Supplemental Table S1. Enrichment of transcripts in MYB134-overexpressing transgenic poplar relative to controls

Affymetrix Probeset	P. tricho gene model	Annotation	Fold change	T statistic	P-value
Ptp.8030.1.S1_s_at	Potri.014G019200	cytochrome b5	163.2833	16.85894	3.53E-08
PtpAffx.7896.4.A1_a_at	Potri.003G176900	chalcone synthase (CHS6)	93.77203	21.83764	3.53E-09
PtpAffx.18705.2.A1_a_at	Potri.015G050200	leucoanthocyanidin reductase (LAR3)	60.59532	37.65457	2.60E-11
Ptp.8030.1.S1_at	Potri.014G019200	cytochrome b5	48.05178	20.64396	5.83E-09
Ptp.3138.2.A1_a_at	Potri.009G133300	udp-glucose:flavonoid 3-o-glucosyltransferase	45.80734	22.09157	3.18E-09
PtpAffx.161181.1.S1_at	Potri.006G178700	cinnamoyl-CoA reductase-like	45.06821	19.59402	9.29E-09
PtpAffx.7896.2.S1_at	Potri.003G176800	chalcone synthase(CHS4)	41.13079	39.03098	1.88E-11
PtpAffx.37082.1.A1_at	Potri.002G033600	dihydroflavonol 4-reductase (DFR1)	39.54137	25.11352	1.01E-09
PtpAffx.6065.2.S1_at	Potri.008G116500	leucoanthocyanidin reductase (LAR1)	38.84044	34.47834	5.77E-11
RPTR-Ptp-U57609-2_s_at	---	---	37.4959	45.21196	4.95E-12
PtpAffx.30659.1.A1_at	Potri.002G173900	transcription factor (MYB115)	35.30178	44.07727	6.23E-12
PtpAffx.120325.1.S1_s_at	Potri.013G073300	flavonoid 3'-hydroxylase (F3H1)	31.51567	16.42893	4.44E-08
Ptp.6057.1.S1_at	Potri.001G113100	anthocyanidin synthase (ANS2)	30.74659	9.198484	6.57E-06
PtpAffx.5092.1.A1_at	Potri.004G030700	anthocyanidin reductase (ANR1)	28.37733	32.38522	1.02E-10
PtpAffx.142603.1.A1_s_at	Potri.013G073300	flavonoid 3'-hydroxylase (F3H1)	27.05796	18.703	1.41E-08
PtpAffx.7896.3.S1_a_at	Potri.001G051600	chalcone synthase (CHS3)	26.52365	14.84038	1.09E-07
Ptp.4863.1.S1_s_at	Potri.013G073300	flavonoid 3'-hydroxylase (F3H1)	26.52258	20.72227	5.64E-09
PtpAffx.5092.2.S1_a_at	Potri.004G030700	anthocyanidin reductase (ANR1)	26.07823	20.50992	6.18E-09
PtpAffx.224485.1.S1_s_at	Potri.005G207600	hydrogen antiporter-proanthocyanidin transport	23.98421	18.42999	1.60E-08
Ptp.1080.1.S1_s_at	Potri.010G129800	leucocyanidin reductase (LAR2)	21.70362	15.29466	8.34E-08
PtpAffx.6065.3.A1_a_at	Potri.010G129800	leucocyanidin reductase (LAR2)	20.60674	17.9467	2.03E-08
PtpAffx.162989.1.S1_at	Potri.009G133300	udp-glucose:flavonoid 3-o-glucosyltransferase	19.52091	21.23703	4.53E-09
PtpAffx.224252.1.S1_at	Potri.002G173900	transcription factor (MYB115)	18.92459	17.57196	2.45E-08
Ptp.1080.1.S1_at	Potri.010G129800	leucocyanidin reductase (LAR2)	18.58252	17.36505	2.72E-08
PtpAffx.25553.1.A1_at	Potri.005G229500	dihydroflavonol 4-reductase (DFR2)	16.5693	17.16159	3.02E-08
Ptp.323.1.S1_s_at	Potri.005G113900	naringenin 3-dioxygenase	14.08321	13.76554	2.10E-07
Ptp.6753.1.S1_s_at	Potri.006G027000	serine hydrolase (PFAM)	10.65876	11.66834	8.79E-07
PtpAffx.160113.1.A1_s_at	Potri.001G006700	AMP-binding enzyme (PFAM)	10.2984	15.74556	6.46E-08
PtpAffx.83404.1.A1_at	Potri.009G069100	flavonoid 3',5'-hydroxylase (CYP75A12|F3'5'H1)	10.19663	18.83537	1.32E-08
PtpAffx.125678.1.A1_at	---	---	9.907653	5.427128	0.000401
PtpAffx.7740.2.A1_a_at	Potri.018G100500	cinnamoyl-CoA reductase-like	8.764517	16.51608	4.24E-08
Ptp.6057.1.S1_s_at	Potri.001G113100	anthocyanidin synthase (ANS2)	8.497491	12.2562	5.76E-07
PtpAffx.8131.6.A1_a_at	Potri.006G221800	transcription factor (MYB134)	8.147172	18.77702	1.36E-08
PtpAffx.222060.1.S1_at	---	---	8.005913	11.85978	7.65E-07
PtpAffx.8131.4.A1_a_at	Potri.006G221800	transcription factor (MYB134)	7.97044	17.22329	2.92E-08
PtpAffx.224602.1.S1_at	Potri.008G128500	transcription factor (MYB194)	7.959252	19.31856	1.05E-08
Ptp.4458.1.S1_s_at	Potri.T035000	glutathione S-transferase (PFAM)	7.807675	19.67796	8.94E-09
Ptp.5716.1.S1_at	Potri.002G095900	monosaccharide transporter	7.806563	20.44209	6.36E-09
PtpAffx.249.83.A1_x_at	Potri.018G114800	unknown protein	7.356863	8.73696	1.01E-05
PtpAffx.94822.1.A1_at	Potri.002G055100	TT12 (TRANSPARENT TESTA 12); antiporter/ solute:hydrogen antiporter	6.795176	19.46291	9.86E-09
PtpAffx.54821.1.A1_at	Potri.006G027000	serine hydrolase (PFAM)	6.690093	11.90532	7.40E-07
PtpAffx.133554.1.A1_s_at	Potri.005G167400	acetyl-CoA carboxylase	6.662745	23.33136	1.95E-09
PtpAffx.156161.1.A1_at	Potri.001G157600	nodulin MtN21 family protein	6.490875	17.18962	2.97E-08
PtpAffx.86545.1.S1_at	Potri.010G223700	unknown protein	6.242573	13.27558	2.88E-07
Ptp.6711.1.S1_s_at	Potri.014G145100	chalcone synthase (CHS1)	6.098726	8.672523	1.07E-05
PtpAffx.157838.2.S1_at	---	---	5.818017	19.25219	1.09E-08
PtpAffx.30128.1.S1_at	Potri.001G140700	cinnamoyl-CoA reductase-like	5.577246	9.935996	3.45E-06
PtpAffx.249.102.A1_x_at	---	---	5.553507	10.39139	2.36E-06
PtpAffx.224746.1.S1_s_at	Potri.011G066800	cysteine proteinase, putative / thiol protease, putative	5.420569	16.5478	4.17E-08
PtpAffx.127289.1.A1_at	Potri.006G209000	WD40 repeat-containing protein (AtAN11 like)	5.219675	12.85534	3.81E-07
Ptp.2833.1.S1_at	---	---	5.208285	20.81995	5.40E-09
PtpAffx.205491.1.S1_at	Potri.005G167400	acetyl-CoA carboxylase	5.184778	20.78798	5.48E-09
Ptp.4450.1.S1_at	---	---	4.952875	2.992692	0.014936
PtpAffx.4850.1.A1_s_at	Potri.010G213000	chalcone isomerase (CHI1)	4.916343	14.30874	1.50E-07
Ptp.1512.1.S1_s_at	Potri.019G057800	chalcone isomerase-like protein (CHIL2)	4.647485	18.35612	1.66E-08
PtpAffx.213439.1.S1_at	Potri.016G075800	WD40 repeat-containing protein (AtAN11 like)	4.619583	16.02367	5.54E-08
PtpAffx.160901.1.S1_s_at	Potri.004G057700	XBCP3 (xylem bark cysteine peptidase 3); cys endopeptidase/ cys-type peptidase	4.199214	9.064349	7.42E-06
PtpAffx.205684.1.S1_at	Potri.005G208600	bHLH TT8-like	3.987209	17.13424	3.06E-08
PtpAffx.65824.1.A1_at	Potri.001G001600	pyruvate kinase, putative	3.930125	12.19123	6.03E-07
PtpAffx.19596.1.S1_at	---	---	3.924788	12.80954	3.93E-07
PtpAffx.33535.2.A1_at	Potri.002G029300	PAP10 (PURPLE ACID PHOSPHATASE 10); acid phosphatase/ protein ser/thr phosphatase	3.833496	14.69616	1.18E-07
PtpAffx.5685.1.S1_x_at	Potri.005G045300	unknown protein	3.64408	16.10165	5.30E-08
PtpAffx.224650.1.S1_s_at	Potri.010G114000	transcription factor (MYB165)	3.551603	15.47316	7.53E-08
PtpAffx.256.2.S1_at	Potri.005G208600	bHLH TT8-like	3.536714	17.06229	3.18E-08
PtpAffx.137746.1.S1_at	Potri.004G088100	transcription factor (MYB182)	3.533906	16.28853	4.79E-08
Ptp.6918.1.S1_at	---	---	3.517449	5.197493	0.000544
Ptp.8024.1.S1_at	Potri.005G208600	bHLH TT8-like	3.51615	8.051025	1.96E-05
PtpAffx.105254.1.S1_at	---	---	3.461575	4.538652	0.001366
PtpAffx.200035.1.S1_at	Potri.001G006700	AMP-binding enzyme	3.402119	12.04395	6.70E-07
PtpAffx.12056.3.S1_a_at	Potri.T071600	4-Coumarate:CoA ligase (Ptr4CL4)	3.400256	13.62235	2.30E-07
PtpAffx.30743.1.A1_a_at	Potri.013G031900	unknown protein	3.343919	12.13628	6.27E-07
PtpAffx.225544.1.S1_s_at	Potri.016G031000	p-coumaroyl shikimate 3'- hydroxylase (CYP98A23)	3.332724	15.8947	5.95E-08
PtpAffx.30743.5.A1_at	Potri.013G031900	unknown protein	3.260588	7.824444	2.46E-05
PtpAffx.224878.1.S1_at	Potri.014G100800	transcription factor (MYB201)	3.20616	11.03236	1.42E-06
PtpAffx.5685.1.S1_a_at	Potri.005G045300	unknown protein	3.16919	16.22155	4.97E-08
PtpAffx.47237.2.A1_a_at	Potri.001G181700	unknown protein	3.162376	13.22467	2.98E-07
PtpAffx.200755.1.S1_s_at	Potri.001G247400	ceramidase family protein	3.159078	8.161898	1.75E-05
PtpAffx.224381.1.S1_at	Potri.004G069600	quercetin O-glucosyltransferase activity	3.122538	8.973053	8.07E-06

