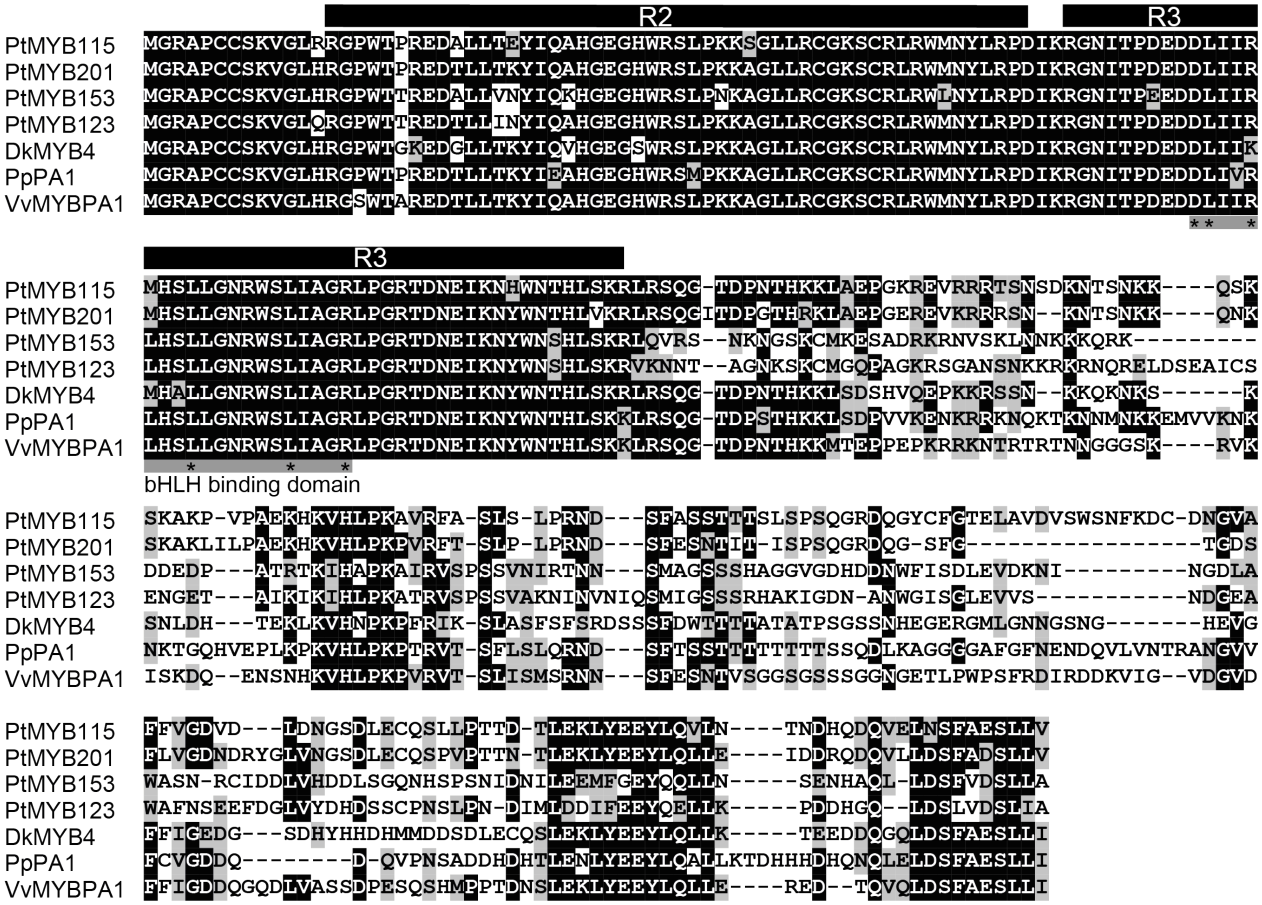

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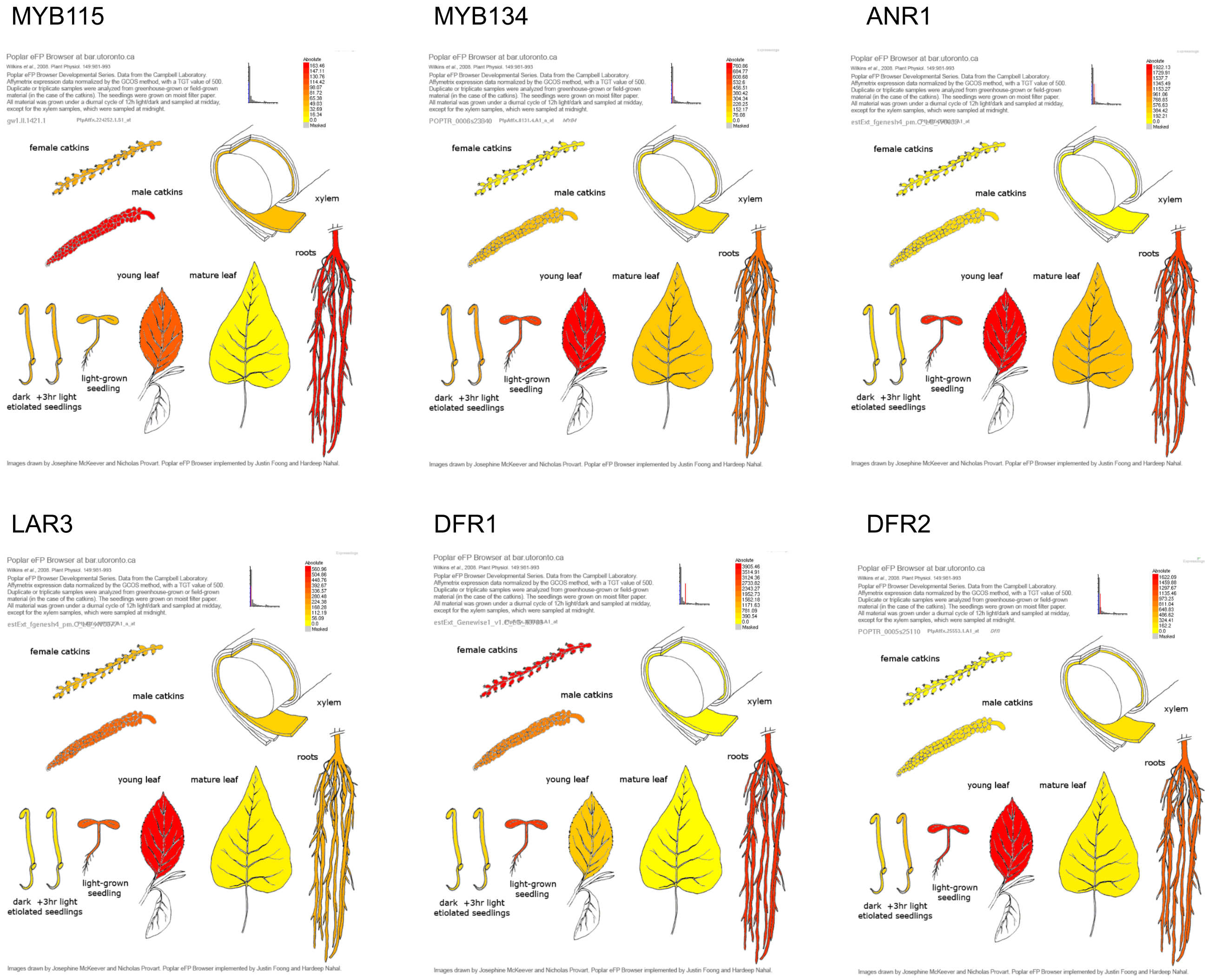
                                         R2                                      R3
PtMYB115   MGRAPCCSKVGLRRGPWTPREDALLTEYIQAHGEGHWRSLPKKSGLLRCGKSCRLRWMNYLRPDIKRGNITPDEDDLIIR
PtMYB201   MGRAPCCSKVGLHRGPWTPREDTLLTKYIQAHGEGHWRSLPKKAGLLRCGKSCRLRWMNYLRPDIKRGNITPDEDDLIIR
PtMYB153   MGRAPCCSKVGLHRGPWTTREDALLVNYIQKHGEGHWRSLPNKAGLLRCGKSCRLRWLNYLRPDIKRGNITPEEDDLIIR
PtMYB123   MGRAPCCSKVGLQRGPWTTREDTLLINYIQAHGEGHWRSLPKKAGLLRCGKSCRLRWMNYLRPDIKRGNITPDEDDLIIR
DkMYB4     MGRAPCCSKVGLHRGPWTGKEDGLLTKYIQVHGEGSWRSLPKKAGLLRCGKSCRLRWMNYLRPDIKRGNITPDEDDLIIK
