

Supplemental Table 1 *PgUGT* homologs found in *P. glauca* PG29 organ and tissue transcriptome libraries

<i>PgUGT</i>	PG29 hit	E-value	HSP length	%Identity
<i>UGT1</i>	PG29_Flush_Bud_comp132287_c2_seq4	0	569	100
<i>UGT1</i>	PG29_Flush_Bud_comp132287_c2_seq3	0	569	100
<i>UGT1</i>	PG29_Flush_Bud_comp132287_c2_seq1	0	1476	99
<i>UGT1</i>	PG29_Flush_Bud_comp132287_c1_seq3	0	1476	99
<i>UGT1</i>	PG29_Young_Buds_comp170110_c0_seq1	0	1476	99
<i>UGT1</i>	PG29_MatureNeedle_comp189895_c0_seq1	0	1476	99
<i>UGT1</i>	PG29_Flush_Bud_comp132287_c1_seq2	0	1476	99
<i>UGT1</i>	PG29_Flush_Bud_comp132287_c1_seq1	0	1476	99
<i>UGT1</i>	PG29_Bark_comp321308_c0_seq1	0	1476	99
<i>UGT2</i>	PG29_MatureNeedle_comp192578_c0_seq8	0	1452	99
<i>UGT2</i>	PG29_MatureNeedle_comp192578_c0_seq4	0	1452	99
<i>UGT2</i>	PG29_MatureNeedle_comp192578_c0_seq16	0	1137	99
<i>UGT2</i>	PG29_MatureNeedle_comp192578_c0_seq13	0	1137	99
<i>UGT2</i>	PG29_MatureNeedle_comp192578_c0_seq2	0	1440	97
<i>UGT2</i>	PG29_MatureNeedle_comp192578_c0_seq11	0	1420	97
<i>UGT2</i>	PG29_MatureNeedle_comp192578_c0_seq7	0	1420	97
<i>UGT2</i>	PG29_MatureNeedle_comp192578_c0_seq12	0	1125	96
<i>UGT3</i>	PG29_Flush_Bud_comp134798_c0_seq2	0	490	100
<i>UGT3</i>	PG29_Flush_Bud_comp134798_c0_seq1	0	490	100
<i>UGT3</i>	PG29_Bark_comp316885_c2_seq1	3.66E-137	273	100
<i>UGT3</i>	PG29_Flush_Bud_comp134798_c0_seq5	0	1467	100
<i>UGT3</i>	PG29_Flush_Bud_comp134798_c0_seq3	0	1467	100
<i>UGT3</i>	PG29_Flush_Bud_comp134798_c0_seq2	0	978	100
<i>UGT3</i>	PG29_Flush_Bud_comp134798_c0_seq1	0	978	100

