Supplementary Table 1. Group L UGTs included in phylogenetic analysis

GT	Species	Acc. no.	Activity	Source
UGT74B1	*Arabidopsis thaliana*	AAC00570	Thiohydroximate glucosyltransferase	1
UGT74C1	*Arabidopsis thaliana*	AAD32293	-	3
UGT74D1	*Arabidopsis thaliana*	AEC08580	Jasmonate glucosyltransferase	2
UGT74E1	*Arabidopsis thaliana*	POC7P7	-	3
UGT74F2	*Arabidopsis thaliana*	AAB64024	Salicylic acid and anthranilic acid glucosyltransferase	4-6
UGT75B1	*Arabidopsis thaliana*	AEE27854	Indole-3-acetic acid glucosyltransferase	29
UGT75C1	*Arabidopsis thaliana*	CAB10189	Anthocyanin-5-*O*-glucosyltransferase	7
UGT75D1	*Arabidopsis thaliana*	CAB10333	Flavonoid glucosyltransferase	8
UGT84A1	*Arabidopsis thaliana*	AEE83609	Hydroxybenzoate glucosyltransferase	4
UGT84B1	*Arabidopsis thaliana*	AAB87119	Indole-3-acetic acid glucosyltransferase	9
UGT74H5	*Avena strigosa*	ACD03250	N-methylanthranilate glucosyltransferase	This study
UGT74H6	*Avena strigosa*	ACD03261	Benzoic acid glucosyltransferase	This study
UGT74H7	*Avena strigosa*	ACD03246	-	This study
UGT84C2	*Avena strigosa*	ACD03236	-	This study
UGT75E2	*Avena strigosa*	ACD03260	-	This study
UGT75E3	*Avena strigosa*	ACD03251	-	This study
UGT75D1 like6	*Brachypodium distachyon*	XP_003576359	-	*
UGT75D1 like5	*Brachypodium distachyon*	XP_003560621	-	*
UGT75D1 like4	*Brachypodium distachyon*	XP_003571494	-	*
UGT84A2 like	*Brachypodium distachyon*	XP_003565946	-	*
Cinnamate-GT like2	*Brachypodium distachyon*	XP_003567004	-	*
Cinnamate-GT like1	*Brachypodium distachyon*	XP_003571042	-	*
IAA-GT like	*Brachypodium distachyon*	XP_003559553	-	*
UGT74F1 like1	*Brachypodium distachyon*	XP_003578449	-	*
UGT74F1 like2	*Brachypodium distachyon*	XP_003576736	-	*
UGT74F2 like	*Brachypodium distachyon*	XP_003578448	-	*
UGT84A9a	*Brassica napus*	CAS03354	Sinapate glucosyltransferase	10
CsGT45	*Crocus sativus*	ACM66950	Flavonoid glucosyltransferase	11
EpGT-1	*Eucalyptus perriniana*	BAD90934	Monoterpene glucosyltransferase	12
EpGT-2	*Eucalyptus perriniana*	BAD90935	Monoterpene glucosyltransferase	12
5GT-A	*Eustoma grandiflorum*	BAF49285	Anthocyanin 5-O-glucosyltransferase	13
FaGT2	*Fragaria x ananassa*	Q66PF4	Cinnamate glucosyltransferase	14
5GT7	*Gentiana triflora*	BAG32255	Anthocyanin 5-O-glucosyltransferase	15
HGT8	*Glandularia x hybrida*	BAA36423	Anthocyanin 5-O-glucosyltransferase	16
GgSGT	*Gomphrena globosa*	BAG14302	Sinapate glucosyltransferase	17
ant5GT	*Iris hollandica*	BAD06874	Anthocyanin 5-O-glucosyltransferase	18
HCA1GT-1	*Lobelia erinus*	BAF99686	Hydroxycinnamate-O-glucosyltransferase	19
SAGTase	*Nicotiana tabacum*	AAF61647	Salicylic acid glucosyltransferase	21
Os11g0145200	*Oryza sativa*	NP_001065729	-	*
Os02g0203300	*Oryza sativa*	NP_001046237	-	*

Supplementary Table 1 continued…

Os01g0686300	*Oryza sativa*	NP_001043905	-	*
Os01g0686200	*Oryza sativa*	NP_001043904	-	*
Os03g0693600	*Oryza sativa*	NP_001050964	-	*
Os09g0518000	*Oryza sativa*	NP_001063684	-	*
Os09g0518200	*Oryza sativa*	NP_001063685	-	*
Pf3R4	*Perilla frutescens*	BAA36421	Anthocyanin 5-O-glucosyltransferase	16
F7GT	*Pyrus comunnis*	AAY27090	Flavonoid 7-O-glucosyltransferase	22
GAGT	*Solanum lycopersicum*	CAI62049	Gentisic acid xylosyltransferase	20
UGT74M1	*Vaccaria hispanica*	ABK76266	Triterpene carboxylic acid glucosyltransferase	24
ResOGT	*Vitis labrusca*	ABH03018	Resveratrol/hydroxycinnamic acid O-glucosyltransferase	25
IAGLU	*Zea mays*	NP_001150551	Indole-3-acetate beta-glucosyltransferase	26, 27
IAGT	*Zea mays*	NP_001150551	-	26
UGT2	*Crocus sativus*	AAP94878	Crocetin glucosyltransferase	28

