey	0.858531581	3.6092×10^{-13}	9.279992054
<i>MYB016</i>	Green yellow	0.64811754	3.475×10^{-6}	2.610396418
<i>MYB033</i>	Green yellow	0.853808065	6.65017×10^{-13}	8.248200096
<i>MYB063</i>	Green yellow	0.658571509	2.12641×10^{-6}	3.254886124
<i>MYB112</i>	Green yellow	0.668417671	1.31541×10^{-6}	7.197803629
<i>MYB120</i>	Green yellow	0.841283983	3.04726×10^{-12}	7.522774903

MYB138	Green yellow	0.765045512	3.64962×10^{-9}	2.811832622
MYB143	Green yellow	0.650599848	3.09771×10^{-6}	7.052251591
MYB001	Tan	0.822748742	2.31442×10^{-11}	6.502160014
MYB051	Tan	0.664747826	1.57653×10^{-6}	0.846210199
MYB056	Tan	0.855966881	5.04304×10^{-13}	18.03535892
MYB183	Tan	0.513535281	0.000504893	0.258778325
MYB028	Saddle brown	0.683972041	5.93304×10^{-7}	0.318682777
MYB100	Purple	0.496613535	0.00082225	0.182491614
MYB104	Purple	0.505321012	0.000641773	0.44486522
MYB137	Purple	0.809318227	8.73506×10^{-11}	5.771470494
MYB011	Yellow	0.499643351	0.000754882	1.15363062
MYB024	Yellow	0.758543616	5.89815×10^{-9}	21.6127707
MYB046	Yellow	0.520234654	0.0004133	1.469734894
MYB057	Yellow	-0.676471503	8.76182×10^{-7}	2.822597637
MYB129	Yellow	0.746125485	1.41704×10^{-8}	7.43202027
MYB169	Yellow	0.91953606	8.10418×10^{-18}	72.80582519
MYB194	Yellow	0.821901673	2.52483×10^{-11}	43.12610329
MYB086	Light cyan	0.876147463	2.99211×10^{-14}	15.07189018
MYB162	Light cyan	0.845889234	1.76861×10^{-12}	19.16848834
MYB202	Light cyan	0.650749964	3.07615×10^{-6}	1.626475004
MYB003	Brown	0.611872665	1.66628×10^{-5}	1.951836834
MYB074	Brown	0.386196337	0.011531569	0.691630934
MYB091	Brown	0.775155927	1.67702×10^{-9}	18.34457102
MYB128	Brown	0.727383384	4.85817×10^{-8}	12.72568448
MYB147	Brown	0.849794757	1.09941×10^{-12}	22.93717879
MYB168	Brown	0.832724208	8.01376×10^{-12}	16.72255939
MYB196	Brown	0.672047291	1.09699×10^{-6}	4.475039914
MYB204	Brown	0.82668119	1.53587×10^{-11}	21.19399754
MYB079	Cyan	0.847831677	1.39849×10^{-12}	4.094024561
MYB002	Red	0.531120952	0.000295876	1.25309318
MYB032	Green	0.695425926	3.19843×10^{-7}	11.19969889
MYB047	Green	0.652183719	2.8771×10^{-6}	3.650958675
MYB092	Green	0.382589649	0.012398762	0.121792178
MYB099	Green	0.693972145	3.46478×10^{-7}	9.400057022
MYB102	Green	0.682983199	6.25003×10^{-7}	6.937926254
MYB142	Green	-0.702201488	2.18943×10^{-7}	5.117675703
MYB210	Green	0.706820406	1.6807×10^{-7}	13.91098084
MYB049	Grey60	0.864654156	1.58049×10^{-13}	7.450822935
MYB013	Orange	0.678467242	7.90716×10^{-7}	1.504720346
MYB109	Orange	0.816284534	4.44536×10^{-11}	2.894595267
MYB123	Orange	0.920719564	6.09298×10^{-18}	9.832437567
MYB023	Sky blue	0.802831327	1.59918×10^{-10}	2.333643224

Table S6. Top 10 pathways for genes that *R2R3-MYB* genes had weight values with in each module.

Module	KEGG A class	KEGG B class	Pathway	Count	Pathway ID
Black	Metabolism	Global and overview maps	Metabolic pathways	66	ko01100
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	38	ko01110
	Environmental Information Processing	Signal transduction	Plant hormone signal transduction	21	ko04075
	Organismal Systems	Environmental adaptation	Plant-pathogen interaction	9	ko04626
	Metabolism	Biosynthesis of other secondary metabolites	Phenylpropanoid biosynthesis	8	ko00940
	Cellular Processes	Transport and catabolism	Endocytosis	8	ko04144
	Metabolism	Carbohydrate metabolism	Pentose and glucuronate interconversions	7	ko00040
	Metabolism	Carbohydrate metabolism	Starch and sucrose metabolism	7	ko00500
	Metabolism	Lipid metabolism	Cutin, suberine and wax biosynthesis	6	ko00073
	Metabolism	Lipid metabolism	Glycerophospholipid metabolism	5	ko00564
White	Metabolism	Global and overview maps	Metabolic pathways	2	ko01100
	Metabolism	Energy metabolism	Photosynthesis - antenna proteins	1	ko00196
	Metabolism	Carbohydrate metabolism	Starch and sucrose metabolism	1	ko00500
Magenta	Metabolism	Global and overview maps	Metabolic pathways	19	ko01100
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	12	ko01110
	Genetic Information Processing	Translation	mRNA surveillance pathway	3	ko03015
	Organismal Systems	Environmental adaptation	Plant-pathogen interaction	3	ko04626
	Metabolism	Carbohydrate metabolism	Glycolysis / Gluconeogenesis	2	ko00010
	Metabolism	Carbohydrate metabolism	Starch and sucrose metabolism	2	ko00500
	Metabolism	Metabolism of cofactors and vitamins	Vitamin B6 metabolism	2	ko00750
	Metabolism	Metabolism of terpenoids and polyketides	Zeatin biosynthesis	2	ko00908
	Metabolism	Biosynthesis of other secondary metabolites	Phenylpropanoid biosynthesis	2	ko00940
	Metabolism	Biosynthesis of other secondary metabolites	Flavonoid biosynthesis	2	ko00941
Dark orange	Metabolism	Global and overview maps	Metabolic pathways	2	ko01100
	Metabolism	Amino acid metabolism	Arginine and proline metabolism	1	ko00330
	Metabolism	Metabolism of cofactors and vitamins	Riboflavin metabolism	1	ko00740
	Metabolism	Metabolism of cofactors and vitamins	Folate biosynthesis	1	ko00790
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	1	ko01110
Steel blue	Metabolism	Global and overview maps	Metabolic pathways	23	ko01100
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	15	ko01110
	Metabolism	Global and overview maps	Biosynthesis of amino acids	4	ko01230
	Metabolism	Metabolism of terpenoids and polyketides	Terpenoid backbone biosynthesis	3	ko00900
	Metabolism	Global and overview maps	Carbon metabolism	3	ko01200
	Metabolism	Lipid metabolism	alpha-Linolenic acid metabolism	2	ko00592
	Metabolism	Lipid metabolism	Sphingolipid metabolism	2	ko00600
	Metabolism	Carbohydrate metabolism	Glyoxylate and dicarboxylate metabolism	2	ko00630
	Metabolism	Biosynthesis of other secondary metabolites	Phenylpropanoid biosynthesis	2	ko00940
	Metabolism	Biosynthesis of other secondary metabolites	Isoflavonoid biosynthesis	2	ko00943
Blue	Metabolism	Global and overview maps	Metabolic pathways	168	ko01100
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	68	ko01110

	Environmental Information	Signal transduction	Plant hormone signal transduction	28	ko04075
	Processing				
	Metabolism	Carbohydrate metabolism	Pentose and glucuronate interconversions	25	ko00040
	Metabolism	Carbohydrate metabolism	Starch and sucrose metabolism	25	ko00500
	Environmental Information	Signal transduction	MAPK signaling pathway - plant	19	ko04016
	Processing				
	Metabolism	Carbohydrate metabolism	Amino sugar and nucleotide sugar metabolism	14	ko00520
	Genetic Information Processing	Translation	mRNA surveillance pathway	14	ko03015
	Metabolism	Biosynthesis of other secondary metabolites	Phenylpropanoid biosynthesis	11	ko00940
	Metabolism	Global and overview maps	Carbon metabolism	11	ko01200
Turquoise	Metabolism	Global and overview maps	Metabolic pathways	61	ko01100
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	39	ko01110
	Metabolism	Global and overview maps	Carbon metabolism	9	ko01200
	Genetic Information Processing	Folding, sorting and degradation	RNA degradation	8	ko03018
	Metabolism	Carbohydrate metabolism	Starch and sucrose metabolism	7	ko00500
	Environmental Information	Signal transduction	Plant hormone signal transduction	7	ko04075
	Processing				
	Metabolism	Global and overview maps	Biosynthesis of amino acids	6	ko01230
	Metabolism	Carbohydrate metabolism	Glycolysis / Gluconeogenesis	5	ko00010
	Metabolism	Carbohydrate metabolism	Pentose phosphate pathway	5	ko00030
Sienna 3	Metabolism	Amino acid metabolism	Cysteine and methionine metabolism	5	ko00270
	Metabolism	Global and overview maps	Metabolic pathways	5	ko01100
	Metabolism	Lipid metabolism	Ether lipid metabolism	2	ko00565
	Metabolism	Lipid metabolism	Sphingolipid metabolism	2	ko00600
	Metabolism	Amino acid metabolism	Tryptophan metabolism	1	ko00380
	Metabolism	Lipid metabolism	Glycerolipid metabolism	1	ko00561
	Metabolism	Carbohydrate metabolism	Glyoxylate and dicarboxylate metabolism	1	ko00630
	Metabolism	Carbohydrate metabolism	Butanoate metabolism	1	ko00650
	Metabolism	Global and overview maps	Carbon metabolism	1	ko01200
	Metabolism	Global and overview maps	Metabolic pathways	39	ko01100
Dark grey	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	28	ko01110
	Metabolism	Global and overview maps	Biosynthesis of amino acids	11	ko01230
	Metabolism	Amino acid metabolism	Phenylalanine, tyrosine and tryptophan biosynthesis	9	ko00400
	Cellular Processes	Transport and catabolism	Peroxisome	8	ko04146
	Metabolism	Amino acid metabolism	Tryptophan metabolism	7	ko00380
	Metabolism	Biosynthesis of other secondary metabolites	Phenylpropanoid biosynthesis	6	ko00940
	Metabolism	Biosynthesis of other secondary metabolites	Isoflavonoid biosynthesis	5	ko00943
	Metabolism	Amino acid metabolism	Arginine and proline metabolism	4	ko00330
	Metabolism	Biosynthesis of other secondary metabolites	Flavonoid biosynthesis	4	ko00941
	Metabolism	Global and overview maps	Metabolic pathways	52	ko01100
Green yellow	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	28	ko01110
	Organismal Systems	Environmental adaptation	Circadian rhythm - plant	23	ko04712

	Genetic Information Processing	Folding, sorting and degradation	Ubiquitin mediated proteolysis	8	ko04120
	Metabolism	Biosynthesis of other secondary metabolites	Phenylpropanoid biosynthesis	7	ko00940
	Metabolism	Carbohydrate metabolism	Amino sugar and nucleotide sugar metabolism	6	ko00520
	Metabolism	Carbohydrate metabolism	Fructose and mannose metabolism	5	ko00051
	Metabolism	Carbohydrate metabolism	Starch and sucrose metabolism	5	ko00500
	Metabolism	Metabolism of terpenoids and polyketides	Terpenoid backbone biosynthesis	5	ko00900
	Metabolism	Global and overview maps	Carbon metabolism	5	ko01200
	Metabolism	Global and overview maps	Metabolic pathways	71	ko01100
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	55	ko01110
	Metabolism	Global and overview maps	Carbon metabolism	22	ko01200
Tan	Metabolism	Carbohydrate metabolism	Glyoxylate and dicarboxylate metabolism	11	ko00630
	Metabolism	Energy metabolism	Carbon fixation in photosynthetic organisms	11	ko00710
	Environmental Information Processing	Signal transduction	Plant hormone signal transduction	11	ko04075
	Metabolism	Global and overview maps	Biosynthesis of amino acids	10	ko01230
	Cellular Processes	Transport and catabolism	Peroxisome	9	ko04146
	Metabolism	Carbohydrate metabolism	Glycolysis / Gluconeogenesis	8	ko00010
	Metabolism	Amino acid metabolism	Glycine, serine and threonine metabolism	8	ko00260
	Metabolism	Global and overview maps	Metabolic pathways	14	ko01100
	Environmental Information Processing	Signal transduction	MAPK signaling pathway - plant	11	ko04016
	Organismal Systems	Environmental adaptation	Plant-pathogen interaction	11	ko04626
Purple	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	6	ko01110
	Metabolism	Carbohydrate metabolism	Amino sugar and nucleotide sugar metabolism	5	ko00520
	Metabolism	Metabolism of other amino acids	Glutathione metabolism	4	ko00480
	Environmental Information Processing	Signal transduction	Plant hormone signal transduction	4	ko04075
	Genetic Information Processing	Folding, sorting and degradation	Protein processing in endoplasmic reticulum	4	ko04141
	Metabolism	Biosynthesis of other secondary metabolites	Phenylpropanoid biosynthesis	3	ko00940
	Genetic Information Processing	Folding, sorting and degradation	Protein export	3	ko03060
	Metabolism	Global and overview maps	Metabolic pathways	248	ko01100
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	136	ko01110
	Organismal Systems	Environmental adaptation	Plant-pathogen interaction	56	ko04626
Yellow	Environmental Information Processing	Signal transduction	MAPK signaling pathway - plant	41	ko04016
	Metabolism	Biosynthesis of other secondary metabolites	Phenylpropanoid biosynthesis	39	ko00940
	Metabolism	Carbohydrate metabolism	Starch and sucrose metabolism	31	ko00500
	Metabolism	Carbohydrate metabolism	Amino sugar and nucleotide sugar metabolism	28	ko00520
	Genetic Information Processing	Folding, sorting and degradation	Protein processing in endoplasmic reticulum	28	ko04141
	Environmental Information Processing	Signal transduction	Plant hormone signal transduction	27	ko04075