<i>UGT3</i>	PG29_Young_Buds_comp169337_c0_seq2	0	793	100
<i>UGT4</i>	PG29_Flush_Bud_comp132287_c2_seq1	0	1476	99
<i>UGT4</i>	PG29_Flush_Bud_comp132287_c1_seq3	0	1476	99
<i>UGT4</i>	PG29_Young_Buds_comp170110_c0_seq1	0	1476	99
<i>UGT4</i>	PG29_MatureNeedle_comp189895_c0_seq1	0	1476	99
<i>UGT4</i>	PG29_Flush_Bud_comp132287_c1_seq2	0	1476	99
<i>UGT4</i>	PG29_Flush_Bud_comp132287_c1_seq1	0	1476	99
<i>UGT4</i>	PG29_Bark_comp321308_c0_seq1	0	1476	99
<i>UGT4</i>	PG29_Flush_Bud_comp132287_c2_seq4	0	569	100
<i>UGT4</i>	PG29_Flush_Bud_comp132287_c2_seq3	0	569	100
<i>UGT5</i>	PG29_Flush_Bud_comp135258_c3_seq4	0	468	100
<i>UGT5</i>	PG29_Flush_Bud_comp135258_c3_seq5	0	487	100
<i>UGT5</i>	PG29_Flush_Bud_comp135258_c1_seq1	0	1474	100
<i>UGT5</i>	PG29_Flush_Bud_comp135258_c3_seq6	0	479	96
<i>UGT5b</i>	PG29_MatureNeedle_comp192945_c0_seq1	0	1448	99
<i>UGT5b</i>	PG29_Flush_Bud_comp135175_c0_seq1	0	1023	99
<i>UGT5b</i>	PG29_MatureNeedle_comp192945_c0_seq2	0	1451	98
<i>UGT5b</i>	PG29_Flush_Bud_comp135175_c0_seq2	0	461	98
<i>UGT5d</i>	PG29_Flush_Bud_comp135258_c1_seq3	0	457	97
<i>UGT5b</i>	PG29_MatureNeedle_comp188458_c2_seq3	0	373	98
<i>UGT6</i>	PG29_Young_Buds_comp175679_c0_seq6	0	1422	99
<i>UGT6</i>	PG29_Young_Buds_comp175679_c0_seq5	0	1422	99
<i>UGT6</i>	PG29_Young_Buds_comp175679_c0_seq4	0	1422	99
<i>UGT6</i>	PG29_Young_Buds_comp175679_c0_seq3	0	1422	97
<i>UGT6</i>	PG29_Young_Buds_comp175679_c0_seq2	0	1422	97
<i>UGT6</i>	PG29_Young_Buds_comp175679_c0_seq1	0	1422	97
<i>UGT7</i>	PG29_Bark_comp311149_c0_seq1	0	903	98

<i>UGT7</i>	PG29_Young_Buds_comp170573_c1_seq1	0	1120	97
<i>UGT7</i>	PG29_Flush_Bud_comp130633_c0_seq1	0	1396	97
<i>UGT7</i>	PG29_MatureNeedle_comp192164_c1_seq5	0	1396	97
<i>UGT7</i>	PG29_MatureNeedle_comp192164_c1_seq4	0	1396	97
<i>UGT8</i>	PG29_Flush_Bud_comp121285_c0_seq1	0	667	99
<i>UGT8</i>	PG29_Young_Buds_comp141541_c0_seq1	0	644	99
<i>UGT8</i>	PG29_Bark_comp296235_c1_seq1	0	644	99

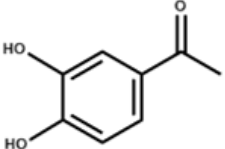
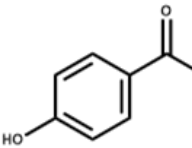
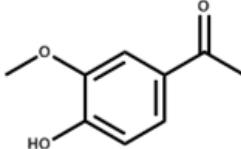
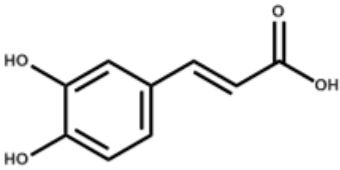
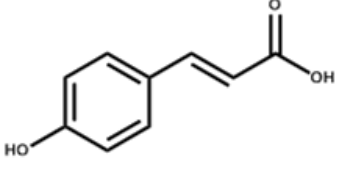
Supplemental Table 2 *PgUGT* homologs found in *P. abies*

PgUGT	PaUGT homolog	% nucleotide id	Tissue with highest expression
UGT1	MA_5002032g0010	98.85 %	needles
UGT2	MA_77583g0010	99.02 %	needles from dried twig
UGT3	MA_10428919g0010	98.91 %	vegetative shoots
UGT4	MA_5002032g0010	98.85 %	needles
UGT5	MA_572042g0010	98.91 %	vegetative shoots
UGT5b	MA_312221g0020	99.20 %	needles from girdled twig
UGT5d	MA_10427806g0010	98.44 %	needles
UGT6	MA_265454g0010	98.50 %	needles
UGT7	MA_10434373g0010	99.04 %	pineapple galls
UGT8	MA_495649g0010	99.22 %	needles