*Predicted by automated computational analysis

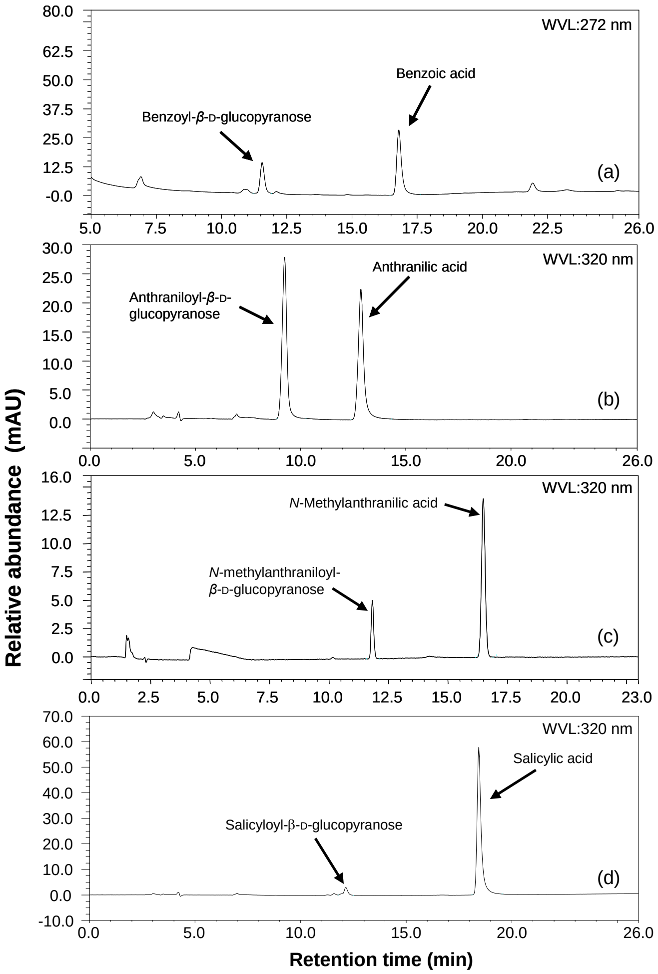
References

1. Grubb, C. D., Zipp, B. J., Ludwig-Muller, J., Masuno, M. N., Molinski, T. F., and Abel, S. (2004) *Plant J* **40**, 893-908
2. Song, J. T., Koo, Y. J., Seo, H. S., Kim, M. C., Choi, Y. D., and Kim, J. H. (2008) *Phytochemistry* **69**, 1128-1134
3. Li, Y., Baldauf, S., Lim, E. K., and Bowles, D. J. (2001) *J Biol Chem* **276**, 4338-4343
4. Lim, E. K., Doucet, C. J., Li, Y., Elias, L., Worrall, D., Spencer, S. P., Ross, J., and Bowles, D. J. (2002) *J Biol Chem* **277**, 586-592
5. Quiel, J. A., and Bender, J. (2003) *J Biol Chem* **278**, 6275-6281
6. Dean, J. V., and Delaney, S. P. (2008) *Physiologia plantarum* **132**, 417-425
7. Gachon, C. M., Langlois-Meurinne, M., Henry, Y., and Saindrenan, P. (2005) *Plant Mol Biol* **58**, 229-245
8. Messner, B., Thulke, O., Schäffner, A. R., (2005) *Planta* **217**, 138-146
9. Jackson, R. G., Lim, E. K., Li, Y., Kowalczyk, M., Sandberg, G., Hoggett, J., Ashford, D. A., and Bowles, D. J. (2001) *j Biol Chem* **276**, 138-146
10. Mittasch, J., Mikolajewski, S., Breuer, F., Strack, D., and Milkowski, C. (2010) *Theor Appl Genet* **276**, 138-146
11. Moraga, A. R., Mozos, A. T., Ahrazem, O., and Gomez-Gomez, L. (2009) *BMC Plant Biol* **9**, 109
12. Nagashima, S., Tomo, S. and Yoshikawa, T. (2005) *NCBI direct submission*
13. Noda, N., Kanno, Y. and Suzuki, M. (2002) *NCBI direct submission*
14. Landmann, C., Fink, B., and Schwab, W. (2007) *Planta* **226**, 417-428
15. Nakatsuka, T., Sato, K., Takahashi, H., Yamamura, S. and Nishihara, M. (2008) *J Exp Bot* **59**, 1241-1252
16. Yamazaki, M., Gong, Z., Fukuchi-Mizutani, M., Fukui, Y., Tanaka, Y.,Kusumi, T. and Saito, K. (1999) *J Biol Chem* **274**, 7405-7411
17. Matsuba, Y., Okuda, Y., Abe, Y., Kitamura, Y., Terasaka, K., Mizukami, H., Kamakura, H., Kawahara, N.,Goda, Y., Sasaki, N. and Ozeki, Y. (2008) *Plant Biotechnol* **25**, 369-375