PpPA1      MGRAPCCSKVGLHRGPWTPREDTLLTKYIEAHGEGHWRSMPKKAGLLRCGKSCRLRWMNYLRPDIKRGNITPDEDDLIVR
VvMYBPA1   MGRAPCCSKVGLHRGSWTAREDTLLTKYIQAHGEGHWRSLPKKAGLLRCGKSCRLRWMNYLRPDIKRGNITPDEDDLIIR
                                                                                    ** *

                    R3
PtMYB115   MHSLLGNRWSLIAGRLPGRTDNEIKNHWNTHLSKRLRSQG-TDPNTHKKLAEPGKREVRRRTSNSDKNTSNKK----QSK
PtMYB201   MHSLLGNRWSLIAGRLPGRTDNEIKNYWNTHLVKRLRSQGITDPGTHRKLAEPGEREVKRRRSN--KNTSNKK----QNK
PtMYB153   LHSLLGNRWSLIAGRLPGRTDNEIKNYWNSHLSKRLQVRS--NKNGSKCMKESADRKRNVSKLNNKKKQRK---------
PtMYB123   LHSLLGNRWSLIAGRLPGRTDNEIKNYWNSHLSKRVKNNT--AGNKSKCMGQPAGKRSGANSNKKRKRNQRELDSEAICS