PtpAffx.157838.2.S1_a_at	---	---	3.066728	13.58878	2.35E-07
PtpAffx.47186.1.S1_at	Potri.004G178100	unknown protein	3.045628	12.80149	3.95E-07
PtpAffx.157838.1.S1_at	---	---	3.045317	8.296294	1.54E-05
PtpAffx.116734.1.A1_at	---	---	3.042291	6.350431	0.000126
Ptp.6632.1.S1_at	Potri.019G130700	cytochrome P450 (CYP73A43|C4H1)	3.04052	6.456998	0.000111
PtpAffx.150025.1.S1_s_at	Potri.013G157900	cytochrome P450 cinnamate 4-hydroxylase (C4H2|CYP73A42)	3.033328	4.516244	0.001411
PtpAffx.83148.2.S1_s_at	Potri.010G145800	ACLB-2 (ATP CITRATE LYASE SUBUNIT B 2); ATP citrate synthase	2.984264	6.906822	6.61E-05
PtpAffx.128519.1.S1_at	Potri.011G076200	GDSL-motif lipase/hydrolase family protein	2.975488	5.181618	0.000556
PtpAffx.211755.1.S1_at	Potri.014G127500	unknown protein	2.96465	11.95119	7.16E-07
Ptp.7328.1.A1_at	Potri.002G203400	unknown protein	2.944334	14.47971	1.35E-07
PtpAffx.206509.1.S1_at	Potri.006G186800	ALDH11A3; 3-chloroallyl aldehyde dehydrogenase/ glyceraldehyde-3-phosphate dehydro	2.842203	12.49547	4.87E-07
Ptp.3325.3.A1_at	Potri.003G219900	ATMYB5 (MYB DOMAIN PROTEIN 5); DNA binding / transcription factor	2.791553	10.70551	1.84E-06
PtpAffx.212895.1.S1_at	Potri.015G100600	unknown protein	2.761163	4.73653	0.001029
PtpAffx.204062.1.S1_at	Potri.004G105000	cinnamoyl-CoA reductase-related	2.734055	10.05732	3.11E-06
PtpAffx.215434.1.S1_s_at	Potri.017G110500	cinnamoyl-CoA reductase-related	2.733339	6.523722	0.000103
PtpAffx.28572.2.S1_at	Potri.001G001600	pyruvate kinase, putative	2.648487	12.02177	6.80E-07
PtpAffx.12874.1.S1_at	Potri.006G232900	GAMMA-VPE (GAMMA VACUOLAR PROCESSING ENZYME); cysteine-type endopeptidase	2.634358	4.594286	0.001261
Ptp.2332.2.A1_a_at	Potri.008G188900	ACLA-2; ATP citrate synthase	2.63431	10.41704	2.31E-06
PtpAffx.21672.1.A1_at	---	---	2.625945	2.804837	0.020317
Ptp.5940.1.S1_at	Potri.016G031100	CYP98A3 (cytochrome P450, family 98, subfamily A)/ p-coumarate 3-hydroxylase	2.61989	11.76116	8.21E-07
PtpAffx.16436.1.S1_at	---	---	2.619259	5.071908	0.000646
PtpAffx.31264.2.S1_a_at	Potri.015G022000	TRY (TRIPTYCHON); DNA binding / transcription factor	2.587293	8.011203	2.04E-05
PtpAffx.6692.7.S1_s_at	Potri.014G020900	protein binding / zinc ion binding	2.550969	11.54143	9.66E-07
PtpAffx.224381.1.S1_s_at	Potri.004G071000	quercetin O-glucosyltransferase activity	2.546403	8.001654	2.06E-05
Ptp.4362.1.S1_at	Potri.017G052400	AtUGT85A2 (UDP-glucosyl transferase 85A2); UDP-glycosyltransferase/ glucuronosyltrans	2.544274	10.51518	2.14E-06
PtpAffx.220100.1.S1_at	Potri.001G133000	anthocyanidin 3-O-glucosyltransferase activity	2.52905	10.23921	2.68E-06
PtpAffx.39332.1.A1_s_at	Potri.004G057700	XBCP3 (xylem bark cysteine peptidase 3); cys-type endopeptidase/ cys-type peptidase	2.526964	11.09185	1.36E-06
PtpAffx.221214.1.S1_s_at	Potri.014G020900	protein binding / zinc ion binding	2.522584	10.93512	1.53E-06
PtpAffx.158517.1.S1_at	Potri.005G004900	ACLA-3; ATP citrate synthase	2.512869	7.281543	4.37E-05
Ptp.7600.1.S1_at	---	---	2.506107	6.885613	6.77E-05
PtpAffx.13946.1.A1_at	Potri.017G043200	unknown protein	2.492587	12.85522	3.81E-07
PtpAffx.162546.1.A1_at	Potri.003G144300	MYB3 (MYB DOMAIN PROTEIN 3); DNA binding / transcription factor	2.491668	7.137922	5.11E-05
PtpAffx.1150.1.A1_s_at	Potri.002G092700	ACC1 (ACETYL-COENZYME A CARBOXYLASE 1); acetyl-CoA carboxylase	2.488203	7.42187	3.76E-05
Ptp.336.1.S1_at	Potri.019G130700	cytochrome P450 (CYP73A43|C4H1)	2.481541	8.496099	1.26E-05
PtpAffx.215434.1.S1_at	Potri.017G110500	cinnamoyl-CoA reductase-related	2.477578	10.77734	1.73E-06
Ptp.4670.1.S1_s_at	Potri.008G105300	ACLB-2 (ATP CITRATE LYASE SUBUNIT B 2); ATP citrate synthase	2.456871	8.442009	1.33E-05
PtpAffx.134162.1.A1_at	Potri.004G067000	alcohol dehydrogenase, putative	2.456086	9.138853	6.93E-06
Ptp.7408.1.A1_a_at	Potri.001G247400	ceramidase family protein	2.432504	11.41054	1.07E-06
PtpAffx.225544.1.S1_x_at	Potri.016G031100	CYP98A3 (cytochrome P450, family 98, subfamily A)/ p-coumarate 3-hydroxylase	2.424918	11.02059	1.43E-06
PtpAffx.1106.1.A1_at	Potri.001G046600	40S ribosomal protein S12 (RPS12C)	2.420823	2.310547	0.045867
PtpAffx.218534.1.S1_at	Potri.007G050500	protein binding / zinc ion binding	2.387301	9.608634	4.57E-06