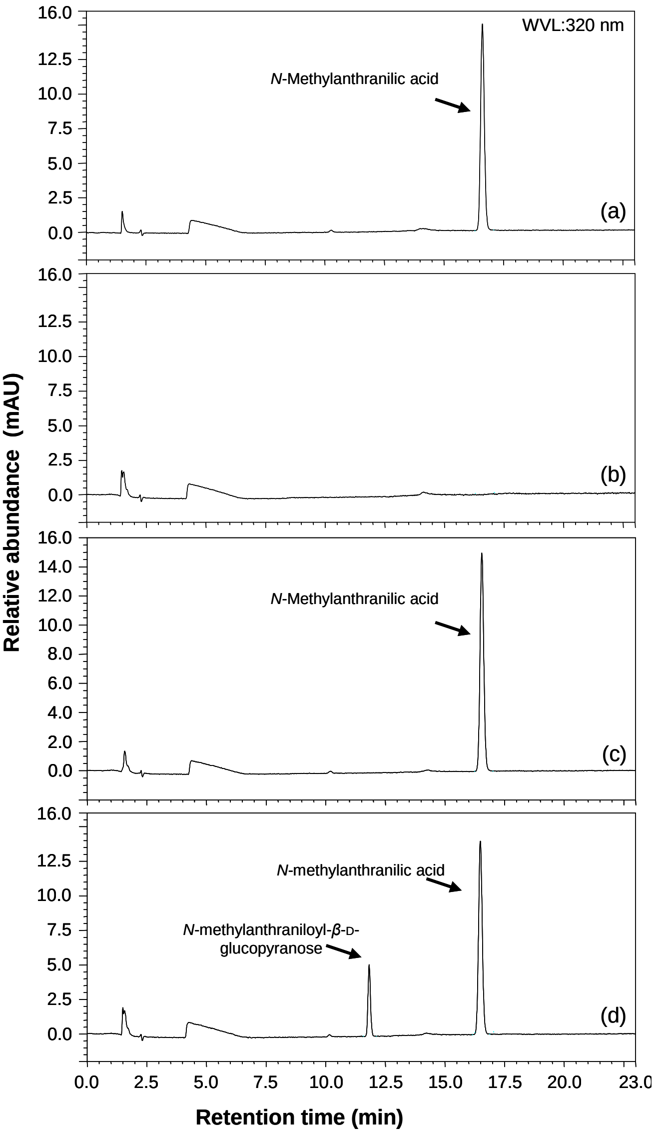
18. Imayama, T., Yoshihara, N., Fukuchi-Mizutani, M., Tanaka, Y., Ino, I. and Yabuya, T. (2004) *Plant Sci* **167**, 1243-1248
19. Noda, N., Kazauma, K. and Suzuki, M. (2005) *NCBI direct submission*
20. Tarraga, S., Lison, P.Lopez-Gresa, M. P., Torres, C., Rodrigo, I., Belles, J. M., and Conejero, V. (2010) *J Exp Bot* **61**, 4325-4338
21. Lee, H. I., and Raskin, I. (1999) *J Biol Chem* **274**, 36637-36642
22. Gosch, C., Halbwirth, H. and Stich, K. (2005) *Trees* **21**, 521-529
23. Richman, A., Swanson, A., Humphrey, T., Chapman, R., McGarvey, B., Pocs, R., and Brandle, J. (2005) *Plant J* **41**, 56-57
24. Meesapyodsuk, D., Balsevich, J., Reed, D. W., and Covello, P. S. (2007) *Plant Physiol* **143**, 959-969
25. Hall, D., De Luca, V., (2007) *Plant J* **49**, 579-591
26. Alexandrov, N. N., Brover, V. V., Freidin, S., Troukhan, M. E.,Tatarinova, T. V., Zhang, H., Swaller, T. J., Lu, Y. P., Bouck, J., Flavell, R. B., and Feldmann, K. A. (2009) *Plant Mol Biol* **69**, 179-194
27. Szerszen, J. B. Szczyglowski, K., and Bandurski, R. S. (1994) *Science* **265**, 1699-1701
28. Moraga, A. R., Nohales, P. F., Perez, J. A., and Gomez-Gomez, L. (2004) *Planta* **219**, 955-966
29. Jackson, R. G., Lim, E. K., Li, Y., Kowalczyk, M., Sandberg, G., Hoggett, J., Ashford, D. A. & Bowles, D. J. (2007) *J Biol Chem* **276**, 4350-4356

