









**Supplemental Figure S1** The intact phylogenetic tree of 156 putative bHLH proteins from *Acer palmatum* and eight reference bHLHs with known function of being involved in anthocyanin biosynthesis in other plants. The clade containing eight reference bHLHs and two putative targets was enclosed by the red dashed rectangle, which was presented as Figure 1 in the main text.

**Supplemental Table S1** The name list of 156 putative bHLH proteins (longer than 60 amino acids) in *Acer palmatum* and 8 reference bHLHs

CL10105.Contig1_All.pro	CL3970.Contig1_All-rev.pro
CL1029.Contig27_All-rev.pro	CL3970.Contig2_All-rev.pro
CL1029.Contig29_All.pro	CL3970.Contig4_All.pro
CL10308.Contig2_All.pro	CL4150.Contig1_All.pro
CL10308.Contig3_All-rev.pro	CL4150.Contig2_All.pro
CL1035.Contig5_All.pro	CL4150.Contig3_All.pro
CL1035.Contig8_All.pro	CL4150.Contig4_All.pro
CL1292.Contig1_All-rev.pro	CL4150.Contig6_All.pro
CL1292.Contig2_All-rev.pro	CL418.Contig1_All.pro
CL1292.Contig3_All.pro	CL418.Contig2_All.pro
CL1616.Contig1_All.pro	CL4334.Contig1_All.pro
CL1616.Contig2_All.pro	CL4334.Contig2_All-rev.pro
CL1616.Contig3_All.pro	CL4514.Contig2_All.pro
CL1616.Contig4_All.pro	CL4738.Contig1_All-rev.pro
CL1616.Contig5_All.pro	CL4738.Contig2_All.pro
CL1833.Contig6_All-rev.pro	CL4849.Contig1_All-rev.pro
CL1833.Contig7_All-rev.pro	CL4849.Contig2_All-rev.pro
CL1848.Contig1_All.pro	CL4849.Contig4_All-rev.pro
CL1848.Contig3_All.pro	CL4849.Contig5_All-rev.pro
CL2907.Contig1_All-rev.pro	CL4857.Contig1_All.pro
CL2907.Contig2_All-rev.pro	CL4857.Contig2_All.pro
CL2929.Contig1_All.pro	CL5039.Contig2_All-rev.pro
CL2929.Contig2_All.pro	CL5039.Contig3_All.pro
CL3127.Contig1_All.pro	CL5039.Contig4_All-rev.pro
CL3127.Contig2_All.pro	CL5039.Contig5_All.pro
CL3151.Contig1_All.pro	CL5186.Contig2_All.pro
CL3151.Contig2_All.pro	CL5186.Contig3_All-rev.pro
CL3182.Contig1_All-rev.pro	CL5696.Contig5_All.pro
CL3182.Contig2_All.pro	CL572.Contig3_All.pro
CL3200.Contig1_All.pro	CL572.Contig35_All.pro
CL3200.Contig2_All.pro	CL572.Contig36_All.pro
CL3457.Contig1_All-rev.pro	CL572.Contig5_All.pro
CL3457.Contig3_All-rev.pro	CL572.Contig60_All.pro
CL3457.Contig5_All-rev.pro	CL572.Contig71_All.pro
CL3457.Contig6_All-rev.pro	CL6183.Contig1_All.pro
CL3641.Contig1_All-rev.pro	CL6183.Contig2_All.pro
CL3641.Contig2_All.pro	CL6183.Contig3_All.pro
CL3665.Contig3_All.pro	CL6463.Contig1_All.pro
	CL6463.Contig2_All.pro
	CL7127.Contig1_All-rev.pro