PtpAffx.223835.1.S1_s_at	Potri.003G030800	unknown protein	2.368963	8.679073	1.06E-05
Ptp.5131.1.S1_at	Potri.017G052000	AtUGT85A2 (UDP-glucosyl transferase 85A2); UDP-glycosyltransferase/ glucuronosyltrans	2.336465	7.194964	4.80E-05
PtpAffx.108534.1.A1_at	---	---	2.29474	6.687691	8.49E-05
Ptp.6482.1.S1_s_at	Potri.002G092700	ACC1 (ACETYL-COENZYME A CARBOXYLASE 1); acetyl-CoA carboxylase	2.291282	9.982337	3.32E-06
PtpAffx.47237.3.S1_at	Potri.003G054000	unknown protein	2.286676	9.091413	7.24E-06
PtpAffx.112345.1.S1_at	Potri.002G059200	KCO6; outward rectifier potassium channel	2.282778	5.927971	0.000211
PtpAffx.148416.1.S1_s_at	Potri.001G214500	strictosidine synthase family protein	2.261869	6.428944	0.000115
PtpAffx.221212.1.S1_at	Potri.014G020900	protein binding / zinc ion binding	2.261332	11.10374	1.34E-06
PtpAffx.160133.2.A1_a_at	Potri.006G007900	unknown protein	2.248776	7.038943	5.70E-05
Ptp.4863.2.A1_at	Potri.013G073300	flavonoid 3'-hydroxylase (F3H1)	2.246906	9.205685	6.53E-06
Ptp.6838.2.S1_a_at	Potri.001G221900	pathogenesis-related thaumatin family protein	2.246468	5.082685	0.000636
PtpAffx.92231.1.S1_at	---	---	2.241896	5.727165	0.000272
PtpAffx.14362.1.A1_s_at	Potri.001G221900	pathogenesis-related thaumatin family protein	2.235652	5.066883	0.00065
Ptp.7408.3.A1_at	Potri.001G247400	ceramidase family protein	2.234739	8.235781	1.63E-05
PtpAffx.31264.2.S1_at	---	---	2.230327	7.104467	5.30E-05
PtpAffx.204049.1.S1_s_at	Potri.004G071000	quercetin O-glucosyltransferase activity	2.226384	6.433038	0.000114
PtpAffx.157532.1.S1_at	Potri.016G014300	UGT71C4 (UDP-GLUCOSYL TRANSFERASE 71C4); quercetin 3-O-glucosyltransferase	2.215982	9.77298	3.96E-06
PtpAffx.158559.1.S1_at	Potri.009G149900	amino acid transporter family protein	2.205333	9.949027	3.41E-06
PtpAffx.152256.1.S1_at	Potri.007G107600	DNAJ heat shock N-terminal domain-containing protein	2.185436	5.20834	0.000537
PtpAffx.106733.1.A1_at	Potri.002G057700	enoyl-CoA hydratase/isomerase family protein	2.16468	9.9674	3.36E-06
PtpAffx.155350.1.S1_s_at	Potri.005G141600	RD21 (responsive to dehydration 21); cys-type endopeptidase/ cys-type peptidase	2.148969	7.781923	2.58E-05
PtpAffx.4938.1.S1_s_at	Potri.017G120300	unknown protein	2.146505	9.207772	6.51E-06
PtpAffx.163838.2.S1_a_at	Potri.008G125900	fructose-bisphosphate aldolase, putative	2.130366	6.109376	0.000169
Ptp.5756.2.S1_at	Potri.010G226300	ARA6; GTP binding / GTPase	2.125576	2.559297	0.030443
PtpAffx.77835.1.S1_at	---	---	2.097136	7.099204	5.33E-05
Ptp.5443.1.S1_s_at	Potri.011G015600	pyrophosphate--fructose-6-phosphate 1-phosphotransferase beta subunit, putative	2.094092	9.804481	3.86E-06
PtpAffx.221492.1.S1_at	Potri.003G030800	unknown protein	2.093571	9.449477	5.25E-06
Ptp.1110.1.A1_s_at	Potri.003G052400	GL2 (GLABRA 2); DNA binding / transcription factor	2.087409	7.167424	4.95E-05
PtpAffx.211115.1.S1_at	Potri.013G069200	(MATE) family transporter-related	2.08731	9.174397	6.71E-06
PtpAffx.134527.1.A1_at	Potri.016G034600	scpl46 (serine carboxypeptidase-like 46); serine-type carboxypeptidase	2.086066	8.284453	1.55E-05
Ptp.2303.1.S1_at	Potri.001G214500	strictosidine synthase family protein	2.08107	8.697285	1.04E-05
PtpAffx.32381.1.S1_s_at	Potri.003G059200	esterase/lipase/thioesterase family protein	2.076343	3.95531	0.00325
PtpAffx.12443.4.A1_s_at	Potri.013G157900	cytochrome P450 cinnamate 4-hydroxylase (C4H2|CYP73A42)	2.064479	4.667058	0.001136
Ptp.3935.2.S1_a_at	Potri.001G286600	membrane protein-related	2.060216	8.334045	1.48E-05
PtpAffx.83148.1.S1_s_at	Potri.010G145800	ACLB-2 (ATP CITRATE LYASE SUBUNIT B 2); ATP citrate synthase	2.055867	6.283631	0.000136
Ptp.1405.1.S1_at	Potri.014G128500	PHR2 (photolyase/blue-light receptor 2); DNA photolyase	2.05493	9.385609	5.56E-06
PtpAffx.43377.1.A1_s_at	Potri.014G074400	RNA binding	2.054092	2.773258	0.0214
PtpAffx.11317.4.A1_at	Potri.008G095300	PDCB3 (PLASMODESMATA CALLOSE-BINDING PROTEIN 3); callose binding / polysaccharid	2.04457	2.525089	0.032209
PtpAffx.8131.5.A1_a_at	---	---	2.038837	5.023013	0.00069
PtpAffx.83148.2.S1_a_at	Potri.008G105300	ACLB-2 (ATP CITRATE LYASE SUBUNIT B 2); ATP citrate synthase	2.036126	4.372222	0.001741