Supplementary Table 2. Oligonucleotide primer sequences

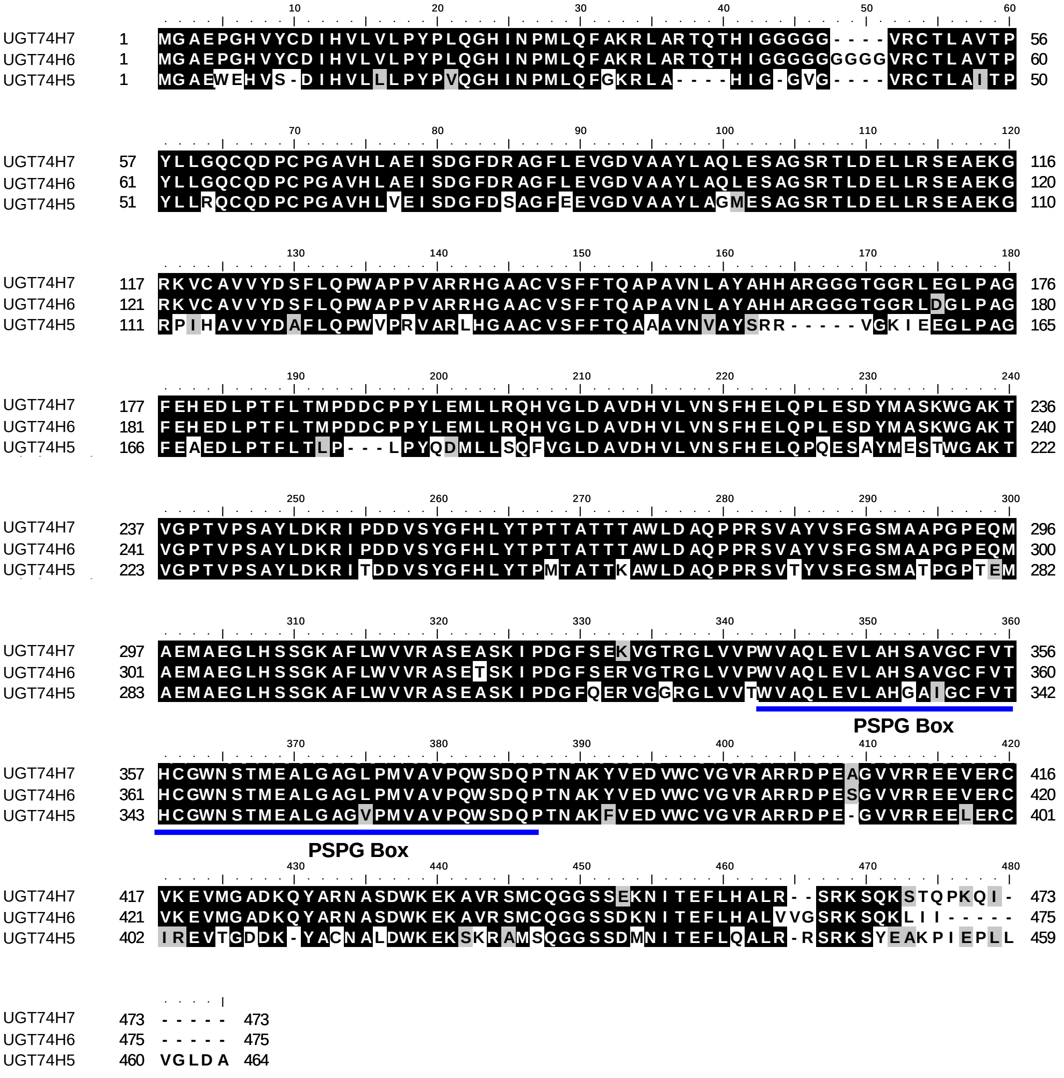
Primer no.	**DNA template**	**Oligonucleotide primer sequence (5’→3’)**
For His$_6$ tags:		
1	*UGT74H5*	GGAATTCCATATGGGGGCTGAGTGGGAG
2	*UGT74H5*	GGAATTCCATATGTCA TGCATCTAACCCCAC
3	*UGT74H7*	GGAATTCCATATGGGGGCTGAGCCGGGCCACGTA
4	*UGT74H7*	GGAATTCCATATGCTAGATTTGTTTGGGCTGAGTTG
5	*UGT74H6*	GGAATTCCATATGGGGGCTGAGCCGGGCCACGTA
6	*UGT74H6*	GGAATTCCATATGTCAGATGATTAATTTCTGGGATTTTC
For native protein:		
7	*UGT74H5*	TTCATATGGGGGCTGAGTGGGAG
8	*UGT74H5*	AGGAATCCATATGTCA TGCATCTAACCCCAC
9	*UGT74H7*	TTCATATGGGGGCTGAGCCGGGCCACGTA
10	*UGT74H7*	CTGAATTCCATATGCTAGATTTGTTTGGGCTGAGTTG
11	*UGT74H6*	TACATATGGGGGCTGAGCCGGGCCACGTA
12	*UGT74H6*	GGAATTCTCAGATGATTAATTTCTGGGATTTTC



Supplementary Figure 1A. HPLC analysis of glucosylated products following assays with purified recombinant UGT74H5. Reactions were performed in 5 mM UDP-D-glucose, pH 6.8 at 30^{O}C for 30 minutes with 100 µM benzoic acid (a), anthranilic acid (b), *N*-methylanthranilic acid (c) or salicylic acid (d). Reactions were analysed by reversed phase HPLC using a LUNA 5-µm C18 column (150 x 4.6 mm, Phenomenex) with a linear gradient of acetonitrile in water (10-40 % for anthranilate and *N*-methylanthranilate; 10-60% for salicylic acid and benzoic acid). The retention times of the glucose conjugates were (a) 11.6 min; (b) 9.2 min; (c) 11.8 min; (d) 12.1 min. Detection wavelengths (WVL) are indicated.



Supplementary Figure 1B. HPLC analysis for assays of purified recombinant UGT74H5 with *N*-methyl-anthranilate. Reactions were performed with 0.5 mM UDP-D-glucose, 0.2 mM *N*-methylanthranilic acid at pH 7.5, 30^{o}C for 30 minutes. Controls include assays with inactivated enzyme (a), minus *N*-methylanthranilic acid (b) and minus UDP-D-glucose (c); (d) reaction with active enzyme. Samples were analysed as for Supplementary Figure 1A. The retention times (R_t) of *N*-methylanthranilic acid and *N*-methylanthraniloyl-β-D-glucopyranose were 16.5 min and 11.8 min, respectively. The detection wavelength (WVL) is indicated.