DkMYB4     MHALLGNRWSLIAGRLPGRTDNEIKNYWNTHLSKRLRSQG-TDPNTHKKLSDSHVQEPKKRSSN--KKQKNKS------K
PpPA1      LHSLLGNRWSLIAGRLPGRTDNEIKNYWNTHLSKKLRSQG-TDPSTHKKLSDPVVKENKRRKNQKTKNNMNKKEMVVKNK
VvMYBPA1   LHSLLGNRWSLIAGRLPGRTDNEIKNYWNTHLSKKLRSQG-TDPNTHKKMTEPPEPKRRKNTRTRTNNGGGSK----RVK
              *    *  *
           bHLH binding domain

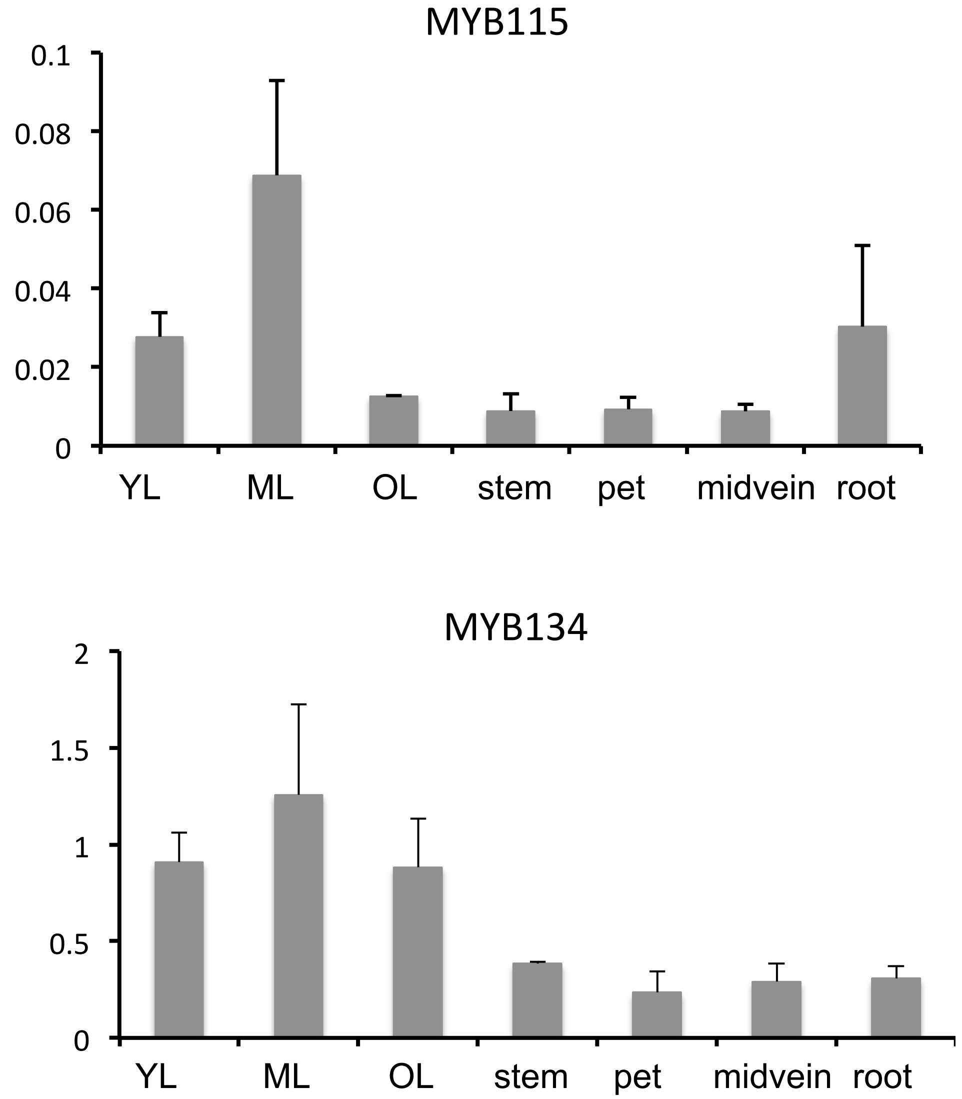
PtMYB115   SKAKP-VPAEKHKVHLPKAVRFA-SLS-LPRND---SFASSTTTSLSPSQGRDQGYCFGTELAVDVSWSNFKDC-DNGVA
PtMYB201   SKAKLILPAEKHKVHLPKPVRFT-SLP-LPRND---SFESNTIT-ISPSQGRDQG-SFG-----------------TGDS
PtMYB153   DDEDP---ATRTKIHAPKAIRVSPSSVNIRTNN---SMAGSSSHAGGVGDHDDNWFISDLEVDKNI---------NGDLA