PtpAffx.138813.1.A1_s_at	Potri.013G004400	ACLA-3; ATP citrate synthase	2.034481	8.003743	2.05E-05
PtpAffx.100093.1.A1_at	---	---	2.032688	3.893763	0.003571
PtpAffx.204541.1.S1_s_at	Potri.009G132000	cold-shock DNA-binding family protein	2.031272	4.480199	0.001487
PtpAffx.220057.1.S1_x_at	Potri.001G141700	unknown protein	2.021024	6.981956	6.08E-05
PtpAffx.51055.1.S1_at	Potri.003G215200	GRIK2 (GEMINIVIRUS REP INTERACTING KINASE 2); kinase	2.020855	8.65247	1.09E-05
PtpAffx.53470.1.S1_at	Potri.006G009200	fumarylacetoacetase, putative	2.018855	8.151667	1.77E-05
Ptp.4791.2.S1_s_at	Potri.009G068600	hydroxymethylglutaryl-CoA lyase, putative / 3-hydroxy-3-methylglutarate-CoA lyase	2.008318	5.157336	0.000575
PtpAffx.155350.1.S1_at	Potri.005G141600	RD21 (responsive to dehydration 21); cys-type endopeptidase/ cys-type peptidase	2.005884	6.031641	0.000186
PtpAffx.47237.3.S1_a_at	Potri.003G054000	unknown protein	2.000407	5.159467	0.000573