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                                    10        20        30        40        50        60
UGT74H7     1  MGAEPGHVYCDIHVLVLPYPLQGHINPMLQFAKRLARTQTHIGGGGG----VRCTLAVTP  56
UGT74H6     1  MGAEPGHVYCDIHVLVLPYPLQGHINPMLQFAKRLARTQTHIGGGGGGGGGVRCTLAVTP  60
UGT74H5     1  MGAEWEHVS-DIHVLLLPYPVQGHINPMLQFGKRLA----HIG-GVG----VRCTLAITP  50

                                    70        80        90       100       110       120
UGT74H7    57  YLLGQCQDPCPGAVHLAEISDGFDRAGFLEVGDVAAYLAQLESAGSRTLDELLRSEAEKG  116
UGT74H6    61  YLLGQCQDPCPGAVHLAEISDGFDRAGFLEVGDVAAYLAQLESAGSRTLDELLRSEAEKG  120
UGT74H5    51  YLLRQCQDPCPGAVHLVEISDGFDSAGFEEVGDVAAYLAGMESAGSRTLDELLRSEAEKG  110

                                   130       140       150       160       170       180
UGT74H7   117  RKVCAVVYDSFLQPWAPPVARRHGAACVSFFTQAPAVNLAYAHHARGGGTGGRLEGLPAG  176
UGT74H6   121  RKVCAVVYDSFLQPWAPPVARRHGAACVSFFTQAPAVNLAYAHHARGGGTGGRLDGLPAG  180
UGT74H5   111  RPIHAVVYDAFLQPWVPRVARLHGAACVSFFTQAAAVNVAYSRR-----VGKIEEGLPAG  165

                                   190       200       210       220       230       240
UGT74H7   177  FEHEDLPTFLTMPDDCPPYLEMLLRQHVGLDAVDHVLVNSFHELQPLESDYMASKWGAKT  236
UGT74H6   181  FEHEDLPTFLTMPDDCPPYLEMLLRQHVGLDAVDHVLVNSFHELQPLESDYMASKWGAKT  240
UGT74H5   166  FEAEDLPTFLTLP---LPYQDMLLSQFVGLDAVDHVLVNSFHELQPQESAYMESTWGAKT  222

                                   250       260       270       280       290       300
UGT74H7   237  VGPTVPSAYLDKRIPDDVSYGFHLYTPTTATTTAWLDAQPPRSVAYVSFGSMAAPGPEQM  296
UGT74H6   241  VGPTVPSAYLDKRIPDDVSYGFHLYTPTTATTTAWLDAQPPRSVAYVSFGSMAAPGPEQM  300
UGT74H5   223  VGPTVPSAYLDKRITDDVSYGFHLYTPMTATTKAWLDAQPPRSVTYVSFGSMATPGPTEM  282

                                   310       320       330       340       350       360
UGT74H7   297  AEMAEGLHSSGKAFLWVVRASEASKIPDGFSEKVGTRGLVVPWVAQLEVLAHSAVGCFVT  356
UGT74H6   301  AEMAEGLHSSGKAFLWVVRASETSKIPDGFSERVGTRGLVVPWVAQLEVLAHSAVGCFVT  360
UGT74H5   283  AEMAEGLHSSGKAFLWVVRASEASKIPDGFQERVGGRGLVVTWVAQLEVLAHGAIGCFVT  342
                                                                  PSPG Box
                                   370       380       390       400       410       420
UGT74H7   357  HCGWNSTMEALGAGLPMVAVPQWSDQPTNAKYVEDVWCVGVRARRDPEAGVVRREEVERC  416
UGT74H6   361  HCGWNSTMEALGAGLPMVAVPQWSDQPTNAKYVEDVWCVGVRARRDPESGVVRREEVERC  420
UGT74H5   343  HCGWNSTMEALGAGVPMVAVPQWSDQPTNAKFVEDVWCVGVRARRDPE-GVVRREELERC  401
                         PSPG Box
                                   430       440       450       460       470       480
UGT74H7   417  VKEVMGADKQYARNASDWKEKAVRSMCQGGSSEKNITEFLHALR--SRKSQKSTQPKQI-  473
UGT74H6   421  VKEVMGADKQYARNASDWKEKAVRSMCQGGSSDKNITEFLHALVVGSRKSQKLII-----  475
UGT74H5   402  IREVTGDDK-YACNALDWKEKSKRAMSQGGSSDMNITEFLQALR-RSRKSYEAKPIEPLL  459