PtMYB123   ENGET---AIKIKIHLPKATRVSPSSVAKNINVNIQSMIGSSSRHAKIGDN-ANWGISGLEVVS-----------NDGEA
DkMYB4     SNLDH---TEKLKVHNPKPFRIK-SLASFSFSRDSSSFDWTTTTATATPSGSSNHEGERGMLGNNGSNG-------HEVG
PpPA1      NKTGQHVEPLKPKVHLPKPTRVT-SFLSLQRND---SFTSSTTTTTTTTSSQDLKAGGGGAFGFNENDQVLVNTRANGVV
VvMYBPA1   ISKDQ--ENSNHKVHLPKPVRVT-SLISMSRNN---SFESNTVSGGSGSSSGGNGETLPWPSFRDIRDDKVIG--VDGVD

PtMYB115   FFVGDVD---LDNGSDLECQSLLPTTD-TLEKLYEEYLQVLN----TNDHQDQVELNSFAESLLV
PtMYB201   FLVGDNDRYGLVNGSDLECQSPVPTTN-TLEKLYEEYLQLLE----IDDRQDQVLLDSFADSLLV
PtMYB153   WASN-RCIDDLVHDDLSGQNHSPSNIDNILEEMFGEYQQLLN-----SENHAQL-LDSFVDSLLA
PtMYB123   WAFNSEEFDGLVYDHDSSCPNSLPN-DIMLDDIFEEYQELLK-----PDDHGQ--LDSLVDSLIA