Supplemental Table S2. Enrichment of transcripts in MYB115-overexpressing transgenic poplar relative to controls

Affymetrix Probeset	P. tricho gene model	Annotation	Fold change	T statistic	P-value
PtpAffx.83404.1.A1_at	Potri.009G069100	flavonoid 3',5'-hydroxylase (CYP75A12|F3'5'H1)	138.3866	16.49887	1.45E-07
PtpAffx.224252.1.S1_at	Potri.002G173900	MYB115	121.7093	33.14042	5.27E-10
PtpAffx.30659.1.A1_at	Potri.002G173900	MYB115	101.6081	28.62251	1.73E-09
Ptp.8030.1.S1_s_at	Potri.014G019200	cytochrome b5-like	81.52364	29.39499	1.39E-09
PtpAffx.7896.2.S1_at	Potri.003G176700	chalcone synthase(CHS4)	64.90673	40.91504	9.49E-11
PtpAffx.7896.4.A1_a_at	Potri.003G176900	chalcone synthase (CHS6)	50.9888	49.33447	2.07E-11
PtpAffx.224485.1.S1_s_at	Potri.005G207600	(MATE) family transporter-related (AtTT12 like [82.6 % identity])	48.93626	33.508	4.81E-10
Ptp.6057.1.S1_at	Potri.001G113100	anthocyanidin synthase (ANS2)	41.48594	27.86099	2.15E-09
PtpAffx.7896.3.S1_a_at	Potri.001G051600	chalcone synthase (CHS3)	39.651	50.18968	1.80E-11
PtpAffx.37082.1.A1_at	Potri.002G033600	dihydroflavonol 4-reductase (DFR1)	38.50957	29.89835	1.21E-09
PtpAffx.161181.1.S1_at	Potri.006G178700	cinnamoyl-CoA reductase-like protein	35.7962	19.69623	3.53E-08
Ptp.6711.1.S1_s_at	Potri.014G145100	chalcone synthase (CHS1)	33.89923	26.52198	3.20E-09
PtpAffx.6065.2.S1_at	Potri.008G116500	leucoanthocyanidin reductase (LAR1)	33.23252	28.99153	1.56E-09
Ptp.8030.1.S1_at	Potri.014G019200	cytochrome b5-like	30.92049	48.15528	2.52E-11
Ptp.3138.2.A1_a_at	Potri.009G133300	UDP-glucose:flavonoid 3-O-glucosyltransferase-like protein	29.8633	12.10333	1.67E-06
RPTR-Ptp-U57609-2_s_at	---	Reporter	24.25004	22.26658	1.32E-08
PtpAffx.142603.1.A1_s_at	Potri.013G073300	flavonoid 3'-hydroxylase (F3’H1)	23.07233	38.05447	1.71E-10
PtpAffx.8131.4.A1_a_at	Potri.006G221800	MYB134	22.59711	37.48789	1.93E-10
PtpAffx.120325.1.S1_s_at	Potri.013G073300	flavonoid 3'-hydroxylase (F3’H1)	22.02849	26.36403	3.36E-09
Ptp.4863.1.S1_s_at	Potri.013G073300	flavonoid 3'-hydroxylase (F3’H1)	21.87519	35.14275	3.27E-10
PtpAffx.18705.2.A1_a_at	Potri.015G050200	leucoanthocyanidin reductase (LAR3)	21.52007	15.15406	2.85E-07
PtpAffx.5092.1.A1_at	Potri.004G030700	anthocyanidin reductase (ANR1)	20.29951	24.47979	6.12E-09
Ptp.4458.1.S1_s_at	Potri.T035000	glutathione s-transferase-like	20.29729	9.953257	7.53E-06
Ptp.5716.1.S1_at	Potri.002G095900	sugar transport protein-like	19.893	25.79752	4.01E-09
PtpAffx.5092.2.S1_a_at	Potri.004G030700	anthocyanidin reductase (ANR1)	19.81152	36.71946	2.29E-10
Ptp.323.1.S1_s_at	Potri.005G113900	flavanone 3-hydroxylase (F3H6)	19.61242	38.31492	1.62E-10
Ptp.6753.1.S1_s_at	Potri.006G027000	serine hydrolase-like	17.94192	19.65876	3.58E-08
PtpAffx.8131.6.A1_a_at	Potri.006G221800	MYB134	17.36366	33.52703	4.79E-10
PtpAffx.127289.1.A1_at	Potri.006G209000	WD40 repeat-containing protein [1] (AtLWD1 like [72.8 % identity])	16.70971	15.75336	2.10E-07
PtpAffx.25553.1.A1_at	Potri.005G229500	dihydroflavonol 4-reductase (DFR2)	15.60789	20.73333	2.33E-08
Ptp.4912.2.A1_at	---	---	12.61972	19.61306	3.65E-08
PtpAffx.160113.1.A1_s_at	Potri.001G006700	acyl-activating enzyme-like protein	11.57284	28.3388	1.87E-09
PtpAffx.7740.2.A1_a_at	Potri.018G100500	cinnamoyl-CoA reductase-like protein	11.3066	22.3608	1.27E-08
Ptp.3754.1.A1_at	Potri.011G097300	transcription elongation factor Elf1-like protein	10.87061	6.018868	0.0002907
PtpAffx.157838.2.S1_at	---	---	10.2875	9.514738	1.06E-05
Ptp.1362.1.S1_at	Potri.001G256900.1	similar to photosystem II 5 kD protein	10.16059	9.289607	1.27E-05
PtpAffx.6065.3.A1_a_at	Potri.010G129800	leucoanthocyanidin reductase (LAR2)	10.10974	24.89133	5.35E-09
Ptp.1080.1.S1_s_at	Potri.010G129800	leucoanthocyanidin reductase (LAR2)	9.148366	25.0298	5.12E-09
PtpAffx.212895.1.S1_at	Potri.015G100600	chitinase-like	8.641889	8.400222	2.69E-05
Ptp.6632.1.S1_at	Potri.019G130700	cinnamate 4-hydroxylase (C4H1|CYP73A43)	8.199498	14.99177	3.11E-07
PtpAffx.92231.1.S1_at	---	---	8.148303	22.42177	1.24E-08
PtpAffx.150025.1.S1_s_at	Potri.013G157900	cinnamate 4-hydroxylase (C4H2|CYP73A42)	7.907291	17.67985	8.37E-08
Ptp.1080.1.S1_at	Potri.010G129800	leucoanthocyanidin reductase (LAR2)	7.835983	18.63607	5.49E-08
PtpAffx.156161.1.A1_at	Potri.001G157600	integral membrane family protein	7.723566	22.44263	1.23E-08
PtpAffx.200035.1.S1_at	Potri.001G006700	acyl-activating enzyme-like protein	7.546858	28.25221	1.92E-09
PtpAffx.94822.1.A1_at	Potri.002G055100	(MATE) family transporter-related (AtTT12 like [81.5 % identity])	7.284551	16.34024	1.57E-07
PtpAffx.222060.1.S1_at	---	---	7.223664	6.776095	0.0001277
Ptp.1512.1.S1_s_at	Potri.019G057800	---	7.201737	18.79384	5.13E-08
Ptp.6057.1.S1_s_at	Potri.001G113100	anthocyanidin synthase (ANS2)	7.027916	18.70538	5.33E-08
PtpAffx.30128.1.S1_at	Potri.001G140700	cinnamoyl-CoA reductase-like protein	6.969607	9.0101	1.60E-05
PtpAffx.12443.4.A1_s_at	Potri.013G157900	cinnamate 4-hydroxylase (C4H2|CYP73A42)	6.967922	15.65616	2.20E-07
Ptp.336.1.S1_at	Potri.019G130700	cinnamate 4-hydroxylase (C4H1|CYP73A43)	6.234563	14.21163	4.74E-07
PtpAffx.7795.1.A1_at	Potri.019G024600	---	6.00181	3.508483	0.0077109
PtpAffx.12353.1.A1_at	Potri.018G146100	trans-cinnamate 4-monooxygenase (C4H3)	5.992858	7.615204	5.54E-05
PtpAffx.7243.1.A1_a_at	Potri.002G212300	---	5.925439	11.8391	1.98E-06
PtpAffx.12056.3.S1_a_at	Potri.T071600	4-Coumarate:CoA ligase (4CL4)	5.802742	15.07739	2.97E-07
PtpAffx.133554.1.A1_s_at	Potri.005G167400	acetyl-CoA carboxylase-like protein	5.629325	18.78839	5.15E-08
PtpAffx.46281.1.S1_at	Potri.019G024600	lipase/acylhydrolase-like protein	5.359818	3.896597	0.0043788
PtpAffx.249.86.A1_a_at	---	---	5.031714	9.119101	1.46E-05
PtpAffx.215434.1.S1_at	Potri.017G110500	flavonol reductase/cinnamoyl-CoA reductase-like	4.837022	16.92189	1.19E-07
PtpAffx.34213.1.S1_at	Potri.013G083600	peroxidase-like protein	4.7162	10.88566	3.79E-06
PtpAffx.211755.1.S1_at	Potri.014G127500	---	4.686047	7.254369	7.86E-05
PtpAffx.162989.1.S1_at	Potri.009G133300	UDP-glucose:flavonoid 3-O-glucosyltransferase-like protein	4.626936	8.275647	3.01E-05
PtpAffx.205491.1.S1_at	Potri.005G167400	acetyl-CoA carboxylase-like protein	4.48875	16.31234	1.59E-07
PtpAffx.157838.2.S1_a_at	---	---	4.461568	7.456369	6.45E-05
PtpAffx.249.102.A1_x_at	Potri.018G114800	---	4.456062	15.85175	2.00E-07
PtpAffx.249.83.A1_x_at	Potri.018G114800	---	4.391304	15.6514	2.21E-07
PtpAffx.104180.1.S1_at	Potri.010G075600	serine protease inhibitor-like	4.238565	7.060771	9.54E-05
Ptp.4912.1.S1_at	---	---	4.19839	12.79569	1.08E-06
Ptp.6847.1.S1_a_at	Potri.013G103700	phenylcoumaran benzylic ether reductase -like protein	4.190316	5.764166	0.0003895