UGT74H7   473  -----  473
UGT74H6   475  -----  475
UGT74H5   460  VGLDA  464
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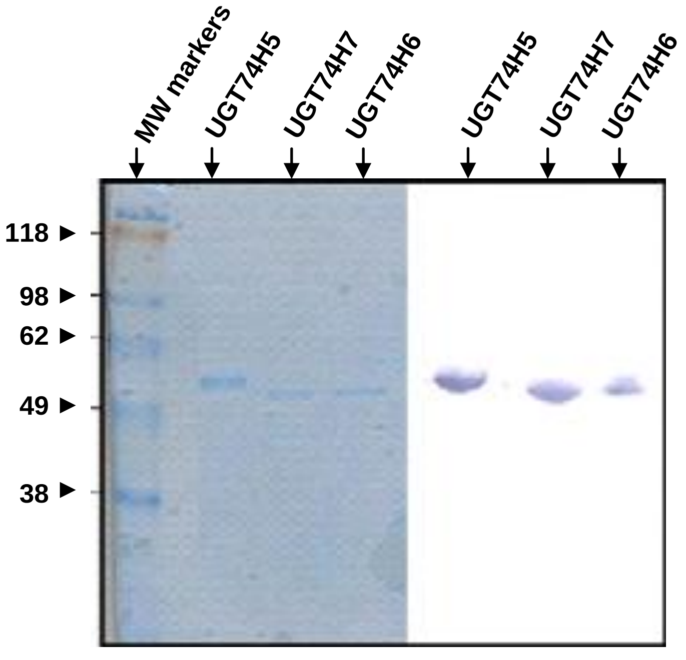
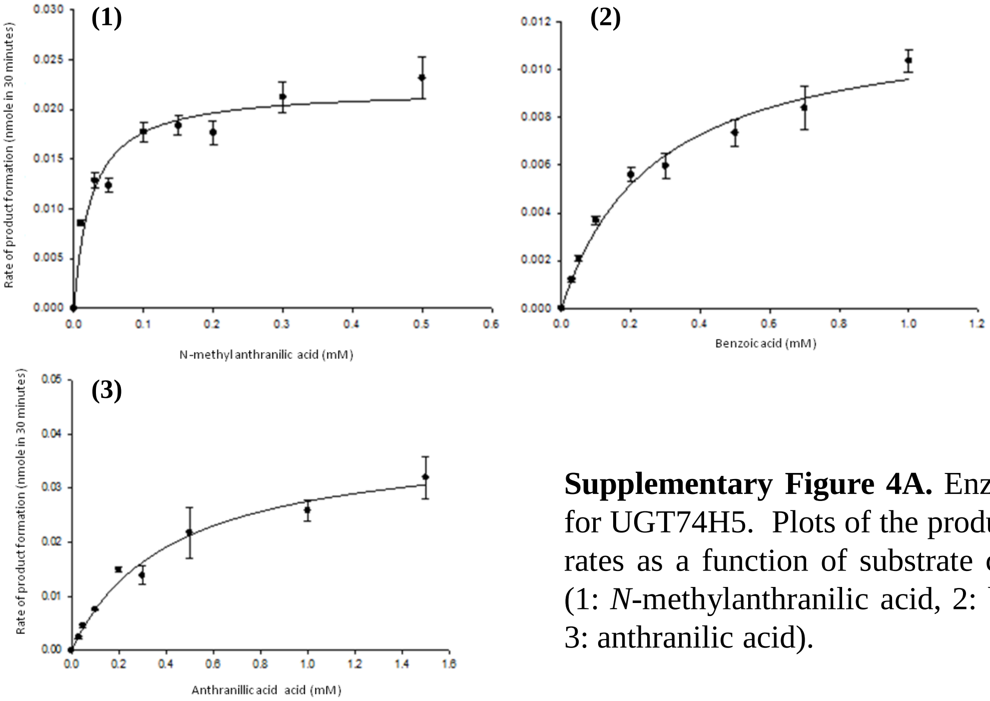
Supplementary Figure 2.

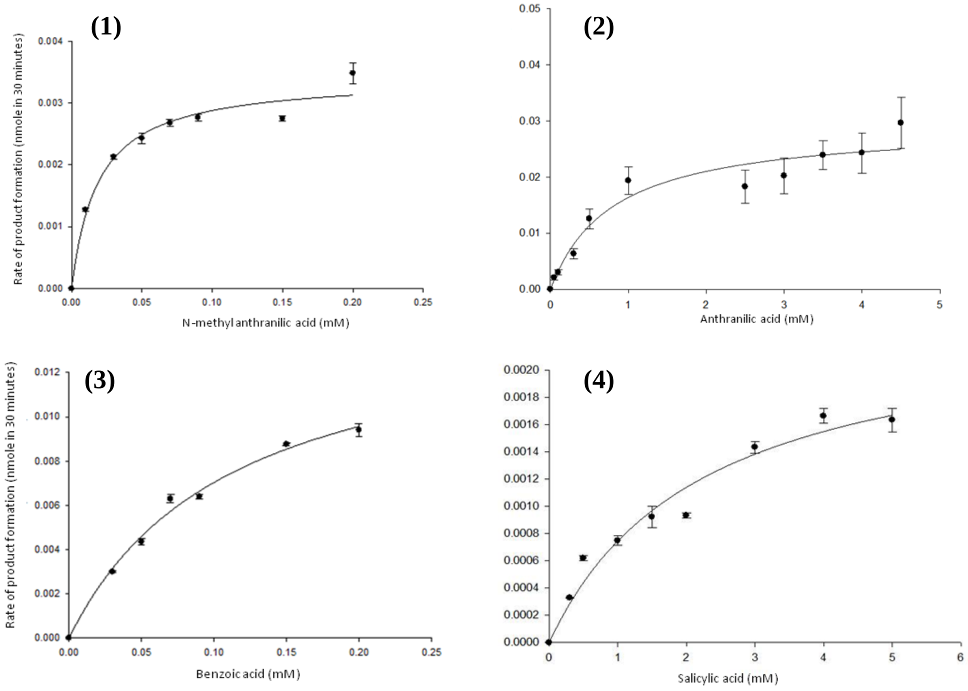
Alignment of amino acid sequences of UGT74H5 and two other closely related GTs expressed in oat roots (UGT74H6 and UGT74H7). Identical amino acids are highlighted in black and similar amino acids in grey. The PSPG box (a conserved region corresponding to the UDP-D-glucose binding domain; Hughes and Hughes, 1994; *DNA Seq* 5: 41-49) is underlined.