	Metabolism	Global and overview maps	Carbon metabolism	21	ko01200
	Metabolism	Global and overview maps	Metabolic pathways	82	ko01100
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	61	ko01110
	Metabolism	Biosynthesis of other secondary metabolites	Flavonoid biosynthesis	25	ko00941
	Organismal Systems	Environmental adaptation	Plant-pathogen interaction	15	ko04626
	Metabolism	Biosynthesis of other secondary metabolites	Phenylpropanoid biosynthesis	9	ko00940
Light cyan	Metabolism	Global and overview maps	Biosynthesis of amino acids	9	ko01230
	Metabolism	Global and overview maps	Carbon metabolism	7	ko01200
	Environmental Information	Signal transduction	MAPK signaling pathway - plant	7	ko04016
	Processing				
	Metabolism	Energy metabolism	Oxidative phosphorylation	6	ko00190
	Environmental Information	Membrane transport	ABC transporters	6	ko02010
	Processing				
	Genetic Information Processing	Translation	RNA transport	46	ko03013
	Genetic Information Processing	Transcription	Spliceosome	43	ko03040
	Metabolism	Global and overview maps	Metabolic pathways	36	ko01100
	Genetic Information Processing	Translation	mRNA surveillance pathway	36	ko03015
Brown	Genetic Information Processing	Folding, sorting and degradation	RNA degradation	28	ko03018
	Genetic Information Processing	Folding, sorting and degradation	Ubiquitin mediated proteolysis	17	ko04120
	Cellular Processes	Transport and catabolism	Endocytosis	16	ko04144
	Genetic Information Processing	Translation	Ribosome biogenesis in eukaryotes	13	ko03008
	Genetic Information Processing	Folding, sorting and degradation	Protein processing in endoplasmic reticulum	13	ko04141
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	12	ko01110
	Metabolism	Global and overview maps	Metabolic pathways	5	ko01100
	Metabolism	Lipid metabolism	Fatty acid biosynthesis	2	ko00061
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	2	ko01110
	Metabolism	Global and overview maps	Fatty acid metabolism	2	ko01212
Cyan	Genetic Information Processing	Folding, sorting and degradation	RNA degradation	2	ko03018
	Cellular Processes	Transport and catabolism	Peroxisome	2	ko04146
	Metabolism	Carbohydrate metabolism	Citrate cycle (TCA cycle)	1	ko00020
	Metabolism	Lipid metabolism	Fatty acid degradation	1	ko00071
	Metabolism	Amino acid metabolism	Cysteine and methionine metabolism	1	ko00270
	Metabolism	Amino acid metabolism	Valine, leucine and isoleucine degradation	1	ko00280
	Genetic Information Processing	Translation	Ribosome	19	ko03010
	Genetic Information Processing	Translation	RNA transport	6	ko03013
Red	Genetic Information Processing	Translation	Aminoacyl-tRNA biosynthesis	3	ko00970
	Genetic Information Processing	Translation	mRNA surveillance pathway	2	ko03015
	Genetic Information Processing	Translation	Ribosome biogenesis in eukaryotes	1	ko03008
	Genetic Information Processing	Transcription	Spliceosome	1	ko03040
	Metabolism	Global and overview maps	Metabolic pathways	111	ko01100
Green	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	63	ko01110
	Metabolism	Global and overview maps	Carbon metabolism	28	ko01200
	Metabolism	Global and overview maps	Biosynthesis of amino acids	18	ko01230

	Environmental Information	Signal transduction	Plant hormone signal transduction	16	ko04075
	Processing				
	Metabolism	Amino acid metabolism	Cysteine and methionine metabolism	13	ko00270
	Metabolism	Carbohydrate metabolism	Glycolysis / Gluconeogenesis	12	ko00010
	Metabolism	Amino acid metabolism	Valine, leucine and isoleucine degradation	11	ko00280
	Metabolism	Amino acid metabolism	Arginine and proline metabolism	11	ko00330
	Metabolism	Carbohydrate metabolism	Galactose metabolism	9	ko00052
	Metabolism	Global and overview maps	Metabolic pathways	19	ko01100
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	12	ko01110
	Environmental Information	Signal transduction	Plant hormone signal transduction	8	ko04075
	Processing				
	Metabolism	Carbohydrate metabolism	Starch and sucrose metabolism	7	ko00500
Grey 60	Environmental Information	Signal transduction	MAPK signaling pathway - plant	6	ko04016
	Processing				
	Genetic Information Processing	Folding, sorting and degradation	Ubiquitin mediated proteolysis	4	ko04120
	Organismal Systems	Environmental adaptation	Plant-pathogen interaction	4	ko04626
	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis	3	ko00906
	Metabolism	Global and overview maps	Carbon metabolism	3	ko01200
	Metabolism	Amino acid metabolism	Cysteine and methionine metabolism	2	ko00270
	Metabolism	Global and overview maps	Metabolic pathways	21	ko01100
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	12	ko01110
	Metabolism	Metabolism of other amino acids	Glutathione metabolism	4	ko00480
	Metabolism	Carbohydrate metabolism	Starch and sucrose metabolism	3	ko00500
Orange	Genetic Information Processing	Folding, sorting and degradation	Ubiquitin mediated proteolysis	3	ko04120
	Metabolism	Carbohydrate metabolism	Galactose metabolism	2	ko00052
	Metabolism	Carbohydrate metabolism	Ascorbate and aldarate metabolism	2	ko00053
	Metabolism	Lipid metabolism	Fatty acid biosynthesis	2	ko00061
	Metabolism	Amino acid metabolism	Cysteine and methionine metabolism	2	ko00270
	Metabolism	Amino acid metabolism	Arginine and proline metabolism	2	ko00330
	Genetic Information Processing	Folding, sorting and degradation	Proteasome	28	ko03050
	Genetic Information Processing	Folding, sorting and degradation	Protein processing in endoplasmic reticulum	2	ko04141
	Metabolism	Carbohydrate metabolism	Glycolysis / Gluconeogenesis	1	ko00010
	Metabolism	Nucleotide metabolism	Purine metabolism	1	ko00230
Sky blue	Metabolism	Carbohydrate metabolism	Pyruvate metabolism	1	ko00620
	Metabolism	Global and overview maps	Metabolic pathways	1	ko01100
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	1	ko01110
	Metabolism	Global and overview maps	Carbon metabolism	1	ko01200
	Metabolism	Global and overview maps	Biosynthesis of amino acids	1	ko01230

Table S7. Differentially expressed *R2R3-MYB* genes.

<i>R2R3-MYB</i> gene	<i>P. trichocarpa</i> gene ID for R2R3-MYB	Module	‘Intolerant’		‘Tolerant 2’		‘Tolerant 2’	
			$\log_2(\text{E4-inoculated/E4-free})$		$\log_2(\text{E4-inoculated/E4-free})$		$\log_2(\text{E4-inoculated/E4-free})$	
			2 dpi	4 dpi	2 dpi	4 dpi	2 dpi	4 dpi
<i>MYB146</i>	Potri.013G001000	Black	0.20	-1.24	-1.43	1.33	-0.55	1.20
<i>MYB069</i>	Potri.005G224100	Dark orange	0.28	0.90	1.00	1.13	1.46	1.43
<i>MYB121</i>	Potri.010G123000	Steel blue	0.70	1.04	-3.92	4.18	1.22	8.58
<i>MYB064</i>	Potri.005G112000	Blue	0.11	-0.85	0.03	1.80	0.40	2.41
<i>MYB080</i>	Potri.006G234200	Blue	0.04	-0.23	-0.86	2.02	-0.07	1.27
<i>MYB063</i>	Potri.005G096600	Green yellow	-0.40	-0.32	5.21	0.42	1.04	-0.35
<i>MYB104</i>	Potri.008G166700	Purple	0.97	0.22	-0.24	7.32	4.83	3.83
<i>MYB137</i>	Potri.012G055600	Purple	-0.10	0.42	0.22	1.92	1.72	2.05
<i>MYB011</i>	Potri.001G219100	Yellow	0.34	0.32	-1.17	4.39	1.63	2.58
<i>MYB024</i>	Potri.002G038500	Yellow	0.16	0.65	1.44	3.59	4.08	4.73
<i>MYB046</i>	Potri.003G189700	Yellow	0.04	0.18	1.32	1.08	1.14	1.04
<i>MYB129</i>	Potri.010G240800	Yellow	0.07	0.39	0.20	2.36	1.13	1.50
<i>MYB169</i>	Potri.015G046200	Yellow	-0.32	1.23	1.33	2.36	2.68	2.30
<i>MYB194</i>	Potri.017G130300	Yellow	0.26	-0.12	0.69	2.75	1.59	2.37
<i>MYB086</i>	Potri.007G067600	Light cyan	-0.55	-0.70	6.25	3.39	-2.42	4.00
<i>MYB099</i>	Potri.008G101400	Green	-0.01	1.31	1.77	0.57	1.28	0.09
<i>MYB101</i>	Potri.008G128500	Black	0.00	-0.24	-1.22	-1.41	-1.19	-1.21
<i>MYB077</i>	Potri.006G221200	Turquoise	0.28	-0.74	-1.58	-1.03	-0.52	-2.33
<i>MYB118</i>	Potri.010G093000	Turquoise	0.00	-0.27	-0.14	-1.47	-0.28	-1.03
<i>MYB140</i>	Potri.012G080400	Turquoise	0.26	-0.76	-1.58	-1.85	-0.29	-2.31
<i>MYB078</i>	Potri.006G221500	Dark grey	0.10	-0.74	-0.08	-3.72	-2.15	-3.45
<i>MYB082</i>	Potri.006G275900	Dark grey	0.23	-0.47	-0.74	-3.79	-0.71	-3.98
<i>MYB156</i>	Potri.013G149200	Dark grey	-0.19	-0.86	-1.87	-5.64	-1.59	-4.67
<i>MYB195</i>	Potri.018G005300	Dark grey	0.01	-1.11	-1.17	-2.56	-1.12	-2.35
<i>MYB214</i>	Potri.019G118900	Dark grey	1.45	0.20	-1.02	-3.57	-2.24	-3.41
<i>MYB112</i>	Potri.009G053900	Green yellow	-0.41	-0.73	1.18	-1.81	-1.12	-3.06
<i>MYB051</i>	Potri.004G088100	Tan	0.16	-0.34	-1.95	-0.93	-1.36	-1.65
<i>MYB183</i>	Potri.017G082500	Tan	-0.07	0.12	0.40	-1.03	0.01	-1.33
<i>MYB162</i>	Potri.014G100800	Light cyan	-0.23	-0.08	0.57	-1.82	-0.13	-1.68
<i>MYB202</i>	Potri.018G127700	Light cyan	-0.19	-0.28	-1.24	-1.06	-1.08	-1.93
<i>MYB074</i>	Potri.006G122100	Brown	-0.14	0.25	-0.20	-1.21	-0.07	-1.19
<i>MYB079</i>	Potri.006G221800	Cyan	-0.12	-0.60	-0.14	-2.19	-0.23	-2.44
<i>MYB032</i>	Potri.002G173900	Green	0.10	0.14	-1.91	-2.95	0.15	-2.85
<i>MYB049</i>	Potri.004G033100	Grey 60	-0.26	0.63	-0.04	-2.81	1.24	-5.11

Table S8. Top 10 pathways for genes that differently expressed *R2R3-MYB* genes had weight values with in each module.