DkMYB4     FFIGEDG---SDHYHHDHMMDDSDLECQSLEKLYEEYLQLLK-----TEEDDQGQLDSFAESLLI
PpPA1      FCVGDDQ--------D-QVPNSADDHDHTLENLYEEYLQALLKTDHHHDHQNQLELDSFAESLLI
VvMYBPA1   FFIGDDQGQDLVASSDPESQSHMPPTDNSLEKLYEEYLQLLE----RED--TQVQLDSFAESLLI
```

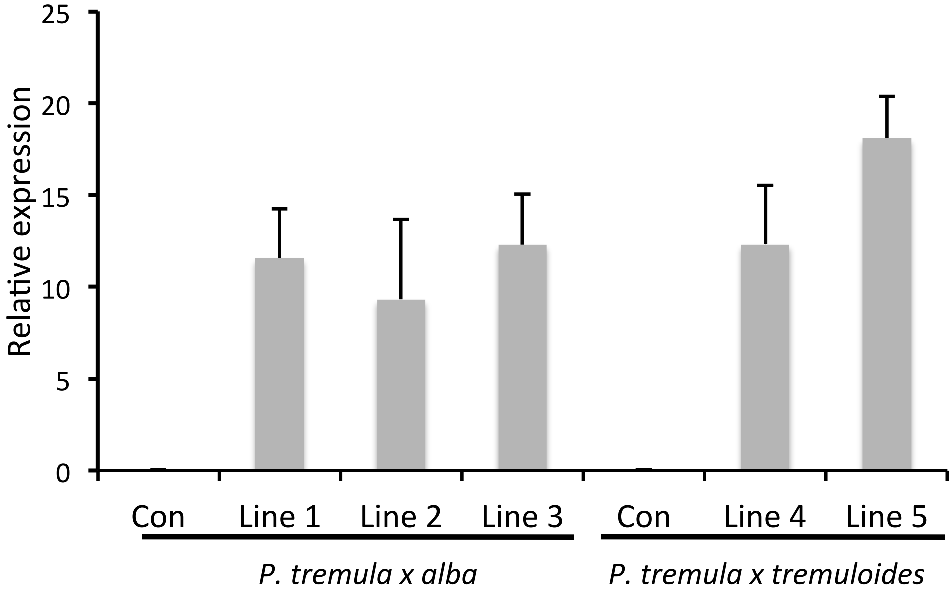
Supplemental Figure S1. Protein sequence alignment of MYB115 with other PA1 clade MYB activators. Sequences of poplar MYBs and characterized MYBs from other species were obtained from Phytozome and aligned by ClustalW. The bHLH binding domain is conserved and indicated by asterisks. For accession numbers and other details, see Materials and Methods.



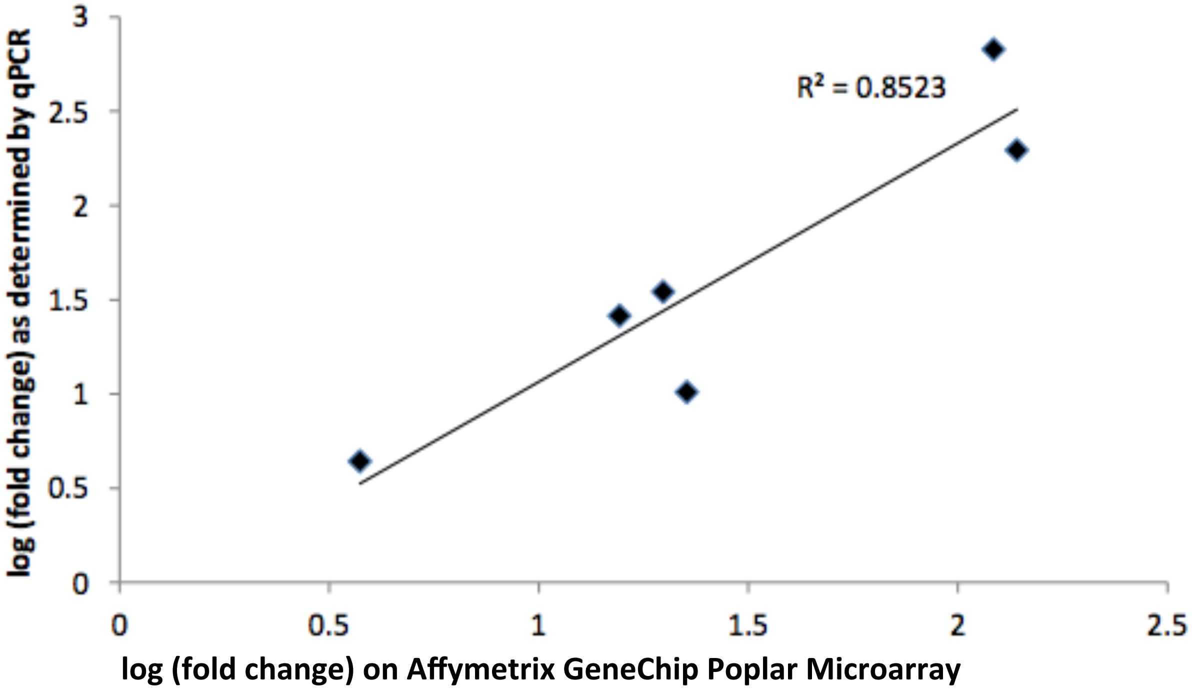
Supplemental Figure S2.