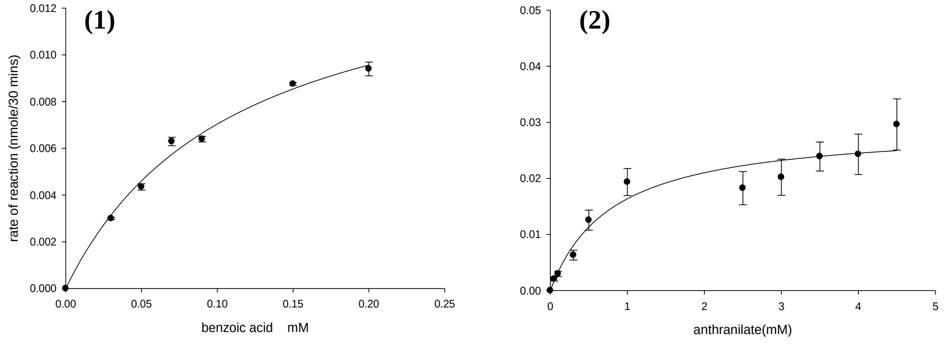
Supplementary Figure 3. Analysis of the three purified His$_6$-tagged oat glycosyltransferases following expression in *E. coli*. Proteins were run on a 4-12% SDS-PAGE gradient gel and detected by staining with Coomassie brilliant blue (left) or by Western blot analysis using polyclonal antisera raised against UGT74H5 (right).



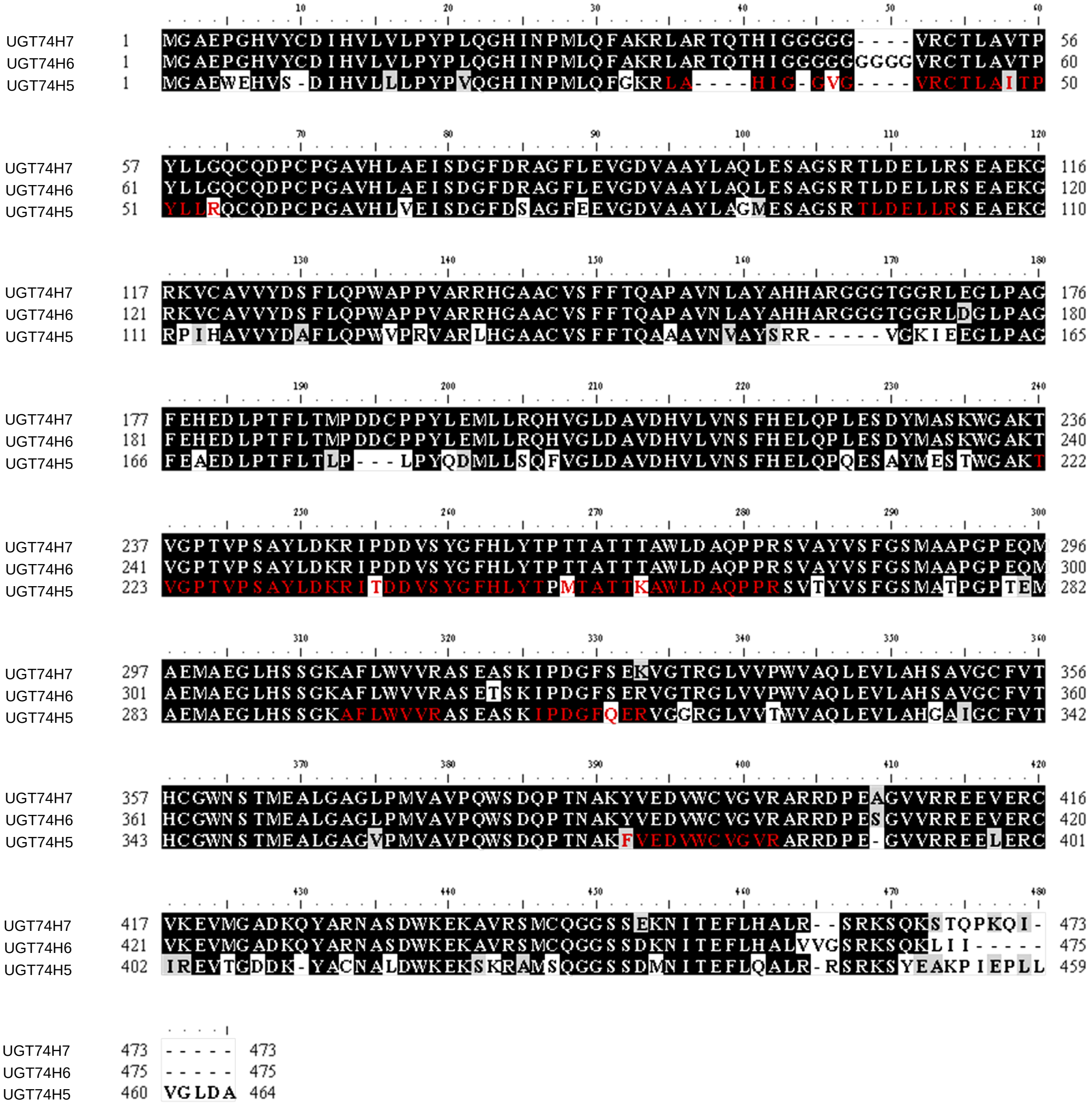
Supplementary Figure 4A. Enzyme kinetics for UGT74H5. Plots of the product formation rates as a function of substrate concentration (1: *N*-methylanthranilic acid, 2: benzoic acid, 3: anthranilic acid).