Module	KEGG A class	KEGG B class	Pathway	Count	Pathway ID
Black	Metabolism	Global and overview maps	Metabolic pathways	34	ko01100
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	18	ko01110
	Environmental Information Processing	Signal transduction	Plant hormone signal transduction	7	ko04075
	Metabolism	Biosynthesis of other secondary metabolites	Phenylpropanoid biosynthesis	6	ko00940
	Metabolism	Carbohydrate metabolism	Starch and sucrose metabolism	5	ko00500
	Metabolism	Lipid metabolism	Cutin, suberine and wax biosynthesis	5	ko00073
	Organismal Systems	Environmental adaptation	Plant-pathogen interaction	4	ko04626
	Genetic Information Processing	Translation	Ribosome	4	ko03010
	Metabolism	Biosynthesis of other secondary metabolites	Flavonoid biosynthesis	3	ko00941
	Metabolism	Carbohydrate metabolism	Pentose and glucuronate interconversions	3	ko00040
Dark orange	Metabolism	Global and overview maps	Metabolic pathways	2	ko01100
	Metabolism	Amino acid metabolism	Arginine and proline metabolism	1	ko00330
	Metabolism	Metabolism of cofactors and vitamins	Riboflavin metabolism	1	ko00740
	Metabolism	Metabolism of cofactors and vitamins	Folate biosynthesis	1	ko00790
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	1	ko01110
Steel blue	Metabolism	Global and overview maps	Metabolic pathways	23	ko01100
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	15	ko01110
	Metabolism	Global and overview maps	Biosynthesis of amino acids	4	ko01230
	Metabolism	Metabolism of terpenoids and polyketides	Terpenoid backbone biosynthesis	3	ko00900
	Metabolism	Global and overview maps	Carbon metabolism	3	ko01200
	Metabolism	Lipid metabolism	alpha-Linolenic acid metabolism	2	ko00592
	Metabolism	Lipid metabolism	Sphingolipid metabolism	2	ko00600
	Metabolism	Carbohydrate metabolism	Glyoxylate and dicarboxylate metabolism	2	ko00630
	Metabolism	Biosynthesis of other secondary metabolites	Phenylpropanoid biosynthesis	2	ko00940
	Metabolism	Biosynthesis of other secondary metabolites	Isoflavonoid biosynthesis	2	ko00943
Blue	Metabolism	Global and overview maps	Metabolic pathways	3	ko01100
	Metabolism	Carbohydrate metabolism	Amino sugar and nucleotide sugar metabolism	2	ko00520
	Metabolism	Energy metabolism	Photosynthesis	1	ko00195
	Genetic Information Processing	Translation	Ribosome	1	ko03010
	Genetic Information Processing	Translation	mRNA surveillance pathway	1	ko03015
Turquoise	Cellular Processes	Transport and catabolism	Phagosome	1	ko04145
	Metabolism	Global and overview maps	Metabolic pathways	34	ko01100
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	22	ko01110
	Metabolism	Global and overview maps	Carbon metabolism	7	ko01200
	Genetic Information Processing	Folding, sorting and degradation	RNA degradation	6	ko03018
	Metabolism	Carbohydrate metabolism	Starch and sucrose metabolism	5	ko00500
	Metabolism	Global and overview maps	Biosynthesis of amino acids	5	ko01230
	Metabolism	Carbohydrate metabolism	Pentose phosphate pathway	4	ko00030

	Environmental Information		Signal transduction	Plant hormone signal transduction	4	ko04075
	Processing					
	Metabolism	Carbohydrate metabolism	Glycolysis / Gluconeogenesis		3	ko00010
	Metabolism	Nucleotide metabolism	Purine metabolism		3	ko00230
Dark grey	Metabolism	Global and overview maps	Metabolic pathways		39	ko01100
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites		28	ko01110
	Metabolism	Global and overview maps	Biosynthesis of amino acids		11	ko01230
	Metabolism	Amino acid metabolism	Phenylalanine, tyrosine and tryptophan biosynthesis		9	ko00400
	Cellular Processes	Transport and catabolism	Peroxisome		8	ko04146
	Metabolism	Amino acid metabolism	Tryptophan metabolism		7	ko00380
	Metabolism	Biosynthesis of other secondary metabolites	Phenylpropanoid biosynthesis		6	ko00940
	Metabolism	Biosynthesis of other secondary metabolites	Isoflavonoid biosynthesis		5	ko00943
	Metabolism	Amino acid metabolism	Arginine and proline metabolism		4	ko00330
	Metabolism	Biosynthesis of other secondary metabolites	Flavonoid biosynthesis		4	ko00941
Green yellow	Metabolism	Global and overview maps	Metabolic pathways		19	ko01100
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites		11	ko01110
	Metabolism	Carbohydrate metabolism	Amino sugar and nucleotide sugar metabolism		6	ko00520
	Cellular Processes	Transport and catabolism	Phagosome		5	ko04145
	Metabolism	Carbohydrate metabolism	Pentose and glucuronate interconversions		3	ko00040
	Metabolism	Carbohydrate metabolism	Ascorbate and aldarate metabolism		3	ko00053
	Metabolism	Carbohydrate metabolism	Starch and sucrose metabolism		3	ko00500
	Metabolism	Biosynthesis of other secondary metabolites	Phenylpropanoid biosynthesis		3	ko00940
	Metabolism	Biosynthesis of other secondary metabolites	Flavonoid biosynthesis		3	ko00941
	Metabolism	Carbohydrate metabolism	Glycolysis / Gluconeogenesis		2	ko00010
Tan	Metabolism	Biosynthesis of other secondary metabolites	Phenylpropanoid biosynthesis		1	ko00940
	Metabolism	Global and overview maps	Metabolic pathways		1	ko01100
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites		1	ko01110
	Genetic Information Processing	Folding, sorting and degradation	Proteasome		1	ko03050
Purple	Metabolism	Global and overview maps	Metabolic pathways		14	ko01100
	Environmental Information		Signal transduction	MAPK signaling pathway - plant	11	ko04016
	Processing					
	Organismal Systems	Environmental adaptation	Plant-pathogen interaction		11	ko04626
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites		6	ko01110
	Metabolism	Carbohydrate metabolism	Amino sugar and nucleotide sugar metabolism		5	ko00520
	Metabolism	Metabolism of other amino acids	Glutathione metabolism		4	ko00480
	Environmental Information		Signal transduction	Plant hormone signal transduction	4	ko04075
	Processing					
	Genetic Information Processing	Folding, sorting and degradation	Protein processing in endoplasmic reticulum		4	ko04141
	Metabolism	Biosynthesis of other secondary metabolites	Phenylpropanoid biosynthesis		3	ko00940
	Genetic Information Processing	Folding, sorting and degradation	Protein export		3	ko03060
Yellow	Metabolism	Global and overview maps	Metabolic pathways		248	ko01100

	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	136	ko01110
	Organismal Systems	Environmental adaptation	Plant-pathogen interaction	56	ko04626
	Environmental Information Processing	Signal transduction	MAPK signaling pathway - plant	41	ko04016
	Metabolism	Biosynthesis of other secondary metabolites	Phenylpropanoid biosynthesis	39	ko00940
	Metabolism	Carbohydrate metabolism	Starch and sucrose metabolism	31	ko00500
	Metabolism	Carbohydrate metabolism	Amino sugar and nucleotide sugar metabolism	28	ko00520
	Genetic Information Processing	Folding, sorting and degradation	Protein processing in endoplasmic reticulum	28	ko04141
	Environmental Information Processing	Signal transduction	Plant hormone signal transduction	27	ko04075
	Metabolism	Global and overview maps	Carbon metabolism	21	ko01200
Light cyan	Metabolism	Global and overview maps	Metabolic pathways	82	ko01100
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	61	ko01110
	Metabolism	Biosynthesis of other secondary metabolites	Flavonoid biosynthesis	25	ko00941
	Organismal Systems	Environmental adaptation	Plant-pathogen interaction	15	ko04626
	Metabolism	Biosynthesis of other secondary metabolites	Phenylpropanoid biosynthesis	9	ko00940
	Metabolism	Global and overview maps	Biosynthesis of amino acids	9	ko01230
	Metabolism	Global and overview maps	Carbon metabolism	7	ko01200
	Environmental Information Processing	Signal transduction	MAPK signaling pathway - plant	7	ko04016
	Metabolism	Energy metabolism	Oxidative phosphorylation	6	ko00190
	Environmental Information Processing	Membrane transport	ABC transporters	6	ko02010
Brown	Genetic Information Processing	Folding, sorting and degradation	RNA degradation	1	ko03018
	Genetic Information Processing	Replication and repair	Homologous recombination	1	ko03440
	Genetic Information Processing	Folding, sorting and degradation	Ubiquitin mediated proteolysis	1	ko04120
Cyan	Metabolism	Global and overview maps	Metabolic pathways	5	ko01100
	Metabolism	Lipid metabolism	Fatty acid biosynthesis	2	ko00061
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	2	ko01110
	Metabolism	Global and overview maps	Fatty acid metabolism	2	ko01212
	Genetic Information Processing	Folding, sorting and degradation	RNA degradation	2	ko03018
	Cellular Processes	Transport and catabolism	Peroxisome	2	ko04146
	Metabolism	Carbohydrate metabolism	Citrate cycle (TCA cycle)	1	ko00020
	Metabolism	Lipid metabolism	Fatty acid degradation	1	ko00071
	Metabolism	Amino acid metabolism	Cysteine and methionine metabolism	1	ko00270
	Metabolism	Amino acid metabolism	Valine, leucine and isoleucine degradation	1	ko00280
Green	Metabolism	Global and overview maps	Metabolic pathways	81	ko01100
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	44	ko01110
	Metabolism	Global and overview maps	Carbon metabolism	24	ko01200
	Metabolism	Global and overview maps	Biosynthesis of amino acids	13	ko01230
	Environmental Information Processing	Signal transduction	Plant hormone signal transduction	12	ko04075
	Metabolism	Carbohydrate metabolism	Glycolysis / Gluconeogenesis	10	ko00010

	Metabolism	Carbohydrate metabolism	Galactose metabolism	9	ko00052
	Metabolism	Amino acid metabolism	Cysteine and methionine metabolism	8	ko00270
	Metabolism	Carbohydrate metabolism	Starch and sucrose metabolism	8	ko00500
	Genetic Information Processing	Folding, sorting and degradation	Protein processing in endoplasmic reticulum	8	ko04141
	Metabolism	Global and overview maps	Metabolic pathways	19	ko01100
	Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	12	ko01110
	Environmental Information Processing	Signal transduction	Plant hormone signal transduction	8	ko04075
	Metabolism	Carbohydrate metabolism	Starch and sucrose metabolism	7	ko00500
	Environmental Information Processing	Signal transduction	MAPK signaling pathway - plant	6	ko04016
	Genetic Information Processing	Folding, sorting and degradation	Ubiquitin mediated proteolysis	4	ko04120
	Organismal Systems	Environmental adaptation	Plant-pathogen interaction	4	ko04626
	Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis	3	ko00906
	Metabolism	Global and overview maps	Carbon metabolism	3	ko01200
	Metabolism	Amino acid metabolism	Cysteine and methionine metabolism	2	ko00270

Grey 60

Table S9. Annotation of differently expressed *R2R3-MYB* genes related-genes that involved in poplar-E4 interaction in the selected modules.