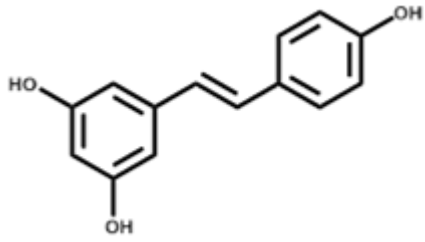
Supplemental Table 3. *PgUGTs* official nomenclature

Common name	Official name	Accession number
PgUGT1	PgUGT721A1	KY963359
PgUGT2	PgUGT722A1	KY963360
PgUGT3	PgUGT74AK1	KY963361
PgUGT5	PgUGT73AP1	KY963363
PgUGT5b	PgUGT73AP3	KY963364
PgUGT5c	PgUGT73AP2	KY963365
PgUGT6	PgUGT715A2	KY963366
PgUGT7	PgUGT73AQ1	KY963367
PgUGT8	PgUGT715B1	KY963368

Supplemental Table 4 Enzyme activity of PgUGT5 and PgUGT5b with different phenolic substrates.

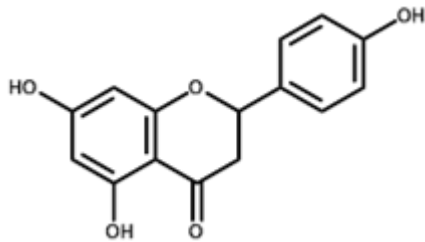
Substrate	PgUGT5	PgUGT5b
Pungenol		
	+	+
Piceol		
	-	-
Acetovanillone		
	-	-
Caffeic acid		
	-	-
Coumaric acid		
	-	-

Resveratrol



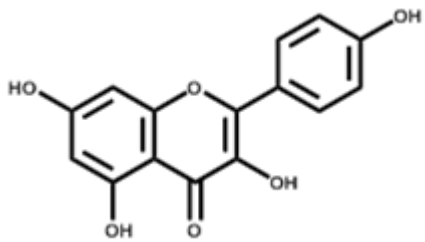
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Naringenin



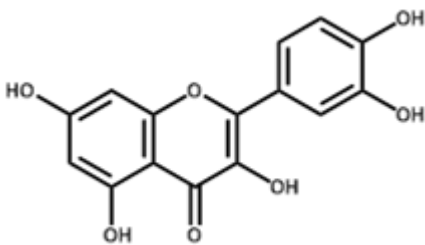
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Kaempferol