CL7127.Contig2_All-rev.pro
CL7209.Contig1_All.pro
CL7209.Contig2_All.pro
CL7338.Contig4_All-rev.pro
CL7338.Contig5_All.pro
CL7338.Contig6_All-rev.pro
CL7338.Contig7_All.pro
CL7601.Contig1_All.pro
CL7601.Contig2_All.pro
CL7601.Contig3_All.pro
CL7601.Contig4_All-rev.pro
CL8408.Contig1_All.pro
CL8408.Contig2_All.pro
CL8881.Contig1_All.pro
CL8881.Contig2_All.pro
CL8881.Contig3_All.pro
CL9162.Contig1_All-rev.pro
CL9162.Contig2_All-rev.pro
CL9889.Contig2_All.pro
Unigene10591_All.pro
Unigene11120_All-rev.pro
Unigene11131_All.pro
Unigene1166_All.pro
Unigene11690_All.pro
Unigene11901_All.pro
Unigene1297_All-rev.pro
Unigene13498_All.pro
Unigene13561_All.pro
Unigene14361_All.pro
Unigene14501_All.pro
Unigene14587_All-rev.pro
Unigene14835_All.pro
Unigene16378_All.pro
Unigene17429_All-rev.pro
Unigene20219_All.pro
Unigene20480_All.pro
Unigene20542_All-rev.pro
Unigene20596_All-rev.pro
Unigene21161_All-rev.pro
Unigene21833_All.pro
Unigene23323_All-rev.pro
Unigene23324_All-rev.pro
Unigene23515_All-rev.pro

Unigene23765_All-rev.pro
Unigene23773_All.pro
Unigene24001_All.pro
Unigene24403_All-rev.pro
Unigene24418_All.pro
Unigene24543_All-rev.pro
Unigene24875_All.pro
Unigene24922_All.pro
Unigene27722_All-rev.pro
Unigene29817_All-rev.pro
Unigene29818_All.pro
Unigene29948_All-rev.pro
Unigene30003_All-rev.pro
Unigene30513_All.pro
Unigene31035_All.pro
Unigene33000_All-rev.pro
Unigene33001_All-rev.pro
Unigene33002_All.pro
Unigene33003_All.pro
Unigene33203_All.pro
Unigene33566_All.pro
Unigene33670_All-rev.pro
Unigene34215_All-rev.pro
Unigene34283_All.pro
Unigene34478_All.pro
Unigene34840_All.pro
Unigene4107_All-rev.pro
Unigene47552_All.pro
Unigene527_All-rev.pro
Unigene7300_All-rev.pro
Unigene7426_All.pro
Unigene7478_All-rev.pro
Unigene7741_All.pro
Unigene842_All-rev.pro
Unigene9470_All.pro
At1g63650-EGL3.pro
<b>At4g09820-TT8.pro</b>
<b>At5g41315-GL3.pro</b>
<b>MdbHLH3.pro</b>
<b>MdbHLH33.pro</b>
<b>MtTT8-KM892777.pro</b>
<b>PhAN1-AAG25928.pro</b>
<b>VvACC68685.pro</b>

**Supplemental Table S2** Percentage of residue identity between two putative target bHLH proteins and five reference proteins

	VvMYC1	MdbHLH3	MtTT8	PhAN1	AtTT8
Unigene13498_All	68.8	65.4	59.5	58.0	55.1
CL8881.contig2_All	54.4	52.8	47.9	47.2	51.1

The deduced protein sequences deduced from assembled transcripts of Unigene13498\_All and CL8881.contig2\_All were aligned with five reference bHLHs using ClustalW of MegAlign (DNASTAR, Madison, USA).

**Supplemental Table S3** Open reading frame of *ApbHLH1* (2130 bp)

ATGGCTGCGCCGCGAGTAGCCGGCTTCAAAGTATGCTGCAGGAGGCGGT  
 GCAATCAGTTCAGTGGACTTACAGTCTCTT  
 TTGGCAAATCTGTCCACAACAAGGGATCCTAATATGGGGAGATGGGTATTAT  
 AATGGAGCAATTAAGACAAGGAAAACAG  
 TGCAACCGATGGAGGTGAGTGCGGAGGAAGCGTCTCTGCAAAGAAGCCA  
 GCAGCTTAGAGAGCTTTACGAGTCATTGTCG  
 GCTGGAGAGACGAACCAGCCAGCAAGGAGGCCTTGTGCTTCGTTGTGCGC  
 GGAGGACTTAACGGAGTCGGAGTGTTCTA  
 TTTGATGTGTGTGTCCTTCTCTTTCCACCTGGCCTCGGGTTACCTGGAAAG  
 GCATACGCAAGGCGGCAACATGTATGGC  
 TTACAGGAGCGAACGAGGTTGACAGCAAAACCTTCTCTAGAGCAATTCTT  
 GCCAAGAGTGCTCGTATACAGACTGTGTTA  
 TGCATTCCTCTTCTTGACGGCGTCGTTGAATTGGGCTCAACAGATAGGATAC  
 AAGAGGACCTTGGATTGGTCCAACAAAT  
 CAAGAGCTTCTTCACAGACCAACACCACCCAAACCCTCAACCACCAAAAC  
 CAGCTCTCTCCGAGCACTCCACCTCCAATC  
 CCGCCACGTCATCCGACCACCGCCGCTTCCACTCACCTCCAATTCCGGCCA  
 TGTACGCCGCTGTTGACCCACCAGCCAAC  
 CCCAACCAAGAAGACGAAGACGACGAAGAAGAGGAGGAAGAGGAAGAA