Module	Pathway	MM	IC	Number		NR Description	Ortholog protein ID
				based	on IC		
Yellow	Plant-pathogen interaction	0.731667828	28.18601891	543		enhanced disease susceptibility 1 family protein [<i>Populus trichocarpa</i>]	XP_002322142.1
	Plant-pathogen interaction	0.920409544	73.66890421	200		PREDICTED: probable WRKY transcription factor 75 [<i>Populus euphratica</i>]	XP_011036106.1
	Plant-pathogen interaction	0.790612977	42.31868736	380		PREDICTED: probable leucine-rich repeat receptor-like protein kinase At1g35710 isoform X1 [<i>Populus euphratica</i>]	XP_011015511.1
	Plant-pathogen interaction	0.815077509	41.64267491	386		PREDICTED: LRR receptor-like serine/threonine-protein kinase FLS2 isoform X1 [<i>Populus euphratica</i>]	XP_011009761.1
	Plant-pathogen interaction	0.667695698	4.931313422	1208		PREDICTED: receptor-like protein 12 isoform X3 [<i>Populus euphratica</i>]	XP_011005453.1
	Plant-pathogen interaction	0.889471294	53.54928705	297		NBS-LRR type disease resistance protein [<i>Populus trichocarpa</i>]	ABF81442.1
	Plant-pathogen interaction	0.862561453	37.82865827	428		PREDICTED: disease resistance protein RPM1-like [<i>Populus euphratica</i>]	XP_011018453.1
	Plant-pathogen interaction	0.843737683	31.2957153	506		PREDICTED: disease resistance protein RPM1-like [<i>Populus euphratica</i>]	XP_011018453.1
	Plant-pathogen interaction	0.811863051	30.49046349	516		NBS-LRR type disease resistance protein [<i>Populus trichocarpa</i>]	ABF81442.1
	Plant-pathogen interaction	0.817070696	80.12273631	164		Pathogenesis-related family protein [<i>Populus trichocarpa</i>]	XP_002300292.2
	Plant-pathogen interaction	0.86679066	86.94001381	141		pathogenesis-related family protein [<i>Populus trichocarpa</i>]	XP_006379156.1
	Plant-pathogen interaction	0.807783874	65.26983883	237		pathogenesis related protein-1 [<i>Populus tomentosa</i>]	ADP69172.1
	Plant-pathogen interaction	0.784610472	23.47694776	626		pathogenesis-related family protein [<i>Populus trichocarpa</i>]	XP_002313936.2
	Plant-pathogen interaction	0.87124103	74.55316647	196		calcium-binding family protein [<i>Populus trichocarpa</i>]	XP_002306659.1
	Plant-pathogen interaction	0.924338746	82.70309515	151		calcium-binding family protein [<i>Populus trichocarpa</i>]	XP_002302215.1
	Plant-pathogen interaction	0.910754749	52.21008024	304		Calmodulin-like family protein [<i>Populus trichocarpa</i>]	XP_002323262.1
	Plant-pathogen interaction	0.771866458	19.32932604	699		calmodulin-like protein 6a [<i>Populus trichocarpa</i>]	XP_006382787.1
	Plant-pathogen interaction	0.878423746	33.9678179	479		PREDICTED: chitin elicitor receptor kinase 1-like isoform X1 [<i>Populus euphratica</i>]	XP_011007196.1
	Plant-pathogen interaction	0.802700927	51.63109975	305		PREDICTED: probable WRKY transcription factor 72 [<i>Populus euphratica</i>]	XP_011047157.1
	Plant-pathogen interaction	0.828369029	31.14320615	509		WRKY transcription factor 47 family protein [<i>Populus trichocarpa</i>]	XP_002302808.1
	Plant-pathogen interaction	0.847419889	46.26933536	341		calcium-dependent protein kinase [<i>Populus trichocarpa</i>]	XP_002308958.1
	Plant-pathogen interaction	0.643976498	5.920144683	1133		C2 domain-containing family protein [<i>Populus trichocarpa</i>]	XP_002298742.1
	Plant-pathogen interaction	0.812906595	17.18310314	745		calcium-dependent protein kinase 2 [<i>Populus trichocarpa</i>]	XP_002310978.1
	Plant-pathogen interaction	0.7475023	10.62517782	933		putative protein phosphatase [<i>Populus trichocarpa</i>]	XP_002305278.1
	Plant-pathogen interaction	0.913559135	118.2384071	32		K ⁺ rectifying channel family protein [<i>Populus trichocarpa</i>]	XP_002324257.1

Plant-pathogen interaction	0.814849558	22.49225624	641	hypersensitive reaction associated Ca ²⁺ -binding family protein [<i>Populus trichocarpa</i>]	XP_002312322.1
Plant-pathogen interaction	0.861358228	40.70620812	394	glycerol kinase family protein [<i>Populus trichocarpa</i>]	XP_006385291.1
MAPK signaling pathway - plant	0.518589069	1.937251373	1505	1-aminocyclopropane-1-carboxylate synthase [<i>Populus × canadensis</i>]	BAA94600.1
MAPK signaling pathway - plant	0.798081648	56.42464725	286	polygalacturonase inhibiting family protein [<i>Populus trichocarpa</i>]	XP_006381051.1
MAPK signaling pathway - plant	0.630398059	1.689317551	1533	kinase family protein [<i>Populus trichocarpa</i>]	XP_002301811.1
MAPK signaling pathway - plant	0.79909467	25.76591877	582	mitogen-activated protein kinase kinase [<i>Populus trichocarpa</i>]	XP_006374251.1
MAPK signaling pathway - plant	-0.626342368	2.161108756	1476	bZIP family transcription factor family protein [<i>Populus trichocarpa</i>]	XP_002304048.2
MAPK signaling pathway - plant	0.856081459	81.53406183	159	chitinase family protein [<i>Populus trichocarpa</i>]	XP_002306220.1
MAPK signaling pathway - plant	0.866493169	77.21039046	179	PREDICTED: pathogenesis-related protein PR-4-like isoform X2 [<i>Populus euphratica</i>]	XP_011038566.1
MAPK signaling pathway - plant	0.760667478	13.51184245	842	HEV1.2 family protein [<i>Populus trichocarpa</i>]	XP_002319076.1
MAPK signaling pathway - plant	0.825903067	24.23732173	615	Chain A family protein [<i>Populus trichocarpa</i>]	XP_002312923.2
MAPK signaling pathway - plant	0.817070696	80.12273631	164	Pathogenesis-related family protein [<i>Populus trichocarpa</i>]	XP_002300292.2
MAPK signaling pathway - plant	0.86679066	86.94001381	141	pathogenesis-related family protein [<i>Populus trichocarpa</i>]	XP_006379156.1
MAPK signaling pathway - plant	0.807783874	65.26983883	237	pathogenesis related protein-1 [<i>Populus tomentosa</i>]	ADP69172.1
MAPK signaling pathway - plant	0.784610472	23.47694776	626	pathogenesis-related family protein [<i>Populus trichocarpa</i>]	XP_002313936.2
MAPK signaling pathway - plant	0.802700927	51.63109975	305	PREDICTED: probable WRKY transcription factor 72 [<i>Populus euphratica</i>]	XP_011047157.1
MAPK signaling pathway - plant	0.828369029	31.14320615	509	WRKY transcription factor 47 family protein [<i>Populus trichocarpa</i>]	XP_002302808.1
MAPK signaling pathway - plant	0.777463046	19.53603974	690	catalase family protein [<i>Populus trichocarpa</i>]	XP_002306976.2
MAPK signaling pathway - plant	0.814849558	22.49225624	641	hypersensitive reaction associated Ca ²⁺ -binding family protein [<i>Populus trichocarpa</i>]	XP_002312322.1
Plant hormone signal transduction	0.703421135	5.414907325	1164	kinase family protein [<i>Populus trichocarpa</i>]	XP_002320126.1
Plant hormone signal transduction	0.752709001	34.12659493	476	hsr203J family protein [<i>Populus trichocarpa</i>]	XP_002297728.1
Plant hormone signal transduction	0.88292853	46.22514919	342	putative esterase family protein [<i>Populus trichocarpa</i>]	XP_002322442.1

Plant hormone signal transduction	0.400430536	0.84339733	1709	Two-component response regulator ARR8 family protein [<i>Populus trichocarpa</i>]	XP_002307983.2
Plant hormone signal transduction	0.875778741	35.5276817	461	PREDICTED: probable indole-3-acetic acid-amido synthetase GH3.6 [<i>Populus euphratica</i>]	XP_011033661.1
Plant hormone signal transduction	0.498614074	1.490555166	1583	auxin-responsive GH3 family protein [<i>Populus trichocarpa</i>]	XP_002300248.2
Plant hormone signal transduction	-0.625948872	2.027303877	1494	aux/IAA family protein [<i>Populus trichocarpa</i>]	XP_002315736.1
Plant hormone signal transduction	0.817070696	80.12273631	164	Pathogenesis-related family protein [<i>Populus trichocarpa</i>]	XP_002300292.2
Plant hormone signal transduction	0.86679066	86.94001381	141	pathogenesis-related family protein [<i>Populus trichocarpa</i>]	XP_006379156.1
Plant hormone signal transduction	0.807783874	65.26983883	237	pathogenesis related protein-1 [<i>Populus tomentosa</i>]	ADP69172.1
Plant hormone signal transduction	0.784610472	23.47694776	626	pathogenesis-related family protein [<i>Populus trichocarpa</i>]	XP_002313936.2
Flavonoid biosynthesis	0.763934585	38.01267983	426	pinorensin-laricresinol reductase family protein [<i>Populus trichocarpa</i>]	XP_006368316.1
Flavonoid biosynthesis	0.59538787	2.71519092	1412	oxidoreductase family protein [<i>Populus trichocarpa</i>]	XP_002315155.1
Flavonoid biosynthesis	0.893744069	58.20404986	276	PREDICTED: flavonol synthase/flavanone 3-hydroxylase-like [<i>Populus euphratica</i>]	XP_011038015.1
Flavonoid biosynthesis	0.759146135	18.58025451	723	caffeoyl-CoA O-methyltransferase family protein [<i>Populus trichocarpa</i>]	XP_002298729.1
Flavonoid biosynthesis	0.822044769	31.32271313	505	PREDICTED: flavanone 3-dioxygenase [<i>Populus euphratica</i>]	XP_011003288.1
Flavonoid biosynthesis	0.780783358	24.91547666	602	PREDICTED: flavanone 3-dioxygenase-like [<i>Populus euphratica</i>]	XP_011043760.1
Phenylpropanoid biosynthesis	0.897327324	103.0564442	80	eugenol O-methyltransferase family protein [<i>Populus trichocarpa</i>]	XP_002300513.1
Phenylpropanoid biosynthesis	0.848476816	30.31390747	518	Chain A family protein [<i>Populus trichocarpa</i>]	XP_002317838.1
Phenylpropanoid biosynthesis	0.892015801	71.91612723	207	cytochrome P450 family protein [<i>Populus trichocarpa</i>]	XP_002310288.1
Phenylpropanoid biosynthesis	0.921442207	69.98210626	214	oxidoreductase family protein [<i>Populus trichocarpa</i>]	XP_002316410.2
Phenylpropanoid biosynthesis	0.855361942	73.73566079	199	glycosyl hydrolase family 1 family protein [<i>Populus trichocarpa</i>]	XP_002305597.2
Phenylpropanoid biosynthesis	0.663383016	19.38499632	697	beta-D-glucan exohydrolase family protein [<i>Populus trichocarpa</i>]	XP_002325849.2
Phenylpropanoid biosynthesis	0.913998081	81.33845607	161	4-coumarate-CoA ligase family protein [<i>Populus trichocarpa</i>]	XP_002304825.2
Phenylpropanoid biosynthesis	0.747278609	76.53762831	182	PREDICTED: beta-glucosidase 12-like [<i>Populus euphratica</i>]	XP_011007817.1

	Phenylpropanoid biosynthesis	0.761621094	72.74071515	205	PREDICTED: beta-glucosidase 12-like [<i>Populus euphratica</i>]	XP_011007817.1
	Phenylpropanoid biosynthesis	0.708746328	60.99559201	261	linamarase family protein [<i>Populus trichocarpa</i>]	XP_006369423.1
	Phenylpropanoid biosynthesis	0.759146135	18.58025451	723	caffeoyl-CoA O-methyltransferase family protein [<i>Populus trichocarpa</i>]	XP_002298729.1
	Phenylpropanoid biosynthesis	0.852178741	50.16832122	315	peroxidase family protein [<i>Populus trichocarpa</i>]	XP_002323056.1
	Phenylpropanoid biosynthesis	0.574870863	2.916867939	1386	peroxidase family protein [<i>Populus trichocarpa</i>]	XP_002319968.2
	Phenylpropanoid biosynthesis	0.704513643	40.73234147	393	peroxidase [<i>Populus trichocarpa</i>]	CAA66035.1
	Phenylpropanoid biosynthesis	0.713351543	26.27489042	573	Peroxidase 21 precursor family protein [<i>Populus trichocarpa</i>]	XP_006381476.1
	Phenylpropanoid biosynthesis	0.666249469	39.91035009	408	peroxidase family protein [<i>Populus trichocarpa</i>]	XP_002306459.2
	Phenylpropanoid biosynthesis	0.840111724	33.80920552	482	Peroxidase 17 precursor family protein [<i>Populus trichocarpa</i>]	XP_002310551.1
	Phenylpropanoid biosynthesis	0.832218197	30.23046458	520	mannitol dehydrogenase family protein [<i>Populus trichocarpa</i>]	XP_002322822.1
	Isoflavonoid biosynthesis	0.649190413	11.77266722	902	6a-hydroxymaackiain methyltransferase family protein [<i>Populus trichocarpa</i>]	XP_006388414.1
	Isoflavonoid biosynthesis	0.495451522	2.108082836	1485	6a-hydroxymaackiain methyltransferase family protein [<i>Populus trichocarpa</i>]	XP_006376382.1
Light cyan	Flavonoid biosynthesis	0.869839864	28.06598414	1	dihydroflavonol reductase family protein [<i>Populus trichocarpa</i>]	XP_002300759.1
	Flavonoid biosynthesis	0.897694595	14.60467128	46	quinate O-hydroxycinnamoyltransferase/shikimate O-hydroxycinnamoyltransferase [<i>Populus trichocarpa</i>]	ACC63882.1
	Flavonoid biosynthesis	0.781453646	18.75080987	31	Leucoanthocyanidin reductase family protein [<i>Populus trichocarpa</i>]	XP_002305639.1
	Flavonoid biosynthesis	0.796117511	19.36802935	25	Leucoanthocyanidin dioxygenase family protein [<i>Populus trichocarpa</i>]	XP_002298081.1
	Flavonoid biosynthesis	0.80171592	13.15592229	53	Leucoanthocyanidin dioxygenase family protein [<i>Populus trichocarpa</i>]	XP_002304452.1
	Flavonoid biosynthesis	0.869317253	26.89206239	4	chalcone synthase family protein [<i>Populus trichocarpa</i>]	XP_002321081.1
	Flavonoid biosynthesis	0.841903016	25.09188401	6	naregenin-chalcone synthase family protein [<i>Populus trichocarpa</i>]	XP_002299282.1
	Flavonoid biosynthesis	0.816192968	24.46669246	8	naregenin-chalcone synthase family protein [<i>Populus trichocarpa</i>]	XP_002303821.2
	Flavonoid biosynthesis	0.816182236	23.49437578	12	naregenin-chalcone synthase family protein [<i>Populus trichocarpa</i>]	XP_002299281.2
	Flavonoid biosynthesis	0.809725044	21.26944398	20	naregenin-chalcone synthase family protein [<i>Populus trichocarpa</i>]	XP_002303820.1