+ +

Quercetin



+ +

Supplemental Table 5. Primer sequences for cloning and qRT-PCR

	Gene	Primer direction	sequence	
pIBA	<i>PgUGT1</i>	Forward	CAACAT <u>GGTCTCA</u> <i>GCGC</i> ATGGTCCTTCTTGAGTTTGT	
		Reverse	CAACAT <u>GGTCTCA</u> <i>TATCA</i> CGGCAAATTTGAAGC	
	<i>PgUGT2</i>	Forward	CAACAT <u>GGTCTCA</u> <i>GCGC</i> ATGGATTCCACTCTTTACGcTC	
		Reverse	CAACAT <u>GGTCTCA</u> <i>TATCA</i> TTACTCCGTGGGATTTTCGTTT	
	<i>PgUGT4</i>	Forward	CAACAT <u>GGTCTCA</u> <i>GCGC</i> ATGGATTTATACGGTGCAGGCTG	
		Reverse	CAACAT <u>GGTCTCA</u> <i>TATCA</i> TCAATGGCACCCGTGTCC	
	<i>PgUGT5</i>	Forward	CAACAT <u>GGTCTCA</u> <i>GCGC</i> ATGCAGCCTTGTGAATTGGG	
		Reverse	CAACAT <u>GGTCTCA</u> <i>TATCA</i> TGTGTCAGGCACTG	
	<i>PgUGT5b</i>	Forward	CAACAT <u>GGTCTCA</u> <i>GCGC</i> ATGGGAAGCCGAAAGC	
		Reverse	CAACAT <u>GGTCTCA</u> <i>TATCA</i> TGTCGCTGCTGAGTTTG	
	<i>PgUGT5c</i>	Forward	CAACAT <u>GGTCTCA</u> <i>GCGC</i> ATGGGAAGCCGAAAGC	
		Reverse	CAACAT <u>GGTCTCA</u> <i>TATCA</i> TATATGGGGAATTATAGCGACC	
	<i>PgUGT6</i>	Forward	CAACAT <u>GGTCTCA</u> <i>GCGC</i> ATGGAAAGCAGACCTC	
		Reverse	CAACAT <u>GGTCTCA</u> <i>TATCA</i> TGCAGTGAGATTAATAG	
	<i>PgUGT7</i>	Forward	CAACAT <u>GGTCTCA</u> <i>GCGC</i> ATGGATGCGAGAAAG	
		Reverse	CAACAT <u>GGTCTCA</u> <i>TATCA</i> CTTACAGAAGAGAGC	
	<i>PgUGT8</i>	Forward	CAACAT <u>GGTCTCA</u> <i>GCGC</i> ATGGAAGAAAGCAAACCTTCATG	
		Reverse	CAACAT <u>GGTCTCA</u> <i>TATCA</i> CCAGTTGCAACCCAACTCTG	
		Gene	Primer direction	sequence
	pEAQ	<i>PgUGT5</i>	Forward	CAACAT <u>GGTCTC</u> <u>CAGAGT</u> ATGCAGCCTTGTG
			Reverse	CAACAT <u>GGTCTC</u> A <i>GCTATGTGTCAGGCACTG</i>
		<i>PgUGT5b</i>	Forward1	CAACAT <u>GGTCTC</u> <u>CAGAGT</u> ATGGGAAGCCGAAAGC
			Forward2	TTT <u>GGTCTCA</u> <i>CTgG ACATCCGCTTCG</i>
		Reverse1	TT <u>GGTCTCA</u> <i>CcAG ACCCTGTGGGG</i>	

	Gene	Primer direction	sequence
	<i>PgUGT5c</i>	Reverse2	CAACAT <u>GGTCTC A</u> <i>GCTATGTCGCTGCTGAGTTG</i>
		Forward	CAACAT <u>GGTCTCAGAGTATGGGAAGCCGAAAGC</u>
		Reverse	CAACAT <u>GGTCTC A</u> <i>GCTATATATGGGAATTATAGCGACC</i>
qRT-PCR	<i>GQ03413_J21</i>	Probe	/56-FAM/TGT TCC CCG /ZEN/TCC CCA AGT CTA TCA /3IABkFQ/
		Forward	CTA GTG GAC ATA ACA GAG GTG C
		Reverse	TTG TCC TTC ATA GCC CAG TTG
	<i>PgUGT5</i>	Probe	/56-FAM/ACA TTT ATC /ZEN/CAG TTG GGC CGC TCA /3IABkFQ/
		Forward	AAG CAC TGA GGG AAG GAA AG
		Reverse	CGA AGG CGC TTG GTT ATC TA
	<i>PgUGT5b</i>	Probe	/56-FAM/CGC CCA TGA /ZEN/AGC AAC CAC AAG TC/3IABkFQ/
		Forward	GGA TAC CAG AAT CGA ACC CAA G
		Reverse	CTC TCC AGC GTA GAA TTC CAG
	<i>PgUGT5c</i>	Probe	/56-FAM/TTT CCA TCT /ZEN/TCG CTG CTA TCC CCA C/3IABkFQ/
		Forward	CTT TCC CAA GTC TTA CCT GAG G
		Reverse	CTC TCC CTA CAA ATC CAT CGC

* Underlined bases represent BsaI restriction sites **Italicized* bases represent overhangs resulting from digest ***Bolded** base are gene specific bases