PtpAffx.4850.1.A1_s_at	Potri.010G213000	chalcone isomerase (CHI1)	4.163411	20.33791	2.73E-08
Ptp.6847.2.S1_s_at	Potri.013G103700	phenylcoumaran benzylic ether reductase -like protein	4.108134	6.033845	0.0002858
PtpAffx.159543.1.A1_at	Potri.006G101100	similar to putative ANS in *Ricinus communis* (86.7% identity)	4.057872	6.905437	0.0001117
PtpAffx.160901.1.S1_s_at	Potri.004G057700	cysteine protease-like protein	4.001451	7.908653	4.20E-05
PtpAffx.5685.1.S1_x_at	Potri.005G045300	---	3.945677	15.6539	2.21E-07
PtpAffx.211115.1.S1_at	Potri.013G069200	(MATE) family transporter-related	3.945352	13.54431	6.92E-07
PtpAffx.224943.1.S1_s_at	Potri.019G036400	MYB061	3.897258	15.30864	2.63E-07
Ptp.6482.1.S1_s_at	Potri.002G092700	acetyl-CoA carboxylase-like protein	3.874861	10.27301	5.92E-06
Ptp.1442.1.S1_x_at	---	---	3.86488	8.49947	2.47E-05
PtpAffx.215434.1.S1_s_at	Potri.017G110500	flavonol reductase/cinnamoyl-CoA reductase-like	3.851884	10.07009	6.89E-06
Ptp.5773.1.S1_at	Potri.016G111000	probable anion transporter chloroplastic-like	3.845173	11.14552	3.16E-06
PtpAffx.108534.1.A1_at	Potri.014G145100	chalcone synthase (CHS1)	3.767658	15.10607	2.93E-07
PtpAffx.137746.1.S1_at	Potri.004G088100	MYB182	3.744134	7.41577	6.71E-05
PtpAffx.5685.1.S1_a_at	Potri.005G045300	---	3.62709	16.61348	1.37E-07
PtpAffx.48329.2.S1_at	---	---	3.613938	5.560928	0.0004948
PtpAffx.47237.2.A1_a_at	Potri.001G181700	---	3.606718	13.72643	6.23E-07
PtpAffx.201822.1.S1_at	Potri.002G072600	sugar transporter-like protein	3.570947	9.349286	1.21E-05
Ptp.6610.1.S1_at	---	---	3.467474	10.48192	5.07E-06
PtpAffx.224746.1.S1_s_at	Potri.011G066800	cysteine protease-like protein	3.433912	9.618818	9.76E-06
PtpAffx.256.2.S1_at	Potri.005G208600	bHLH type protein [1] (TT8 like [50.5 % identity])	3.407876	13.26681	8.15E-07
PtpAffx.161412.1.S1_at	Potri.004G054600	lipase-like protein	3.388368	7.43673	6.57E-05
PtpAffx.19596.1.S1_at	---	---	3.299199	13.09167	9.04E-07
PtpAffx.65824.1.A1_at	Potri.001G001600	pyruvate kinase-like protein	3.27352	14.11556	5.00E-07
PtpAffx.224650.1.S1_s_at	Potri.010G114000	MYB165	3.237289	5.234589	0.0007354
PtpAffx.50866.2.A1_s_at	Potri.004G041800	amidohydrolase-like protein	3.233605	5.358508	0.0006316
PtpAffx.249.498.A1_at	Potri.018G114800	---	3.226604	7.564087	5.81E-05
PtpAffx.112345.1.S1_at	Potri.002G059200	ion channel-like protein	3.206058	7.530962	6.00E-05
PtpAffx.160504.1.A1_s_at	Potri.002G092700	acetyl-CoA carboxylase-like protein	3.182847	9.922325	7.71E-06
PtpAffx.224878.1.S1_at	Potri.014G100800	MYB201	3.168808	12.87925	1.03E-06
PtpAffx.225583.1.S1_s_at	Potri.014G033400	Patatin-like phospholipase-like protein	3.136809	11.29783	2.85E-06
Ptp.8024.1.S1_at	Potri.005G208600	bHLH type protein (TT8 like [50.5 % identity])	3.114279	7.363569	7.06E-05
PtpAffx.157838.1.S1_at	---	---	3.0776	9.196645	1.37E-05
PtpAffx.205684.1.S1_at	Potri.005G208600	bHLH type protein (TT8 like [50.5 % identity])	3.059646	7.794288	4.67E-05
PtpAffx.83148.1.S1_s_at	Potri.010G145800	ATP citrate-lyase-like protein	3.057902	9.653389	9.50E-06
PtpAffx.201776.1.S1_at	Potri.002G064100	carboxypeptidase-like protein	3.043018	3.290363	0.0106903
PtpAffx.83148.2.S1_s_at	Potri.010G145800	ATP citrate-lyase-like protein	3.005611	7.956358	4.02E-05
PtpAffx.210644.1.S1_at	Potri.012G096800	cytochrome P450 family	2.961663	3.691066	0.0058936
PtpAffx.30743.1.A1_a_at	Potri.013G031900	---	2.9584	11.44653	2.57E-06
PtpAffx.101397.1.A1_at	Potri.013G069200	(MATE) family transporter-related protein	2.943119	10.48001	5.08E-06
PtpAffx.86545.1.S1_at	Potri.010G223700	---	2.891662	8.903977	1.75E-05
PtpAffx.43288.1.A1_at	Potri.004G054600	lipase-like protein	2.869454	6.229325	0.0002297
PtpAffx.204062.1.S1_at	Potri.004G105000	dehydrogenase/isomerase-like	2.852432	9.672841	9.36E-06
Ptp.2571.1.A1_at	Potri.002G092700	acetyl-CoA carboxylase-like protein	2.808251	8.913257	1.73E-05
Ptp.5281.1.S1_s_at	Potri.008G149200	short chain dehydrogenase-like	2.803008	4.7786	0.0013118
PtpAffx.2158.1.S1_at	---	---	2.757472	6.311696	0.0002098
Ptp.6940.1.S1_at	---	---	2.754735	2.882775	0.0199679
PtpAffx.158517.1.S1_at	Potri.005G004900	ATP citrate lyase-like	2.748815	11.35673	2.74E-06
PtpAffx.249.338.A1_a_at	---	---	2.748724	9.3027	1.26E-05
PtpAffx.159543.2.A1_a_at	Potri.006G101100	oxidoreductase-like	2.73983	4.536333	0.001806
PtpAffx.18588.1.S1_at	Potri.013G143300	ribosomal protein-like	2.731795	8.262419	3.05E-05
PtpAffx.216838.1.S1_at	Potri.015G018300	---	2.71574	6.724987	0.0001347
PtpAffx.213439.1.S1_at	Potri.016G075800	WD40 repeat-containing protein (AtLWD1 like [67.5 % identity])	2.690502	6.226195	0.0002305
Ptp.3045.1.S1_at	Potri.004G188100	prephenate dehydratase-like	2.687724	6.638084	0.0001476
PtpAffx.57339.1.A1_at	Potri.016G052200	---	2.671401	7.565747	5.80E-05
PtpAffx.2048.1.S1_a_at	Potri.003G131600	---	2.666177	6.770262	0.0001285
Ptp.5023.1.S1_s_at	Potri.001G293400	adenylyl-sulfate kinase-like	2.657122	2.865447	0.0205126
Ptp.4670.1.S1_s_at	Potri.008G105300	ATP citrate lyase-like	2.642401	8.599119	2.27E-05
PtpAffx.161399.1.S1_at	Potri.012G057500	enolase-like	2.635902	4.351309	0.0023189
PtpAffx.76291.2.A1_a_at	Potri.002G059200	potassium ion channel-like	2.614822	3.716327	0.0056805
Ptp.6352.1.A1_s_at	Potri.002G242500	cytochrome b5-like	2.600035	9.409424	1.15E-05
PtpAffx.4.4.A1_a_at	Potri.009G141800	chitinase-like	2.594996	10.46406	5.14E-06
Ptp.3045.1.S1_s_at	Potri.004G188100	prephenate dehydratase-like	2.594379	7.64156	5.40E-05
Ptp.2979.1.S1_at	Potri.010G124700	---	2.593676	2.829327	0.0216977
PtpAffx.2048.1.S1_x_at	Potri.003G131600	---	2.590999	7.221674	8.12E-05
PtpAffx.225544.1.S1_s_at	Potri.016G031000	p-coumaroyl shikimate 3'- hydroxylase (C3H3)	2.560835	9.862101	8.08E-06
Ptp.2358.1.S1_at	Potri.012G057500	enolase-like	2.557254	4.800596	0.0012748
PtpAffx.106733.1.A1_at	Potri.002G057700	enoyl-CoA hydratase-like	2.555981	10.3781	5.47E-06
PtpAffx.154968.1.S1_at	Potri.015G125100	membrane steroid-binding protein-like	2.538523	10.01741	7.17E-06
PtpAffx.33535.2.A1_at	Potri.002G029300	acid phosphatase-like	2.527966	8.040743	3.72E-05
PtpAffx.224602.1.S1_at	Potri.008G128500	MYB194	2.503994	5.577113	0.0004854
PtpAffx.18295.2.A1_s_at	Potri.010G055400	glyceraldehyde 3-phosphate dehydrogenase-like	2.503507	9.818499	8.35E-06
PtpAffx.138813.1.A1_s_at	Potri.013G004400	ATP citrate-lyase	2.480356	7.139291	8.81E-05
PtpAffx.30278.1.S1_at	Potri.003G061200	---	2.473269	4.448708	0.0020317
PtpAffx.163838.2.S1_a_at	Potri.008G125900	fructose-bisphosphate aldolase-like	2.471575	7.737257	4.93E-05