GAAGAAGACGAAGAGGAGGAGCAAGAGTCTGA  
CTCTGAAGCCGAAACGGGTCGCATCAGAAGCCAAGGCGCCGCTCAAAACC  
CTCAATCCGTGGCTCCACCCATGGCTGAAC  
CGAGTGAGCTCATGCAGCTGGAGATGTCTGAGGATATCCGAGTTGGATCCC  
CCGACGATGCGTCGAATAATTTGGACTCA  
GATTTTCATATGTTGGCCGTGAGCCAAGCCGTGAACCCGGGTGATCACCAG  
CGGCGCTCTGACTCGTTCAGAGCTGAGTC  
GAGTCGAAGGTGGCCGATGCTACAAGAACCATTGACCGGTAGTGGTCTTCC  
ACCACCACCTCCTTCAGCTTCAGGACAAC  
TTGGAATGGAAGAATTGACACAAGAAGACACTCACTACTCCCAAACCGTG  
TCAACCATTATCCAAAAGCAGACAACACGG  
TGGGCCGAATCATCGTCTACCGGCTACGTACGTACTCAACCCAGTCAGCG  
TTTGCCAAGTGGACAAACCGGTCGGACCT  
CCACCTCCAGATTCCCGTGGAAGGCACGTCTCAGTGGCTCCTCAAGTACAT  
TTTGTTTCAGCGTACCTTTTCTACACAGCA  
AATACCGTGATGAAAACCTCCCCCAAGTCACGTGACGCCAGCACCGCCGAC  
GCGGCCTCCAAGTTCCGTAAAGGGACCTCA  
CAAGACGAGCTGAGTGCCAACCACGTGCTGGCGGAGCGCCGCCGCCGCG  
AGAAGTTAAACGAGAGGTTTCATCATTTTAAAG  
GTCATTAGTCCCCTTCGTCACTAAAATGGACAAGGCCTCCATATTGGGTGAC  
ACTATCGAGTACGTCAAACAGTTGCGTA  
AAAAGATTTCAGGATCTCGAGACACGTAACAAGCAGATGGAGACCGATCAA  
CGGTCAAGATTGTCGGATTCTCCAAGGACT  
AGTAGTGGTTTGAAAGAGCAGAGAAGTGGGTTGACTGTTTTGGACCGGGC  
ACGGGTGGGTCTGACCCGGGTCTGATAA  
GAGGAAGATGAGGATAGTGGAGACAAGTAGCGGCGTTGCAAAGCCTAAGA  
CGGTGGAGTCACCGCCACTGCCAACACCAT  
TAACGACAACACCGACGGCGACAACAACGGCTAGTACGGTACAGGTGTCG  
ATCATCGAGAGTGATGCGTTGGTGGAGCTG  
CAATGTGGGTATAGAGAAGGGTTGTTGCTTGATATCATGCTAATGCTAAGGG  
AGCTTCTGATTGAAGTCACAGCAGTTCA  
ATCTTCTCTAACTAATGGAGCTTTTGTAGCTCAGCTAAGGGCAAAGGTGAA  
AGATAATGTAAATGGGAAAAAAGCAAGCA  
TTGTGGAAGTCAAGAGAGCAATACATCAACTGATACCCCAACAATACTGA