	Flavonoid biosynthesis	0.877245813	22.95978242	15	naregenin-chalcone synthase family protein [<i>Populus trichocarpa</i>]	XP_002303819.2
	Flavonoid biosynthesis	0.908122448	11.25612153	67	trans-cinnamate 4-monooxygenase family protein [<i>Populus trichocarpa</i>]	XP_002325638.1
	Plant-pathogen interaction	0.783463538	8.099579659	97	PREDICTED: receptor-like protein 12 isoform X9 [<i>Populus euphratica</i>]	XP_011009855.1
	Plant-pathogen interaction	0.925657951	19.01612327	30	PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At4g36180 isoform X3 [<i>Populus euphratica</i>]	XP_011009849.1
	Plant-pathogen interaction	0.935799789	19.27646008	27	PREDICTED: LRR receptor-like serine/threonine-protein kinase GSO1 isoform X9 [<i>Populus euphratica</i>]	XP_011017634.1
	Plant-pathogen interaction	0.87291484	15.26447911	43	PREDICTED: receptor-like protein 12 isoform X9 [<i>Populus euphratica</i>]	XP_011009855.1
	Plant-pathogen interaction	0.900308426	11.11037355	68	cyclic nucleotide-regulated ion channel family protein [<i>Populus trichocarpa</i>]	XP_002324941.1
	Plant-pathogen interaction	0.614876048	0.450540659	311	hypersensitive reaction associated Ca2+-binding family protein [<i>Populus trichocarpa</i>]	XP_002314958.1
	MAPK signaling pathway - plant	0.813614249	9.521182643	85	PREDICTED: receptor-like protein 12 isoform X9 [<i>Populus euphratica</i>]	XP_011009855.1
	MAPK signaling pathway - plant	0.576407675	0.361306336	317	chitinase class 1 [<i>Vigna unguiculata</i>]	CAA61278.1
	MAPK signaling pathway - plant	0.614876048	0.450540659	311	hypersensitive reaction associated Ca2+-binding family protein [<i>Populus trichocarpa</i>]	XP_002314958.1
	Plant hormone signal transduction	0.929175824	13.57930668	50	PREDICTED: probable carboxylesterase 8 [<i>Populus euphratica</i>]	XP_011034804.1
	Plant hormone signal transduction	0.948171242	17.80931814	33	auxin-responsive family protein [<i>Populus trichocarpa</i>]	XP_002320219.1
	Plant hormone signal transduction	0.667663434	0.813438651	282	PREDICTED: coronatine-insensitive protein 1 [<i>Populus euphratica</i>]	XP_011036007.1
Black	Plant hormone signal transduction	0.905866214	28.33480556	40	auxin-responsive family protein [<i>Populus trichocarpa</i>]	XP_006373010.1
	Plant hormone signal transduction	0.680982154	7.056072276	488	auxin response factor 2 family protein [<i>Populus trichocarpa</i>]	XP_006372205.1
	Plant hormone signal transduction	0.736314383	6.457563294	518	auxin-induced protein IAA4 [<i>Populus trichocarpa</i>]	XP_002319642.1
	Cutin, suberine and wax biosynthesis	0.811431863	21.89080598	95	glucose-methanol-choline oxidoreductase family protein [<i>Populus trichocarpa</i>]	XP_002298074.1
	Cutin, suberine and wax biosynthesis	0.76399666	20.50124	117	Fe(III)-Zn(II) purple acid phosphatase family protein [<i>Populus trichocarpa</i>]	XP_002306126.2
	Cutin, suberine and wax biosynthesis	0.681538135	10.28212828	346	transferase family protein [<i>Populus trichocarpa</i>]	XP_002300751.1
	Cutin, suberine and wax biosynthesis	0.792319785	13.59571293	258	PREDICTED: omega-hydroxypalmitate O-feruloyl transferase-like [<i>Populus euphratica</i>]	XP_011028892.1"
	Plant-pathogen interaction	0.741198502	13.57643424	260	cytochrome P450 family protein [<i>Populus trichocarpa</i>]	XP_002304502.2

	Plant-pathogen interaction	0.768548954	18.10002625	162	beta-ketoacyl-CoA synthase family protein [<i>Populus trichocarpa</i>]	XP_002313455.1
	Plant-pathogen interaction	0.795559546	16.05467483	194	NADPH: QUINONE OXIDOREDUCTASE family protein [<i>Populus trichocarpa</i>]	XP_002304805.1
	MAPK signaling pathway - plant	0.645592062	3.040095467	766	AP2 domain-containing transcription factor family protein [<i>Populus trichocarpa</i>]	XP_002309625.2
	Phenylpropanoid biosynthesis	0.727712786	10.99793286	328	class 4 pathogenesis-related family protein [<i>Populus trichocarpa</i>]	XP_002319077.1
Purple	MAPK signaling pathway - plant	0.931385764	30.71945607	1	leucine-rich repeat family protein [<i>Populus trichocarpa</i>]	XP_002325559.2
	MAPK signaling pathway - plant	0.894960688	12.06581848	102	leucine-rich repeat family protein [<i>Populus trichocarpa</i>]	XP_006376307.1
	MAPK signaling pathway - plant	0.749089696	3.623410892	341	ETHYLENE RESPONSE FACTOR 1 family protein [<i>Populus trichocarpa</i>]	XP_002315707.1
	MAPK signaling pathway - plant	0.688163957	6.507181554	206	WRKY transcription factor 42 family protein [<i>Populus trichocarpa</i>]	XP_006389578.1
	MAPK signaling pathway - plant	0.696430206	4.798575271	279	calcium-binding EF hand family protein [<i>Populus trichocarpa</i>]	XP_002305364.1
	Plant-pathogen interaction	0.796525342	15.71623846	60	WRKY transcription factor 51 family protein [<i>Populus trichocarpa</i>]	XP_002307134.2
	Plant-pathogen interaction	0.688163957	6.507181554	206	WRKY transcription factor 42 family protein [<i>Populus trichocarpa</i>]	XP_006389578.1
	Plant-pathogen interaction	0.696430206	4.798575271	279	calcium-binding EF hand family protein [<i>Populus trichocarpa</i>]	XP_002305364.1
	Plant hormone signal transduction	0.749089696	3.623410892	341	ETHYLENE RESPONSE FACTOR 1 family protein [<i>Populus trichocarpa</i>]	XP_002315707.1
	Flavonoid biosynthesis	0.635153282	1.181190209	566	trans-cinnamate 4-hydroxylase [<i>Populus trichocarpa</i>]	ACC63872.1
Dark grey	Phenylpropanoid biosynthesis	0.640774714	0.866227012	162	transferase family protein [<i>Populus trichocarpa</i>]	XP_006368492.1
	Phenylpropanoid biosynthesis	0.915271671	10.83350347	24	phenylalanine ammonia-lyase family protein [<i>Populus trichocarpa</i>]	XP_002322884.2
	Phenylpropanoid biosynthesis	0.818625197	6.061763881	45	phenylalanine ammonia-lyase family protein [<i>Populus trichocarpa</i>]	XP_006381441.1
	Phenylpropanoid biosynthesis	0.925960179	14.89814754	11	PREDICTED: probable cinnamyl alcohol dehydrogenase 6 [<i>Ricinus communis</i>]	XP_002510582.1
	Flavonoid biosynthesis	0.640774714	0.866227012	162	transferase family protein [<i>Populus trichocarpa</i>]	XP_006368492.1
	Anthocyanin biosynthesis	0.842295608	6.519295227	41	PREDICTED: anthocyanidin 3-O-glucoside 2"-O-glucosyltransferase-like [<i>Populus euphratica</i>]	XP_011045872.1
	Anthocyanin biosynthesis	0.815455568	4.69813241	60	PREDICTED: anthocyanidin 3-O-glucoside 2"-O-glucosyltransferase-like [<i>Populus euphratica</i>]	XP_011045872.1
Grey 60	Plant hormone signal transduction	0.9292512	17.3932998	16	PREDICTED: probable protein phosphatase 2C 51 [<i>Populus euphratica</i>]	XP_011001894.1

Plant hormone signal transduction	0.922541396	16.86370442	18	PREDICTED: probable protein phosphatase 2C 24 [<i>Populus euphratica</i>]	XP_011032242.1
Plant hormone signal transduction	0.82703606	7.434692582	96	Protein phosphatase 2C family protein [<i>Populus trichocarpa</i>]	XP_002316268.2
Plant hormone signal transduction	0.766079188	3.755366035	145	Protein phosphatase 2C family protein [<i>Populus trichocarpa</i>]	XP_002311183.2
Plant hormone signal transduction	0.757233687	3.739213285	146	PREDICTED: probable protein phosphatase 2C 24 [<i>Populus euphratica</i>]	XP_011035254.1
Plant hormone signal transduction	0.94289795	18.86803141	9	bZIP transcription factor 6 family protein [<i>Populus trichocarpa</i>]	XP_002302435.1
MAPK signaling pathway - plant	0.878942482	10.46283728	68	mitogen-activated protein kinase homologue [<i>Populus trichocarpa</i>]	XP_006377705.1
MAPK signaling pathway - plant	0.9292512	17.3932998	16	PREDICTED: probable protein phosphatase 2C 51 [<i>Populus euphratica</i>]	XP_011001894.1
MAPK signaling pathway - plant	0.922541396	16.86370442	18	PREDICTED: probable protein phosphatase 2C 24 [<i>Populus euphratica</i>]	XP_011032242.1
MAPK signaling pathway - plant	0.82703606	7.434692582	96	Protein phosphatase 2C family protein [<i>Populus trichocarpa</i>]	XP_002316268.2
MAPK signaling pathway - plant	0.766079188	3.755366035	145	Protein phosphatase 2C family protein [<i>Populus trichocarpa</i>]	XP_002311183.2
MAPK signaling pathway - plant	0.757233687	3.739213285	146	PREDICTED: probable protein phosphatase 2C 24 [<i>Populus euphratica</i>]	XP_011035254.1
Plant-pathogen interaction	0.783777563	4.282999203	138	calcium binding family protein [<i>Populus trichocarpa</i>]	XP_002317881.2

Table S10. Differently expressed *R2R3-MYB* genes and their related defence-related genes.