PtpAffx.224381.1.S1_s_at	Potri.004G071000	quercetin O-glucosyltransferase-like protein	2.466033	3.451684	0.0083908
PtpAffx.2048.2.S1_a_at	Potri.003G131600	---	2.44478	6.101373	0.0002649
PtpAffx.220100.1.S1_at	Potri.001G133000	UDP-glucosyltransferase-like	2.440327	4.87102	0.0011638
PtpAffx.208112.1.S1_s_at	Potri.008G143600	---	2.435925	7.339616	7.23E-05
PtpAffx.148416.1.S1_s_at	Potri.001G214500	strictosidine synthase-like	2.413321	5.177279	0.0007896
PtpAffx.39332.1.A1_s_at	Potri.004G057700	cysteine protease-like protein	2.412716	10.04581	7.02E-06
PtpAffx.55376.1.S1_at	Potri.014G143200	peroxidase-like	2.409356	3.894272	0.0043934
PtpAffx.225544.1.S1_x_at	Potri.016G031100	p-coumaroyl shikimate 3'- hydroxylase (CYP98A23)	2.381891	9.090713	1.49E-05
PtpAffx.47237.3.S1_a_at	Potri.003G054000	---	2.366469	6.922903	0.0001098
PtpAffx.53470.1.S1_at	Potri.006G009200	fumarylacetoacetase-like	2.359404	7.261286	7.81E-05
Ptp.1405.1.S1_at	Potri.014G128500	DNA photolyase-like	2.35134	6.672576	0.0001424
Ptp.5738.2.S1_s_at	Potri.006G050400	---	2.349355	2.462746	0.0385381
PtpAffx.30743.5.A1_at	Potri.013G031900	---	2.339317	9.759469	8.75E-06
PtpAffx.3539.1.S1_a_at	Potri.001G415100	terpene synthase-like	2.338787	4.857469	0.0011843
PtpAffx.28572.2.S1_at	Potri.001G001600	pyruvate kinase-like protein	2.33414	12.58818	1.23E-06
Ptp.2303.1.S1_at	Potri.001G214500	adipocyte plasma membrane-associated	2.327823	5.399246	0.000601
PtpAffx.6463.1.S1_at	Potri.004G188100	prephenate dehydratase-like	2.312865	8.009599	3.83E-05
PtpAffx.24245.1.A1_at	Potri.006G173500	transketolase-like	2.297136	5.283825	0.0006921
PtpAffx.202703.1.S1_at	Potri.002G252400	---	2.286861	2.337726	0.0469256
PtpAffx.161644.1.S1_s_at	Potri.001G083900	cytochrome P450-like	2.285017	2.753116	0.0244352
PtpAffx.144130.1.S1_s_at	Potri.001G083900	cytochrome P450-like	2.256183	2.606311	0.0307509
Ptp.2573.1.S1_at	Potri.015G034700	glutamine synthetase-like	2.255553	10.77045	4.12E-06
PtpAffx.75249.1.A1_at	Potri.001G161400	H+ ATPase-like	2.252031	8.906533	1.74E-05
PtpAffx.138656.1.A1_at	Potri.018G152100	aquaporin transporter-like	2.217306	6.177865	0.0002432
PtpAffx.208118.1.S1_at	Potri.008G143600	---	2.208126	4.90281	0.0011171
PtpAffx.204049.1.S1_s_at	Potri.004G071000	quercetin O-glucosyltransferase-like	2.207924	4.23344	0.0027263
PtpAffx.154968.1.S1_s_at	Potri.015G125100	membrane steroid-binding protein-like	2.205416	9.405889	1.16E-05
PtpAffx.80486.1.A1_at	Potri.001G212900	serine-type peptidase-like	2.200679	3.322185	0.010189
PtpAffx.25980.1.S1_at	Potri.012G032700	flavonol 3-sulfotransferase-like	2.191155	3.210633	0.0120635
PtpAffx.224381.1.S1_at	Potri.004G069600	quercetin O-glucosyltransferase-like protein	2.177728	2.541405	0.034052
PtpAffx.82668.1.A1_at	Potri.013G157400	cytochrome P450-like	2.168596	2.53337	0.0344849
PtpAffx.7243.1.A1_at	Potri.018G050400	---	2.16432	7.836895	4.49E-05
Ptp.5100.1.S1_at	---	---	2.152981	2.570649	0.0325223
PtpAffx.138813.2.A1_at	Potri.005G004900	ATP citrate lyase-like	2.150635	10.83039	3.95E-06
PtpAffx.47186.1.S1_at	Potri.004G178100	---	2.146189	5.161314	0.0008055
PtpAffx.3369.1.S1_a_at	---	---	2.134089	3.341739	0.0098933
PtpAffx.221214.1.S1_s_at	Potri.014G020900	zinc finger containing protein-like	2.133073	5.415362	0.0005894
PtpAffx.210754.1.S1_at	Potri.012G137500	fatty acyl CoA reductase-like	2.128173	7.412361	6.73E-05
PtpAffx.221212.1.S1_at	Potri.014G020900	zinc finger containing protein-like	2.126047	3.904663	0.0043286
PtpAffx.1270.1.A1_s_at	Potri.019G014800	phosholipase-like	2.121991	3.03659	0.015743
PtpAffx.220135.1.S1_at	Potri.001G126700	aminotransferase-like	2.121586	4.62623	0.0016023
Ptp.4791.2.S1_s_at	Potri.009G068600	hydroxymethylglutaryl-CoA lyase-like	2.112712	6.398702	0.0001908
PtpAffx.57056.1.A1_at	Potri.008G005500	---	2.112061	6.628964	0.0001491
Ptp.3327.1.S1_s_at	Potri.015G128700	plant invertase/pectin methylesterase inhibitor-like	2.104611	4.300874	0.0024846
PtpAffx.87960.1.S1_s_at	Potri.005G257800	phosphofructokinase-like	2.101025	5.244652	0.0007263
Ptp.4812.1.S1_at	Potri.005G257800	phosphofructokinase-like	2.083296	5.945701	0.0003159
PtpAffx.136901.1.S1_at	Potri.005G072500	lanthionine synthetase-like	2.077674	9.310869	1.25E-05
PtpAffx.217589.1.S1_at	Potri.006G170400	aminotransferase-like	2.07073	4.182782	0.0029246
Ptp.1556.1.A1_at	Potri.006G009200	fumarylacetoacetase-like	2.067807	7.129322	8.90E-05
PtpAffx.3539.3.S1_a_at	Potri.001G415100	terpene synthase-like	2.060775	3.509797	0.0076959
PtpAffx.223051.1.S1_s_at	Potri.013G052900	amino acid decarboxylase-like	2.05813	3.615169	0.0065867
PtpAffx.5931.1.A1_a_at	Potri.010G003800	thioesterase-like	2.058092	5.861012	0.0003481
PtpAffx.200334.1.S1_s_at	Potri.001G083900	cytochrome P450-like	2.033199	2.482165	0.037378
Ptp.6228.1.S1_at	Potri.003G100500	UDP-glycosyltransferase-like	2.032942	3.670273	0.0060754
PtpAffx.224177.1.S1_at	Potri.001G274600	flavonoid 3',5'-hydroxylase-like	2.031447	4.57172	0.0017226
PtpAffx.52548.1.A1_at	Potri.009G148800	prephenate dehydratase-like	2.030137	5.558171	0.0004965
Ptp.4667.1.S1_s_at	Potri.001G059900	glucose-6-phosphate dehydrogenase-like	2.029568	3.287616	0.0107348
Ptp.1017.1.A1_at	Potri.016G062700	hydrolase-like	2.02316	6.171412	0.0002449
PtpAffx.254.1.S1_s_at	Potri.014G115200	---	2.018906	7.152407	8.70E-05
PtpAffx.12443.3.A1_at	Potri.013G157900	cinnamate 4-hydroxylase (C4H2|CYP73A42)	2.018016	4.709989	0.0014348
PtpAffx.51055.1.S1_at	Potri.003G215200	protein kinase-like	2.015053	7.918406	4.16E-05
PtpAffx.2542.1.S1_at	Potri.003G158500	---	2.011455	9.347136	1.21E-05
PtpAffx.23401.1.S1_at	Potri.010G177700	alcohol dehydrogenase-like	2.009995	7.954195	4.03E-05
Ptp.323.1.S1_at	---	---	2.000638	2.621361	0.0300331