**Supplemental Table S4** Primers used in this study

Name	Sequence (5' to 3')	Application
bH-f1	CCACTGAAATTTGGAAGTGAGA	Cloning <i>ApbHLH1</i>
bH-f2	GAAGTGAGAATTCAATCCCAAGTTA	Cloning <i>ApbHLH1</i>
bH-f3	TTCAATCCCAAGTTAGTGAAGAAG	Cloning <i>ApbHLH1</i>
bH-f4	GTGAAGAAGATCTACCGTTGAATAC AG	Cloning <i>ApbHLH1</i>
bH-f5	AGATCATTGCTAGGACTGCTTTG	Cloning <i>ApbHLH1</i>
bH-f6	TTTGTAAGCACACATGGTGGAC	Cloning <i>ApbHLH1</i>
bH-f7	AGGGTCAAACAGGGAGACAAC	Cloning <i>ApbHLH1</i>
bH-r1	GGCGACTCGAATGATTAGAACA	Cloning <i>ApbHLH1</i>
bH-r2	TGCAAATTACCTGACACAGTTTG	Cloning <i>ApbHLH1</i>
bH-r3	ATTGGCATGCTTTCTTGAGC	Cloning <i>ApbHLH1</i>
bH-r4	CCTGATTACTCGTGAGTTGTGAAA	Cloning <i>ApbHLH1</i>
qAcUBQ-f	AGGCCAAAATTCAGGACAAG	qPCR
qAcUBQ-r	CGAAGGACAAGATGCAGAGTAG	qPCR
qApbHLH1-f	CGTAACAAGCAGATGGAGACC	qPCR
qApbHLH1-r	CCAAAACAGTCAACCCACTTC	qPCR
PCCL-bHLH-f	ACGGGGGACGAGCTCGGTACCATGGCTG CGCCGCCGAGT	Generating PCCL-ApbHLH1 construct
PCCL-bHLH-r	CGCGTACGAGATCTGGTCGACGTATTGTT	Generating

	GGGGTATCAGTTGATGTAT	PCCL-ApbHLH1 construct
PHNL-bHLH-F	ACGGGGGACGAGCTCGGTACCATGGCTG CGCCGCCGAGT	Generating PHNL-ApbHLH1 construct
PHNL-bHLH-R	AACATCGTATGGGTAGTCGACGTATTGTT GGGGTATCAGTTGATGTAT	Generating PHNL-ApbHLH1 construct
PCCL-MYB-F	ACGGGGGACGAGCTCGGTACCATGACCA TGGTAGAGGGATTTGTAG	Generating PCCL-ApMYB1 construct
PCCL-MYB-R	CGCGTACGAGATCTGGTCGACAATTGCAT ATTCTTCTTCTGTGTTAAGA	Generating PCCL-ApMYB1 construct
PHNL-MYB-F	ACGGGGGACGAGCTCGGTACCATGACCA TGGTAGAGGGATTTGTAG	Generating PHNL-ApMYB1 construct
PHNL-MYB-R	AACATCGTATGGGTAGTCGACAATTGCAT ATTCTTCTTCTGTGTTAAGA	Generating PHNL-ApMYB1 construct
PCCL-bHLH1T-f	ACGGGGGACGAGCTCGGTACCATGGGAG ATGGGTATTATAATGGAG	Paired with PCCL-bHLH-r to generate PCCL-ApbHLH1T
PCCL-MYB1D-R1	GTTCTTCCAGGGACTTCATCTTCAGTGAA CTCTCCTCT	Paired with PCCL-MYB-f to get fragment before bHLH binding domain in <i>ApMYB1</i>
PCCL-MYB1D-2F1	GATGAAGTCCCTGGAAGAACAGCAAATG ATGT	Paired with PCCL-MYB-r to get fragment after bHLH binding domain in <i>ApMYB1</i>
ApbHLH1-F	<u>ttagatct</u> GAATACAGTTTCTAAACAATGGCT G (underlined nucleotides as BglII site)	Generating pCAMIA1305-ApbHLH1 construct ( <i>35S::ApbHLH1</i> )
ApbHLH1-R	<u>tcgtttaaac</u> TCAGTATTGTTGGGGTATCAGTT G (underlined nucleotides as PmeI site)	Generating pCAMIA1305-ApbHLH1 construct ( <i>35S::ApbHLH1</i> )