Module	Gene annotation	Number	<i>Populus</i>	MM	IC
		based on IC	<i>trichocarpa</i> gene ID for <i>R2R3-MYB</i>		
Yellow	<i>Enhanced disease susceptibility 1 family protein</i>	543	Potri.015G069600	0.731667828	28.18601891
	<i>Leucine-rich repeat receptor-like protein kinase</i>	380	Potri.T041300	0.790612977	42.31868736
	<i>LRR receptor-like serine/threonine-protein kinase</i>	386	Potri.003G028200	0.815077509	41.64267491
	<i>Receptor-like protein</i>	1208	Potri.015G025800	0.667695698	4.931313422
	<i>Disease resistance protein</i>	428	Potri.T130000	0.862561453	37.82865827
	<i>Disease resistance protein</i>	506	Potri.T129800	0.843737683	31.2957153
	<i>NBS-LRR type disease resistance protein</i>	516	Potri.001G134700	0.811863051	30.49046349
	<i>Pathogenesis-related family protein</i>	164	Potri.001G288600	0.817070696	80.12273631
	<i>Pathogenesis-related family protein</i>	141	Potri.009G083300	0.86679066	86.94001381
	<i>Pathogenesis related family protein</i>	237	Potri.T131500	0.807783874	65.26983883
	<i>Pathogenesis-related family protein</i>	626	Potri.009G082900	0.784610472	23.47694776
	<i>Calcium-binding family protein</i>	196	Potri.005G183300	0.87124103	74.55316647
	<i>Calmodulin-like protein</i>	699	Potri.005G052800	0.771866458	19.32932604
	<i>WRKY transcription factor 72</i>	305	Potri.015G064100	0.802700927	51.63109975
	<i>Calcium-dependent protein kinase</i>	341	Potri.006G052900	0.847419889	46.26933536
	<i>Pathogenesis-related family protein</i>	179	Potri.013G041900	0.866493169	77.21039046
	<i>WRKY transcription factor 47 family protein</i>	509	Potri.002G186600	0.828369029	31.14320615
	<i>Auxin-responsive GH3 family protein</i>	1583	Potri.001G298300	0.498614074	1.490555166
	<i>Aux/IAA family protein</i>	1494	Potri.010G078300	-0.625948872	2.027303877
	<i>Flavonol synthase/flavanone 3- hydroxylase-like</i>	276	Potri.001G451300	0.893744069	58.20404986
	<i>Flavanone 3-dioxygenase-like</i>	602	Potri.012G006300	0.780783358	24.91547666
	<i>Cytochrome P450 family protein</i>	207	Potri.007G016400	0.892015801	71.91612723
	<i>Peroxidase family protein</i>	315	Potri.016G132900	0.852178741	50.16832122
	<i>Peroxidase family protein</i>	408	Potri.005G135300	0.666249469	39.91035009
	<i>MYB169</i>	204	Potri.015G046200	0.91953606	72.80582519
	<i>MYB194</i>	371	Potri.017G130300	0.821901673	43.12610329
	<i>MYB024</i>	653	Potri.002G038500	0.758543616	21.6127707

	<i>MYB129</i>	1040	Potri.010G240800	0.746125485	7.43202027
	<i>MYB011</i>	1654	Potri.001G219100	0.499643351	1.15363062
Light cyan	<i>Receptor-like protein</i>	97	Potri.018G124400	0.783463538	8.099579659
	<i>LRR receptor-like serine/threonine-protein kinase</i>	30	Potri.001G063300	0.925657951	19.01612327
	<i>LRR receptor-like serine/threonine-protein kinase</i>	27	Potri.001G064600	0.935799789	19.27646008
	<i>Receptor-like protein</i>	43	Potri.001G064100	0.87291484	15.26447911
	<i>Receptor-like protein</i>	85	Potri.T114300	0.813614249	9.521182643
	<i>Chitinase</i>	317	Potri.009G141900	0.576407675	0.361306336
	<i>MYB162</i>	28	Potri.014G100800	0.845889234	19.16848834
	<i>MYB086</i>	44	Potri.007G067600	0.876147463	15.07189018
Black	<i>Cytochrome P450 family protein</i>	258	Potri.003G129100	0.792319785	13.59571293
	<i>Pathogenesis-related family protein</i>	766	Potri.013G041700	0.645592062	3.040095467
	<i>MYB146</i>	511	Potri.013G001000	0.648559262	6.579215683
	<i>MYB101</i>	984	Potri.008G128500	0.566304327	1.171477162
Purple	<i>Leucine-rich repeat family protein</i>	1	Potri.019G084800	0.931385764	30.71945607
	<i>WRKY transcription factor 42 family protein</i>	206	Potri.011G007800	0.688163957	6.507181554
	<i>MYB137</i>	230	Potri.012G055600	0.809318227	5.771470494
	<i>MYB104</i>	681	Potri.008G166700	0.505321012	0.44486522
Dark grey	<i>Phenylalanine ammonia-lyase family protein</i>	24	Potri.016G091100	0.915271671	10.83350347
	<i>Cinnamyl alcohol dehydrogenase</i>	11	Potri.002G018300	0.925960179	14.89814754
	<i>MYB078</i>	27	Potri.006G221500	0.885749529	9.303088284
	<i>MYB214</i>	28	Potri.019G118900	0.858531581	9.279992054
	<i>MYB195</i>	34	Potri.018G005300	0.842065172	7.616312535
	<i>MYB156</i>	46	Potri.013G149200	0.818967892	6.00625534
Grey 60	<i>Protein phosphatase</i>	16	Potri.012G002700	0.9292512	17.3932998
	<i>Protein phosphatase</i>	18	Potri.009G037300	0.922541396	16.86370442
	<i>Protein phosphatase</i>	96	Potri.010G199600	0.82703606	7.434692582
	<i>Protein phosphatase</i>	145	Potri.008G059200	0.766079188	3.755366035
	<i>Protein phosphatase</i>	146	Potri.001G245200	0.757233687	3.739213285
	<i>BZIP transcription factor 6 family protein</i>	9	Potri.002G125400	0.94289795	18.86803141
	<i>Calcium binding family protein</i>	138	Potri.012G048200	0.783777563	4.282999203
	<i>MYB049</i>	95	Potri.004G033100	0.864654156	7.450822935

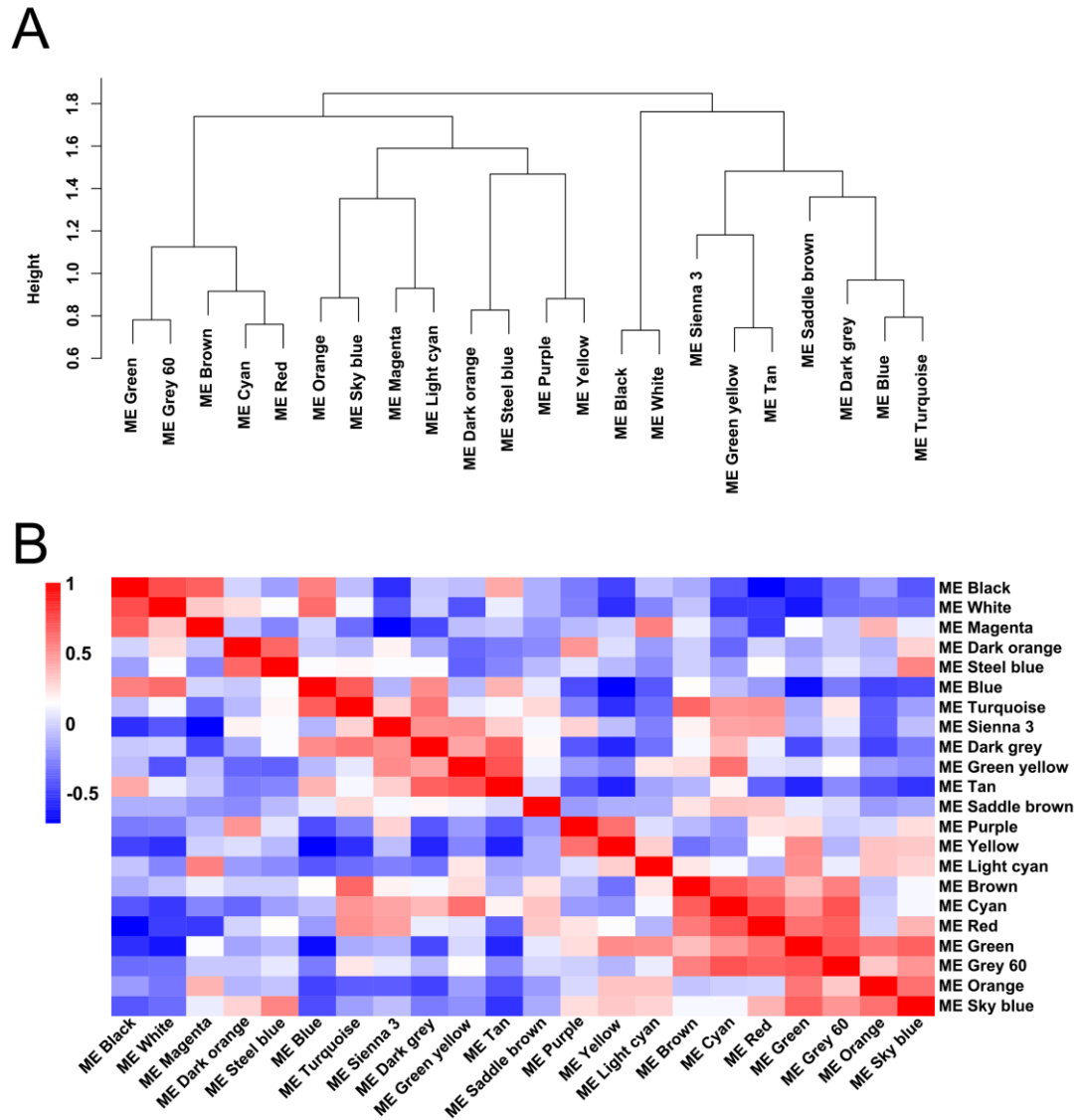


Figure S1. Correlation of module eigengenes of the modules to which the *R2R3-MYB* genes were assigned. **(A)** Hierarchical clustering dendrogram of the module eigengenes. **(B)** Heatmap of the correlation of the module eigengenes. ME, module eigengene.

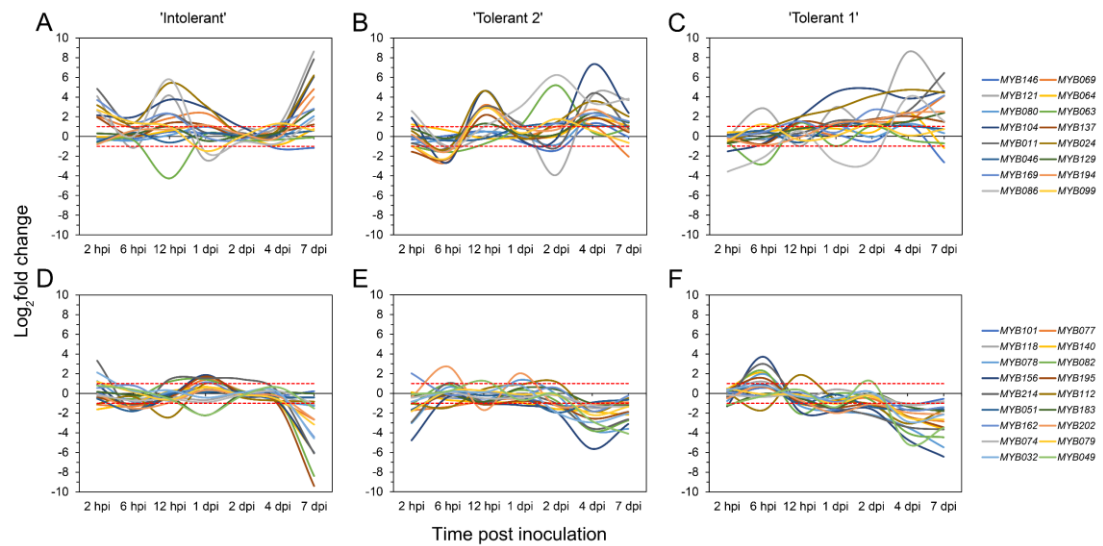


Figure S2. Comparison (\log_2 E4-inoculated/E4-free) of the differentially expressed *R2R3-MYB* genes at different time points in different poplars after E4 infection (colours of the lines represent different genes). (A, D) Expression of the differentially expressed *R2R3-MYB* genes in 'Intolerant'. (B, E) Expression of the differentially expressed *R2R3-MYB* genes in 'Tolerant 2'. (C, F) Expression of the differentially expressed *R2R3-MYB* genes in 'Tolerant 1'.