Analysis of *in silico* expression of MYB115, MYB134 and other major proanthocyanidin pathway genes using the *P. trichocarpa* eFP browser (Wilkins et al., 2009). Red color shows greatest transcript abundance. Note that the scales vary in each panel.



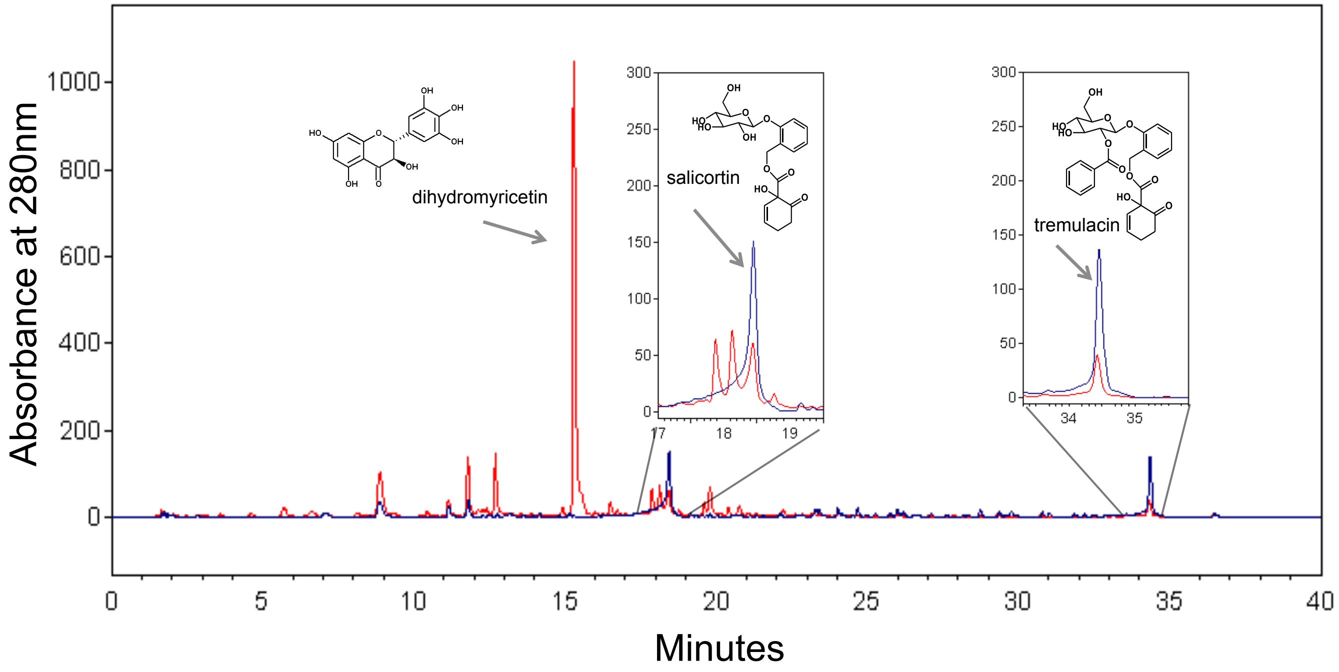
Supplemental Figure S3. RT-qPCR expression profile of MYB115 and MYB134 in wild-type *P. tremula x tremuloides* (353-38) grown in the greenhouse. Relative expression is shown normalized to the mean of elongation factor-1ß and actin. YL, young leaf (LPI 7-10); ML, medium leaf (LPI11-12); OL, old leaf (LPI21-22); pet, petiole. Error bars indicate S.E. (n=4)



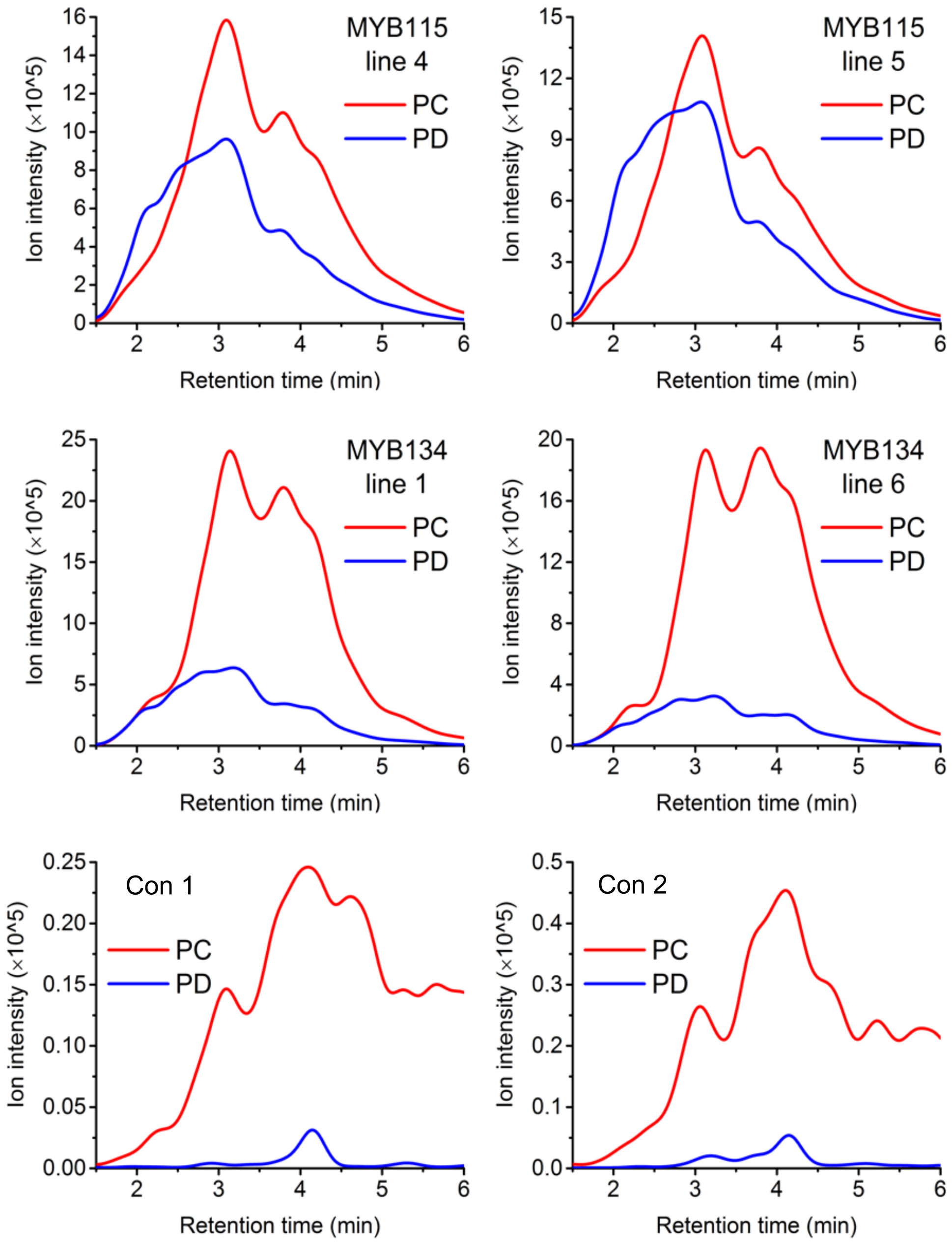
Supplemental Figure S4. Expression of MYB115 transgene in MYB115-overexpressing poplar lines. Relative expression is shown normalized to the poplar elongation factor 1ß. Each bar represents the means from at least three clonal copies of each transgenic line. Two different *Populus* genetic backgrounds, *P. tremula x alba* (INRA 717-1B4) and *P. tremula x tremuloides* (353-38), were transformed. n.d, not detected. Error bars indicate S.E.



Supplemental Figure S5. Validation of microarray results using qPCR The log fold change of Affymetrix microarray results and qPCR analysis of six genes of biological interest (ANR1, DFR2, F3'5'H, MYB134, and MYB182) was plotted. For both analyses, three *P. tremula x tremuloides* MYB115-overexpressors (line 5) were compared with three wild-type plants.



Supplemental Figure S6. Overlay of sample HPLC profiles comparing MYB115-overexpressing (red) and control (blue) poplar leaf extracts. Major compounds which are quantified in Table 4 as showing a significant increase or decrease as a result of MYB115 transgene expression are indicated.



Supplemental Figure S7. Sample chromatograms showing procyanidin (PC) and prodelphinidin (PD) subunits used to determine PA subunit concentrations in MYB115-overexpressors (top), MYB134-overexpressors, and control (bottom). The different proportions of PDs and PCs are clearly seen. Quantitative data are presented in Supplemental Table S3 and the percent delphinidin shown in Fig. 7.