Supplementary Figure 4B. Enzyme kinetics for UGT74H6. Plots of the product formation rates as a function of substrate concentration (1: *N*-methylanthranilic acid, 2: benzoic acid, 3: anthranilic acid, 4: salicylic acid).



Supplementary Figure 4C. Enzyme kinetics for UGT74H7. Plots of the product formation rates as a function of substrate concentration (1: benzoic acid, 2: anthranilic acid).



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                 10        20        30        40        50        60
UGT74H7    1   MGAEPGHVYCDIHVLVLPYPLQGHINPMLQFAKRLARTQTHIGGGGG----VRCTLAVTP   56
UGT74H6    1   MGAEPGHVYCDIHVLVLPYPLQGHINPMLQFAKRLARTQTHIGGGGGGGGGVRCTLAVTP   60
UGT74H5    1   MGAEWEHVS-DIHVLLLPYPVQGHINPMLQFGKRLA----HIG-GVG----VRCTLAITP   50

                 70        80        90       100       110       120
UGT74H7   57   YLLGQCQDPCPGAVHLAEISDGFDRAGFLEVGDVAAYLAQLESAGSRTLDELLRSEAEKG  116
UGT74H6   61   YLLGQCQDPCPGAVHLAEISDGFDRAGFLEVGDVAAYLAQLESAGSRTLDELLRSEAEKG  120
UGT74H5   51   YLLRQCQDPCPGAVHLVEISDGFDSAGFEEVGDVAAYLAGMESAGSRTLDELLRSEAEKG  110

                130       140       150       160       170       180
UGT74H7  117   RKVCAVVYDSFLQPWAPPVARRHGAACVSFFTQAPAVNLAYAHHARGGGTGGRLEGLPAG  176
UGT74H6  121   RKVCAVVYDSFLQPWAPPVARRHGAACVSFFTQAPAVNLAYAHHARGGGTGGRLDGLPAG  180
UGT74H5  111   RPIHAVVYDAFLQPWVPRVARLHGAACVSFFTQAAAVNVAYSRR-----VGKIEEGLPAG  165

                190       200       210       220       230       240
UGT74H7  177   FEHEDLPTFLTMPDDCPPYLEMLLRQHVGLDAVDHVLVNSFHELQPLESDYMASKWGAKT  236
UGT74H6  181   FEHEDLPTFLTMPDDCPPYLEMLLRQHVGLDAVDHVLVNSFHELQPLESDYMASKWGAKT  240
UGT74H5  166   FEAEDLPTFLTLP---LPYQDMLLSQFVGLDAVDHVLVNSFHELQPQESAYMESTWGAKT  222

                250       260       270       280       290       300
UGT74H7  237   VGPTVPSAYLDKRIPDDVSYGFHLYTPTTATTTAWLDAQPPRSVAYVSFGSMAAPGPEQM  296
UGT74H6  241   VGPTVPSAYLDKRIPDDVSYGFHLYTPTTATTTAWLDAQPPRSVAYVSFGSMAAPGPEQM  300
UGT74H5  223   VGPTVPSAYLDKRITDDVSYGFHLYTPMTATTKAWLDAQPPRSVTYVSFGSMATPGPTEM  282

                310       320       330       340       350       360
UGT74H7  297   AEMAEGLHSSGKAFLWVVRASEASKIPDGFSEKVGTRGLVVPWVAQLEVLAHSAVGCFVT  356
UGT74H6  301   AEMAEGLHSSGKAFLWVVRASETSKIPDGFSERVGTRGLVVPWVAQLEVLAHSAVGCFVT  360
UGT74H5  283   AEMAEGLHSSGKAFLWVVRASEASKIPDGFQERVGGRGLVVTWVAQLEVLAHGAIGCFVT  342

                370       380       390       400       410       420
UGT74H7  357   HCGWNSTMEALGAGLPMVAVPQWSDQPTNAKYVEDVWCVGVRARRDPEAGVVRREEVERC  416
UGT74H6  361   HCGWNSTMEALGAGLPMVAVPQWSDQPTNAKYVEDVWCVGVRARRDPESGVVRREEVERC  420
UGT74H5  343   HCGWNSTMEALGAGVPMVAVPQWSDQPTNAKFVEDVWCVGVRARRDPE-GVVRREELERC  401

                430       440       450       460       470       480
UGT74H7  417   VKEVMGADKQYARNASDWKEKAVRSMCQGGSSEKNITEFLHALR--SRKSQKSTQPKQI-  473
UGT74H6  421   VKEVMGADKQYARNASDWKEKAVRSMCQGGSSDKNITEFLHALVVGSRKSQKLII-----  475
UGT74H5  402   IREVTGDDK-YACNALDWKEKSKRAMSQGGSSDMNITEFLQALR-RSRKSYEAKPIEPLL  459

UGT74H7  473   -----  473
UGT74H6  475   -----  475
UGT74H5  460   VGLDA  464
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Supplementary Figure 5. LC-MS/MS analysis of trypsin-digested protein from oat roots (excised following SDS-PAGE) reveals protein fragments corresponding to UGT74H5 (shown in red).