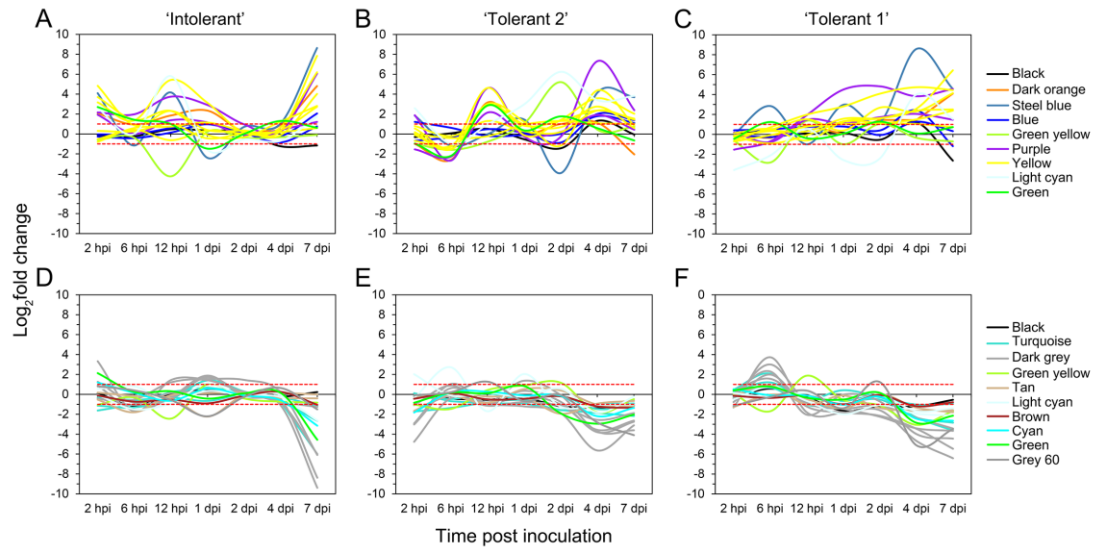


Figure S3. Comparison (\log_2 E4-inoculated/E4-free) of the differentially expressed *R2R3-MYB* genes at different time points in different poplars after E4 infection (colours of the lines represent different modules). (A, D) Expression of the differentially expressed *R2R3-MYB* genes in 'Intolerant'. (B, E) Expression of the differentially expressed *R2R3-MYB* genes in 'Tolerant 2'. (C, F) Expression of the differentially expressed *R2R3-MYB* genes in 'Tolerant 1'.

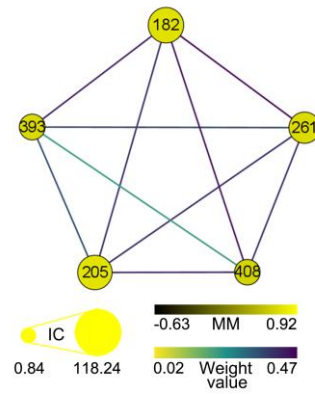


Figure S4. High weight value genes in yellow module (detailed in Table S9). The size of the dots represents IC. The color of the dot represents MM. The color of the line represents the weight value between two genes. The label of dot is listed based on IC for the specific gene in the specific module. *Linamarase family protein* (No. 261), *beta-glucosidase 12-like* genes (No. 182 and 205), and *peroxidase* genes (No. 393 and 408).

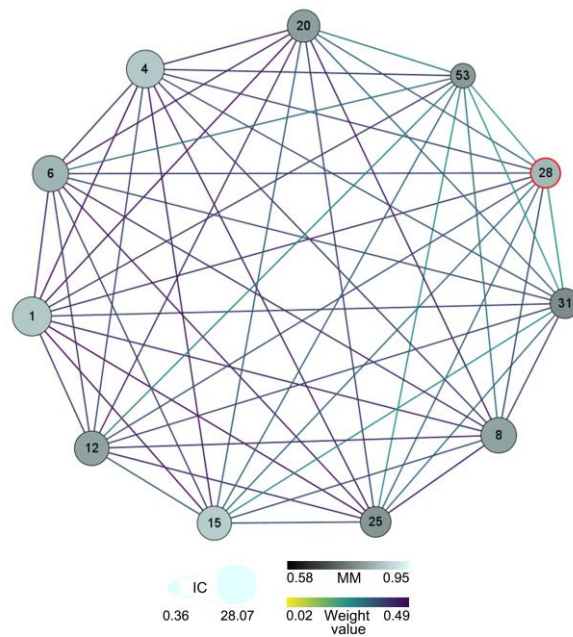


Figure S5. High weight value genes in light cyan module (detailed in Table S9). The size of the dots represents IC. The color of the dot represents MM. The color of the line represents the weight value between two genes. The label of dot is listed based on IC for the specific gene in the specific module. The *R2R3-MYB* genes are highlighted with red borders. *MYB162* (No. 28), *dihydroflavonol reductase family protein* (No. 1), *chalcone synthase family protein* (No. 4), *naregenin-chalcone synthase family protein* genes (No. 6, 8, 12, 15, 20 and 53), *leucoanthocyanidin dioxygenase family protein* (No. 25), *MYB162* (No. 28), and *leucoanthocyanidin reductase family protein* (No. 31).

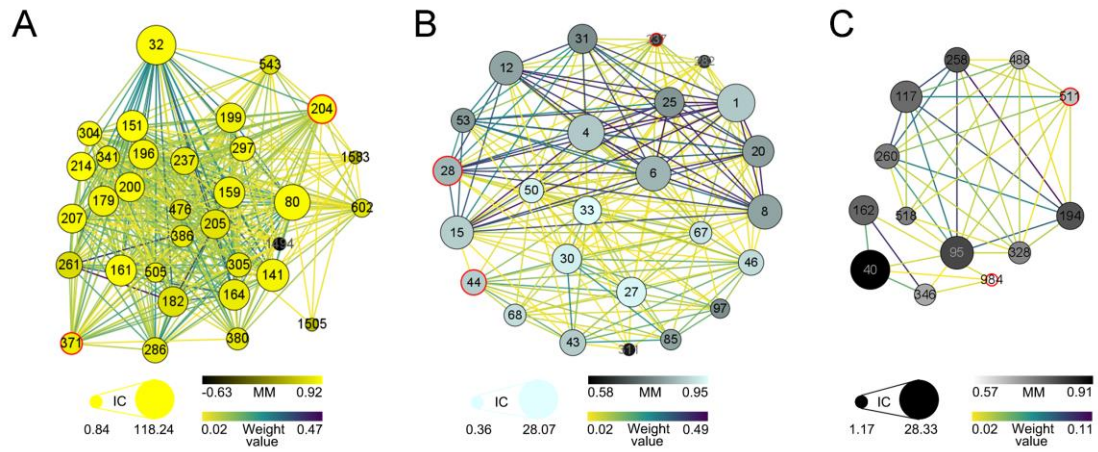


Figure S6. Gene networks for auxin-related genes (detailed in Table S9). (A). The yellow module. (B) The 'light cyan' module. (C) The black module. The size of the dots represents IC. The color of the dot represents MM. The color of the line represents the weight value between two genes. The label of dot is listed based on IC for the specific gene in the specific module. The *R2R3-MYB* genes are highlighted with red borders.

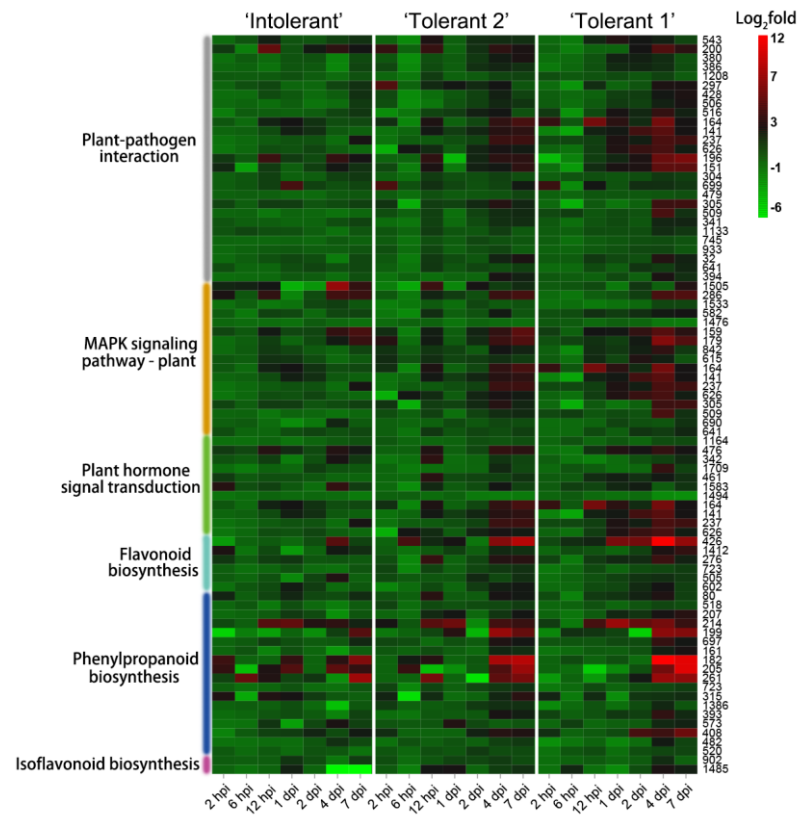


Figure S7. Expression characteristics of *R2R3-MYB* genes related genes that involved in poplar-E4 interaction in yellow module.

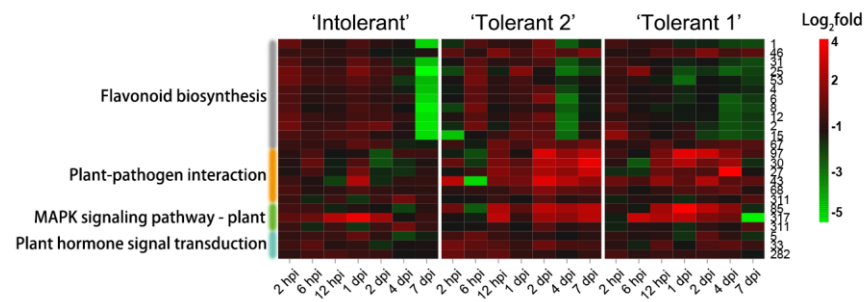


Figure S8. Expression characteristics of *R2R3-MYB* genes related genes that involved in poplar-E4 interaction in light cyan module.

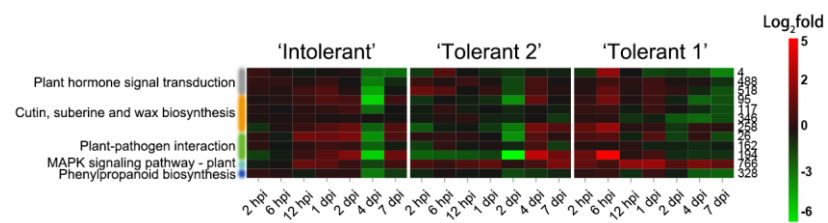


Figure S9. Expression characteristics of *R2R3-MYB* genes related genes that involved in poplar-E4 interaction in black module.

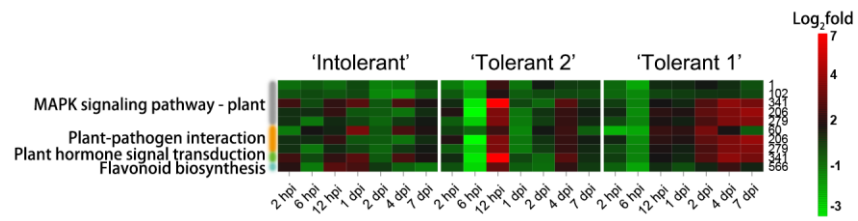


Figure S10. Expression characteristics of *R2R3-MYB* genes related genes that involved in poplar-E4 interaction in purple module.

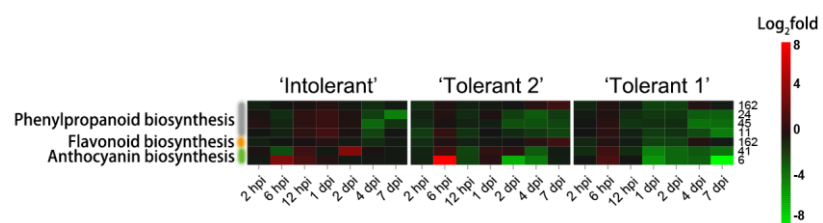


Figure S11. Expression characteristics of *R2R3-MYB* genes related genes that involved in poplar-E4 interaction in dark grey module.

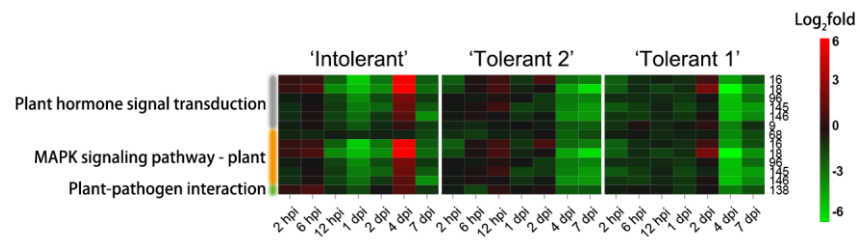


Figure S12. Expression characteristics of *R2R3-MYB* genes related genes that involved in poplar-E4 interaction in grey 60 module.