Supplemental Table S3. Prodelphidin and procyanidin concentrations within PAs of MYB115- and MYB134-overexpressing transgenics in both *P. tremula x P. tremuloides* (t x t) and *P. tremula x P. alba* (t x a) hybrid backgrounds. Means of several independently transformed lines with standard errors are shown.

	***P. tremula x tremuloides* (353-38)**					***P. tremula x alba* (717-B4)**		
	Control (t x t)	MYB134 Line 1	MYB134 Line 6	MYB115 Line 4	MYB115 Line 5	control (t x a)	MYB115 Line 1	MYB115 Line 3
prodelphinidin (mg/g DW)	0.012 ± 0.004	5.2 ± 0.3	3.5 ± 0.2	9.2 ± 0.9	10.4 ± 1.5	0.010 ± 0.002	0.40 ± 0.2	0.60 ± 0.03
procyanidin (mg/g DW)	0.23 ± 0.04	21.6 ± 1.4	18.0 ± 1.4	13.4 ± 1.1	13.5 ± 2.4	0.30 ± 0.07	3.0 ± 1.1	4.2 ± 0.6
percent prodelphinidin	4.3 ± 0.6	19.7 ± 1.5	16.2 ± 0.5	40.9 ± 4.3	44.2 ± 7.7	3.6 ± 0.6	10.6 ± 4.9	12.0 ± 1.1

Supplemental Table S4. Kaempferol, quercetin, and myricetin glycoside concentrations (mg/g DW) in PAs in *tremula x P. alba* (t x a) hybrid backgrounds. Means of multiple independently transformed lines with standard errors are shown. n.d., not detected (below limit of detection).

	***P. tremula x tremuloides* (353-38)**				
	Control (t x t)	MYB134 Line 1	MYB134 Line 6	MYB115 Line 4	MYB115 Line 5
kaempferol glycosides	0.25 ± 0.033	0.13 ± 0.005	0.12 ± 0.004	0.16 ± 0.016	0.13 ± 0.012
quercetin glycosides	0.24 ± 0.14	0.65 ± 0.023	0.58 ± 0.022	0.62 ± 0.018	0.56 ± 0.029
myricetin glycosides	n.d.	0.63 ± 0.025	0.54 ± 0.012	1.02 ± 0.133	1.05 ± 0.19

Supplemental Table S5. Primers used for this work

MYB115 plant-overexpressing constructs

MYB115-F	5'-GAGTCATACCAGCAGTGACTC-3'
MYB115-R	5'-TCCTGGGAAGGGCTCCTTGTT-3'

Promoter cloning

LAR1-PROMS-F	5'- CGGGGTACCAGAACTACTTATGGGCGGGT-3'
LAR1-PROMS-R	5'-CGCGGATCCGCTTGCAACTATATAAATAGTTTCTTG-3'
DFR2-PROMS-F	5'-CCCAAGCTTTTAGGAACTTATTAGTGTGGGGGT-3'
DFR2-PROMS-R	5'-GGACTAGTGTTTAATTCTCAAGCTGATGATGAGT-3'
DFR1-PROM-F	5'-ggaGGTACCGAAAATGATAACGGATGATTCCAC-3'
DFR1-PROM-R	5'-ggACTAGTCTTTAATTTTCAGACAGATGGTGG-3'
MYB115-PROM-F	5'-CAAACTCATACCCGAGTC-3
MYB115-PROM-R	5-AAGACTCTGAACCACATCAC-3
MYB134-PROM-F:	5'-CTGTCTGAAGACTCTGAACCACATCAC-3'
MYB134-PROM-R:	5'-TCTCTACGATCACCACACACGCG -3'
F3', 5' H- PROM-F	5'- CGGGATCCCATGGCGTGAGATGGTGCAAAAGC-3'
F3', 5' H- PROM-R	5'- CGGGATCCCATGGCGTGAGATGGTGCAAAAGC-3'
CytoB5-PROM-F:	5'- GC GTCGAC TCTTTTATGTTACCTGGGCCAATCG
CytoB5-PROM-R:	5'- CC CCCGGGCATGGGAATCCAAGATAGTCGTG-3'

Yeast two-hybrid assay cloning

MYB134- delet-F	5'- TTCCATATGATGGGGAGGAGTCCATGTTG-3'
MYB134- delet -R	5'- GCGTCGACTCAGGTTGCCAGTGTTGGCTTTG-3'
MYB115- delet -F	5'- TTCCATATGATGGGAAGGGCTCCTTGTTG-3'
MYB115- delet -R	5'- GCGTCGACTCATGGTTTAGCCTTGCTCTTGC-3'
bHLH131-F	5'- CGGAATTCATGGCTACCCCGCCT-3'
bHLH131-R	5'- GAAGGATCCTCAATCATGGGGTATTATTTTATG-3'