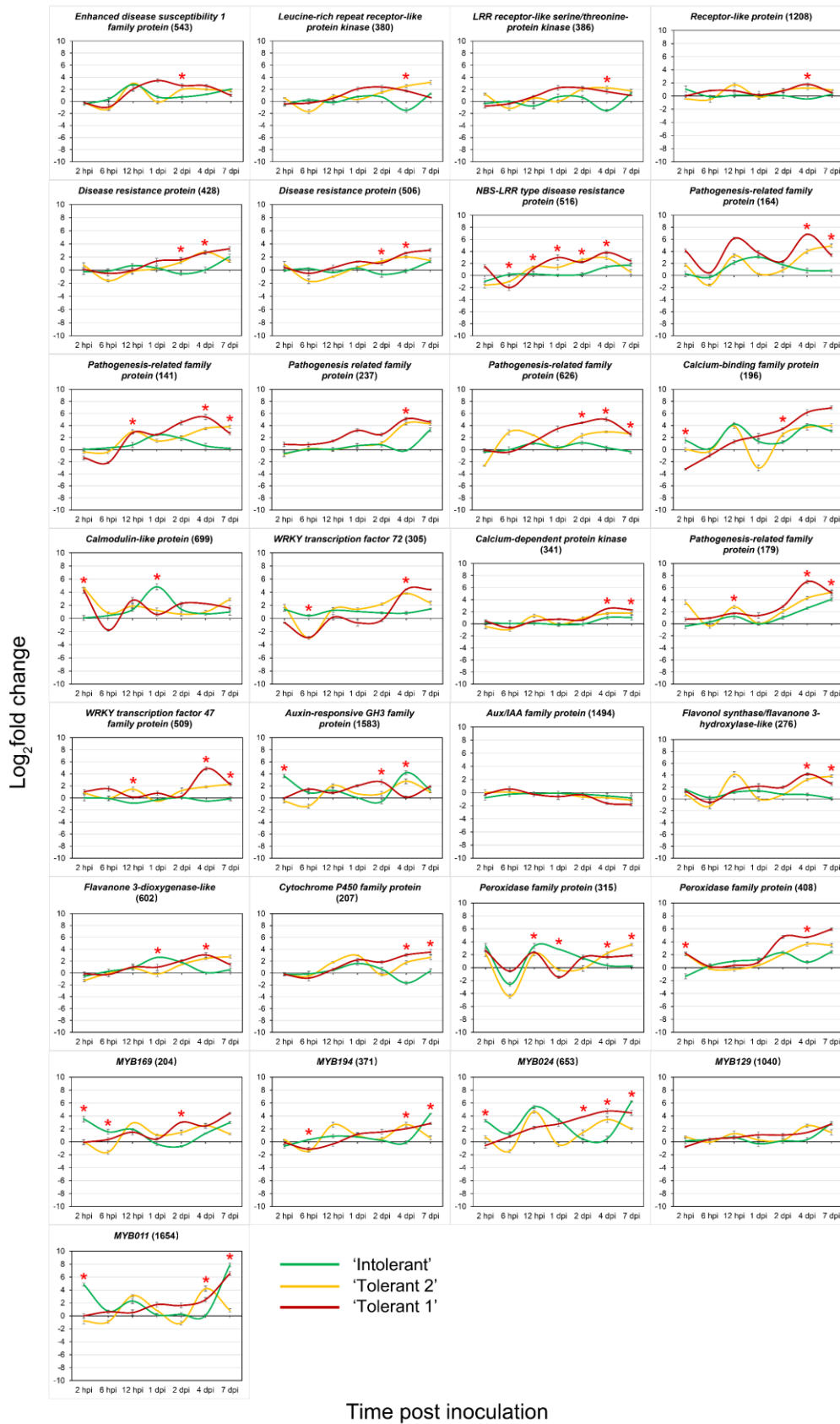


Figure S13. Expression validation of genes in yellow module by RT-qPCR. Data are given as mean with s.d. ($n=3$; *, p value of 'Intolerant' and 'Tolerant 2' or 'Intolerant' and 'Tolerant 1' were both less than 0.05).

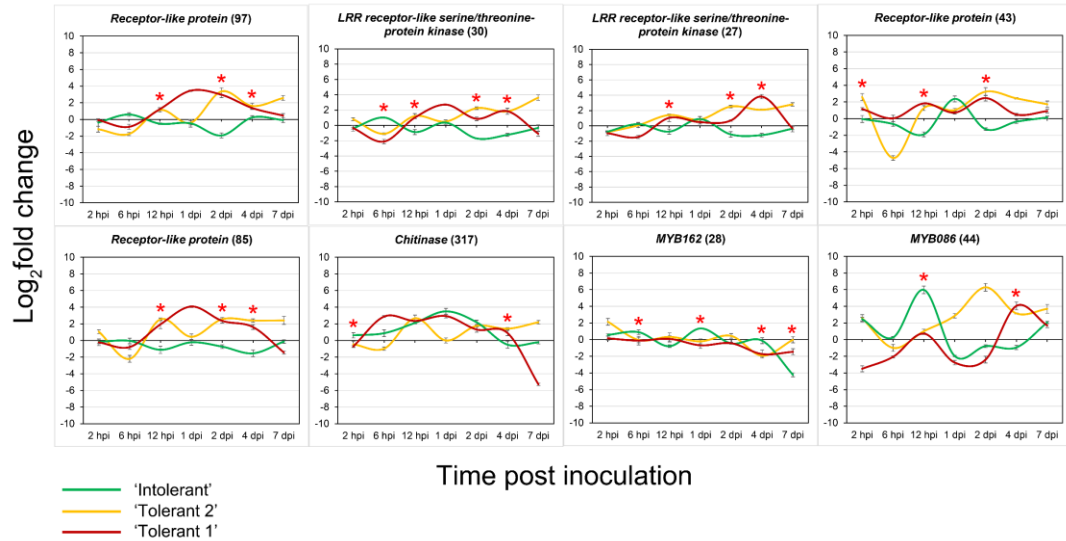


Figure S14. Expression validation of genes in light cyan module by RT-qPCR. Data are given as mean with s.d. ($n=3$; *, p value of 'Intolerant' and 'Tolerant 2' or 'Intolerant' and 'Tolerant 1' were both less than 0.05).

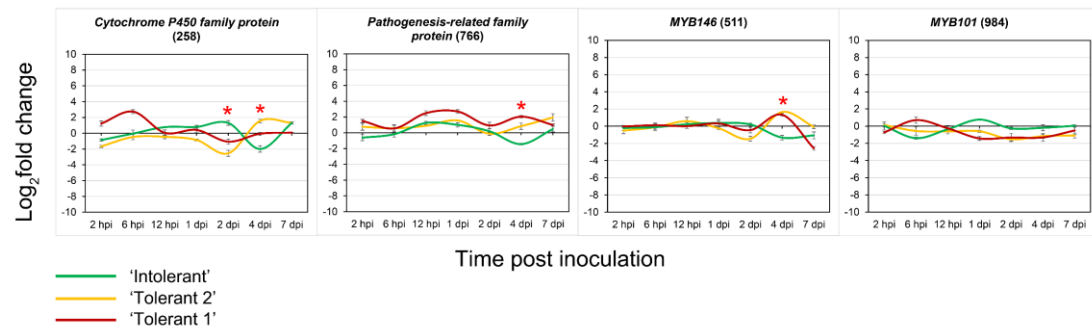


Figure S15. Expression validation of genes in black module by RT-qPCR. Data are given as mean with s.d. ($n=3$; *, p value of 'Intolerant' and 'Tolerant 2' or 'Intolerant' and 'Tolerant 1' were both less than 0.05).

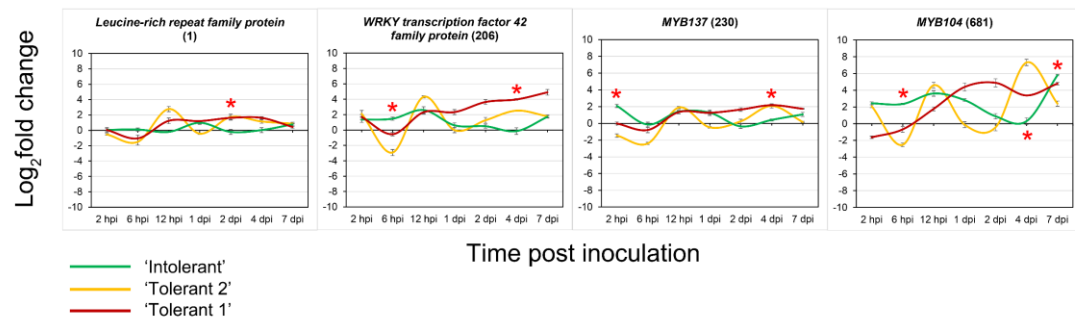


Figure S16. Expression validation of genes in purple module by RT-qPCR. Data are given as mean with s.d. ($n=3$; *, p value of 'Intolerant' and 'Tolerant 2' or 'Intolerant' and 'Tolerant 1' were both less than 0.05).

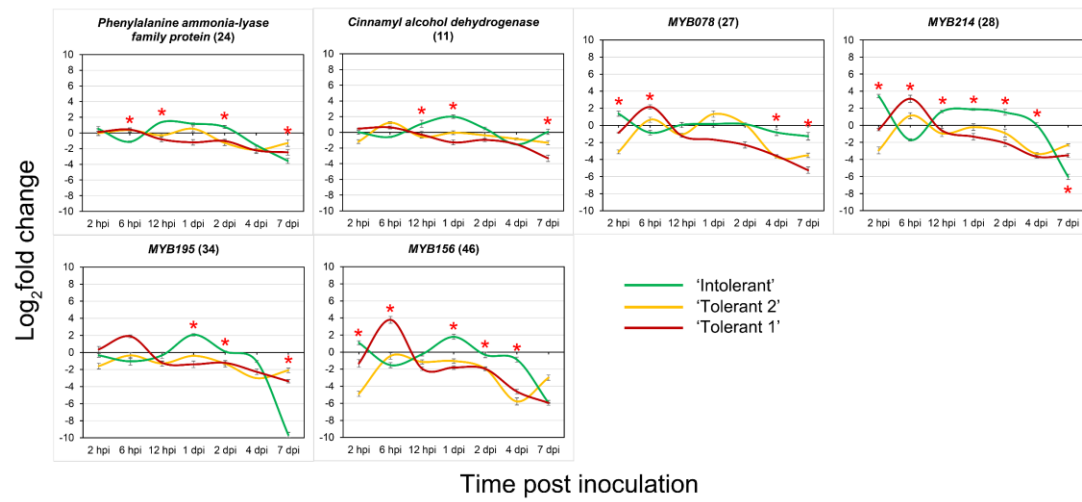


Figure S17. Expression validation of genes in dark grey module by RT-qPCR. Data are given as mean with s.d. ($n=3$; *, p value of 'Intolerant' and 'Tolerant 2' or 'Intolerant' and 'Tolerant 1' were both less than 0.05).

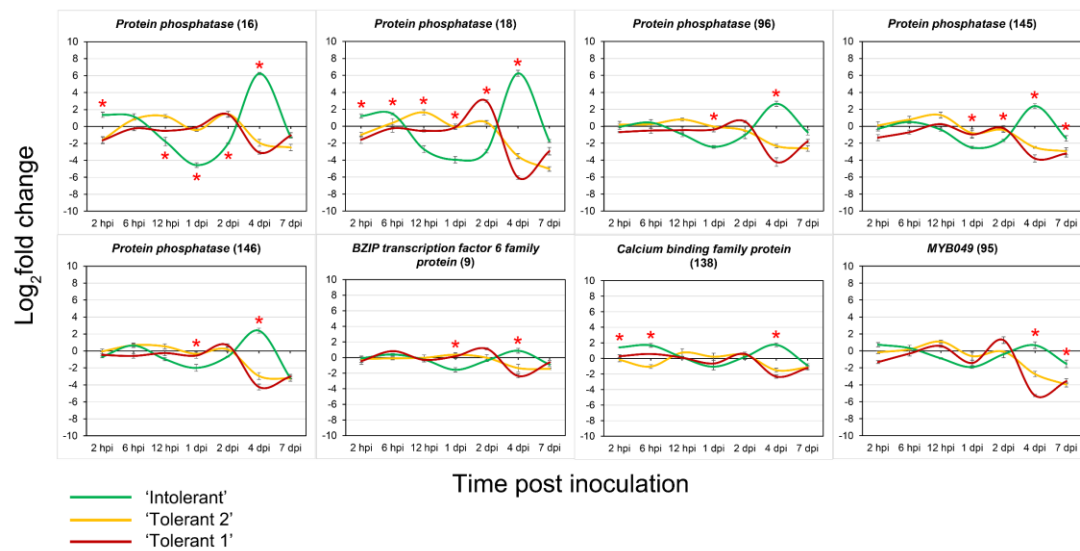


Figure S18. Expression validation of genes in grey 60 module by RT-qPCR. Data are given as mean with s.d. ($n=3$; *, p value of 'Intolerant' and 'Tolerant 2' or 'Intolerant' and 'Tolerant 1' were both less than 0.05).